```
RESULT 1703
AX320075
LOCUS       AX320075                  16 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 11 from Patent WO0188116.
ACCESSION   AX320075
VERSION     AX320075.1  GI:17901576
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stoika,R., Horwitz,G.A., Zhang,X. and Melmed,S.
  TITLE     Method of modulating activation of lymphocytes via modulation of
            pituitary tumor transforming gene, related screeining methods
  JOURNAL   Patent: WO 0188116-A 11 22-NOV-2001;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Anchored primer sequence."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1704
AX352386
LOCUS       AX352386                  16 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 11 from Patent WO0187934.
ACCESSION   AX352386
VERSION     AX352386.1  GI:18617657
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Horwitz,G.A., Zhang,X., Heaney,A. and Melmed,S.
  TITLE     Treatment of neoplasia / transformation using pituitary tumor
            transforming gene carboxy terminal peptides
  JOURNAL   Patent: WO 0187934-A 11 22-NOV-2001;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Anchored primer sequence."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1705
AX391467
LOCUS       AX391467                  16 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 3 from Patent WO0216632.
ACCESSION   AX391467
VERSION     AX391467.1  GI:19700077
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Pharmaceutical compositions comprising a modulator of adamts-1
  JOURNAL   Patent: WO 0216632-A 3 28-FEB-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1706
AX394754
LOCUS       AX394754                  16 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 5 from Patent WO0218568.
ACCESSION   AX394754
VERSION     AX394754.1  GI:21065833
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Molecules involved in the regulation of insulin resistance syndrome
            (irs)
  JOURNAL   Patent: WO 0218568-A 5 07-MAR-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="H-T11-G"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1707
AX394785
LOCUS       AX394785                  16 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 9 from Patent WO0218421.
ACCESSION   AX394785
VERSION     AX394785.1  GI:21065859
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brodin,P. and Thelin,A.
  TITLE     Human and mouse e2-protein, nucleic acids coding therefor and uses
            thereof
  JOURNAL   Patent: WO 0218421-A 9 07-MAR-2002;
            AstraZeneca AB (SE)
FEATURES             Location/Qualifiers
     source          1. .16
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  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 21 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1699
AX235176
LOCUS       AX235176                  16 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 9 from Patent WO0163282.
ACCESSION   AX235176
VERSION     AX235176.1  GI:15593767
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
  TITLE     Analysis of biological targets using a biochip comprising a
            fluorescent marker
  JOURNAL   Patent: WO 0163282-A 9 30-AUG-2001;
            COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence synthetique"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1700
AX235176/c
LOCUS       AX235176                  16 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 9 from Patent WO0163282.
ACCESSION   AX235176
VERSION     AX235176.1  GI:15593767
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
  TITLE     Analysis of biological targets using a biochip comprising a
            fluorescent marker
  JOURNAL   Patent: WO 0163282-A 9 30-AUG-2001;
            COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence synthetique"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 1701
AX253409
LOCUS       AX253409                  16 bp    DNA     linear   PAT 10-OCT-2001
DEFINITION  Sequence 21 from Patent WO0171013.
ACCESSION   AX253409
VERSION     AX253409.1  GI:16073943
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Clendennen,S.K. and Kellogg,J.A.
  TITLE     Melon promoters for expression of transgenes in plants
  JOURNAL   Patent: WO 0171013-A 21 27-SEP-2001;
            Exelixis Plant Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1702
AX306362
LOCUS       AX306362                  16 bp    DNA     linear   PAT 11-DEC-2001
DEFINITION  Sequence 11 from Patent WO0187039.
ACCESSION   AX306362
VERSION     AX306362.1  GI:17645594
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Prezant,T.R., Heaney,A.P. and Melmed,S.
  TITLE     Treatment of neoplasia / transformation using pituitary tumor
            transforming gene 2
  JOURNAL   Patent: WO 0187039-A 11 22-NOV-2001;
            CEDARS-SINAI MEDICAL CENTER (US)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Anchored primer sequence."

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16
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  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1694
AR429377
LOCUS       AR429377                  16 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 15 from patent US 6642438.
ACCESSION   AR429377
VERSION     AR429377.1  GI:40189570
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and
            Webb,N.M.
  TITLE     Melon promoters for expression of transgenes in plants
  JOURNAL   Patent: US 6642438-A 15 04-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1695
AX039049
LOCUS       AX039049                  16 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 2 from Patent WO0061594.
ACCESSION   AX039049
VERSION     AX039049.1  GI:11228345
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beier,M. and Hoheisel,J.
  TITLE     Nucleoside derivatives with photo-unstable protective groups
  JOURNAL   Patent: WO 0061594-A 2 19-OCT-2000;
            DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG
            (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotid"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1696
AX039049/c
LOCUS       AX039049                  16 bp    DNA     linear   PAT 16-NOV-2000
DEFINITION  Sequence 2 from Patent WO0061594.
ACCESSION   AX039049
VERSION     AX039049.1  GI:11228345
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Beier,M. and Hoheisel,J.
  TITLE     Nucleoside derivatives with photo-unstable protective groups
  JOURNAL   Patent: WO 0061594-A 2 19-OCT-2000;
            DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG
            (DE)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotid"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1697
AX127437
LOCUS       AX127437                  16 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 80 from Patent WO0130999.
ACCESSION   AX127437
VERSION     AX127437.1  GI:14133900
KEYWORDS    .
SOURCE      Bruguiera gymnorrhiza
  ORGANISM  Bruguiera gymnorrhiza
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Malpighiales; Rhizophoraceae; Bruguiera.
REFERENCE   1
  AUTHORS   Karube,I. and Hanagata,N.
  TITLE     Salt tolerance genes
  JOURNAL   Patent: WO 0130999-A 80 03-MAY-2001;
            EBARA CORPORATION (JP)
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Bruguiera gymnorrhiza"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:39984"
                     /note="Artificially Synthesized Primer Sequence"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1698
AX146679
LOCUS       AX146679                  16 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 21 from Patent WO0134834.
ACCESSION   AX146679
VERSION     AX146679.1  GI:14285072
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  JOURNAL   Patent: US 6486308-A 2 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1689
AR257437/c
LOCUS       AR257437                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6486308.
ACCESSION   AR257437
VERSION     AR257437.1  GI:27307448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6486308-A 2 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 1690
AR266618
LOCUS       AR266618                 16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 56 from patent US 6495319.
ACCESSION   AR266618
VERSION     AR266618.1  GI:29695682
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 56 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1691
AR266645
LOCUS       AR266645                 16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 83 from patent US 6495319.
ACCESSION   AR266645
VERSION     AR266645.1  GI:29695709
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   McClelland,M., Welsh,J. and Trenkle,T.
  TITLE     Reduced complexity nucleic acid targets and methods of using same
  JOURNAL   Patent: US 6495319-A 83 17-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1692
AR282683
LOCUS       AR282683                 16 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 4 from patent US 6521750.
ACCESSION   AR282683
VERSION     AR282683.1  GI:29719309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Hair,G.A. and Boden,S.D.
  TITLE     Bone mineralization proteins, DNA, vectors, expression systems
  JOURNAL   Patent: US 6521750-A 4 18-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1693
AR369775
LOCUS       AR369775                 16 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 4 from patent US 6300127.
ACCESSION   AR369775
VERSION     AR369775.1  GI:34606215
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Hair,G.A. and Boden,S.D.
  TITLE     Bone mineralization proteins, DNA, vectors, expression systems
  JOURNAL   Patent: US 6300127-A 4 09-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 2 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 1684
AR222462
LOCUS       AR222462                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 22 from patent US 6429300.
ACCESSION   AR222462
VERSION     AR222462.1  GI:23329993
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 22 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1685
AR222462/c
LOCUS       AR222462                 16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 22 from patent US 6429300.
ACCESSION   AR222462
VERSION     AR222462.1  GI:23329993
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 22 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1686
AR227681
LOCUS       AR227681                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 4 from patent US 6444803.
ACCESSION   AR227681
VERSION     AR227681.1  GI:27266260
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Hair,G.A. and Boden,S.D.
  TITLE     Bone mineralization proteins, DNA, vectors, expression systems
  JOURNAL   Patent: US 6444803-A 4 03-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1687
AR232208
LOCUS       AR232208                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6455305.
ACCESSION   AR232208
VERSION     AR232208.1  GI:27274198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Melmed,S. and Pei,L.
  TITLE     Pituitary-tumor-transforming-genes, and related products
  JOURNAL   Patent: US 6455305-A 5 24-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1688
AR257437
LOCUS       AR257437                 16 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 2 from patent US 6486308.
ACCESSION   AR257437
VERSION     AR257437.1  GI:27307448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
```

```
VERSION     I38682.1  GI:2084736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 42 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1679
I38682/c
LOCUS       I38682                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 42 from patent US 5614617.
ACCESSION   I38682
VERSION     I38682.1  GI:2084736
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 42 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 1680
I38700
LOCUS       I38700                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 60 from patent US 5614617.
ACCESSION   I38700
VERSION     I38700.1  GI:2084754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 60 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1681
I38700/c
LOCUS       I38700                    16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 60 from patent US 5614617.
ACCESSION   I38700
VERSION     I38700.1  GI:2084754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 60 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 1682
AR221692
LOCUS       AR221692                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 2 from patent US 6426408.
ACCESSION   AR221692
VERSION     AR221692.1  GI:23328764
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor groove binder conjugates
  JOURNAL   Patent: US 6426408-A 2 30-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1683
AR221692/c
LOCUS       AR221692                  16 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 2 from patent US 6426408.
ACCESSION   AR221692
VERSION     AR221692.1  GI:23328764
KEYWORDS    .
```

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REFERENCE   1  (bases 1 to 16)
  AUTHORS   Boden,S.D. and Hair,G.A.
  TITLE     LIM mineralization protein splice variants
  JOURNAL   Patent: JP 2002542802-A 3 17-DEC-2002;
            EMORY UNIVERSITY
COMMENT     OS   MMLV
            PN   JP 2002542802-A/3
            PD   17-DEC-2002
            PF   28-APR-2000 JP 2000615061
            PR   30-APR-1999 US    60/132021
            PI   SCOTT D BODEN,GREGORY A HAIR
            PC   C12N15/09,A61K38/00,A61K39/395,A61K48/00,A61P19/08,A61P19/10,
            PC   C07K14/51,
            PC
            C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/ PC
             08//
            PC   A61K35/76,C12N15/00,A61K37/02,C12N5/00
            CC   LIM mineralization protein splice variants
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='MMLV'.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1675
BD268989
LOCUS       BD268989                 16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Banana promoter and melon promoter for expression of transgene in
            plant.
ACCESSION   BD268989
VERSION     BD268989.1  GI:33078757
KEYWORDS    JP 2002539779-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Clendennen,S.K., Kellogg,J.A., Phan,C.B., Mathews,H.V. and
            Webb,N.M.
  TITLE     Banana promoter and melon promoter for expression of transgene in
  JOURNAL   Patent: JP 2002539779-A 15 26-NOV-2002;
            EXELIXIS PLANT SCIENCES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002539779-A/15
            PD   26-NOV-2002
            PF   17-MAR-2000 JP 2000606722
            PR   19-MAR-1999 US    60/125310
            PI   STEPHANIE K CLENDENNEN,JILL A KELLOGG,CHAU B PHAN,HELENA V  PI
              MATHEWS,
            PI   NANCY M WEBB
            PC   C12N15/09,A01H1/00,C12N5/10,C12Q1/68//(C12N5/10,C12R1:91), PC
             C12N15/00,
            PC   C12N5/00,(C12N5/00,C12R1:91)
            CC   oligonucleotide primer
            FH   Key             Location/Qualifiers
            FT   source          1. .16
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTG 1782
              ||||||||||||||||
Db          1 AAGCTTTTTTTTTTTG 16


RESULT 1676
I38676
LOCUS       I38676                   16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 36 from patent US 5614617.
ACCESSION   I38676
VERSION     I38676.1  GI:2084730
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 36 25-MAR-1997;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16


RESULT 1677
I38676/c
LOCUS       I38676                   16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 36 from patent US 5614617.
ACCESSION   I38676
VERSION     I38676.1  GI:2084730
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cook,P.D. and Sanghvi,Y.S.
  TITLE     Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
  JOURNAL   Patent: US 5614617-A 36 25-MAR-1997;
FEATURES              Location/Qualifiers
     source           1. .16
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 1678
I38682
LOCUS       I38682                   16 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 42 from patent US 5614617.
ACCESSION   I38682
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ACCESSION   AR037355
VERSION     AR037355.1  GI:5955211
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor grove binder conjugates
  JOURNAL   Patent: US 5801155-A 2 01-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1


RESULT 1670
AR104584
LOCUS       AR104584                 16 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 131 from patent US 6093809.
ACCESSION   AR104584
VERSION     AR104584.1  GI:12817292
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE     Telomerase
  JOURNAL   Patent: US 6093809-A 131 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1671
AR104584/c
LOCUS       AR104584                 16 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 131 from patent US 6093809.
ACCESSION   AR104584
VERSION     AR104584.1  GI:12817292
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE     Telomerase
  JOURNAL   Patent: US 6093809-A 131 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1672
AR175845
LOCUS       AR175845                 16 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 131 from patent US 6309867.
ACCESSION   AR175845
VERSION     AR175845.1  GI:17917144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cech,T.R. and Nakamura,T.
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 131 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db          1 AAAAAAAAAAAAAAAA 16


RESULT 1673
AR175845/c
LOCUS       AR175845                 16 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 131 from patent US 6309867.
ACCESSION   AR175845
VERSION     AR175845.1  GI:17917144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Cech,T.R. and Nakamura,T.
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 131 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db         16 TTTTTTTTTTTTTTTT 1


RESULT 1674
BD259919
LOCUS       BD259919                 16 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  LIM mineralization protein splice variants.
ACCESSION   BD259919
VERSION     BD259919.1  GI:33069689
KEYWORDS    JP 2002542802-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
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ACCESSION   AX043119
VERSION     AX043119.1  GI:11341727
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 685 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              || | ||| ||||||||||||
Db         22 TGTACAAACAAAAAAAAAAA 2

RESULT 1665
AX043642
LOCUS       AX043642                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1208 from Patent WO0065088.
ACCESSION   AX043642
VERSION     AX043642.1  GI:11342257
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1208 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||  || |
Db          1 TTTTTTTTTTTTTTTCCCTGT 21

RESULT 1666
AR027678
LOCUS       AR027678                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5856435.
ACCESSION   AR027678
VERSION     AR027678.1  GI:5938498
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
  TITLE     Nucleic acid-containing composition, its preparation and use
  JOURNAL   Patent: US 5856435-A 15 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16

RESULT 1667
AR027678/c
LOCUS       AR027678                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5856435.
ACCESSION   AR027678
VERSION     AR027678.1  GI:5938498
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Bazile,D., Emile,C., Helene,C. and Spenlehauer,G.
  TITLE     Nucleic acid-containing composition, its preparation and use
  JOURNAL   Patent: US 5856435-A 15 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2801
              ||||||||||||||||
Db         16 AAAAAAAAAAAAAAAA 1

RESULT 1668
AR037355
LOCUS       AR037355                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5801155.
ACCESSION   AR037355
VERSION     AR037355.1  GI:5955211
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
  TITLE     Covalently linked oligonucleotide minor grove binder conjugates
  JOURNAL   Patent: US 5801155-A 2 01-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 8.4e+02;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 16

RESULT 1669
AR037355/c
LOCUS       AR037355                 16 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 2 from patent US 5801155.
```

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REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 823 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              ||| | |||||||||||||| |
Db          1 ATTAAGAAAAAAAAAAAAAGA 21


RESULT 1661
AX042591
LOCUS       AX042591                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 157 from Patent WO0065088.
ACCESSION   AX042591
VERSION     AX042591.1  GI:11341199
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 157 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGA 2194
              |||||||||||||| | | |
Db          1 TTTTTTTTTTTTTAAATCTCA 21


RESULT 1662
AX043292
LOCUS       AX043292                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 858 from Patent WO0065088.
ACCESSION   AX043292
VERSION     AX043292.1  GI:11341900
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 858 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGA 2194
              |||||||||||||| | | |
Db          1 TTTTTTTTTTTTTAAATCTCA 21


RESULT 1663
AJ595474
LOCUS       AJ595474                 25 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            417E08.
ACCESSION   AJ595474
VERSION     AJ595474.1  GI:37945102
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 25)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="417E08"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .25
                     /note="T-DNA flanking sequence
                     left border"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTT 2184
              | |  ||||||||||||||||
Db          1 CATAATTTTTTTTTTTTTTTT 21


RESULT 1664
AX043119/c
LOCUS       AX043119                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 685 from Patent WO0065088.
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  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              :||||||||||||||||
Db         25 BAAAAAAAAAAAAAAA 9


RESULT 1656
AR370671/c
LOCUS       AR370671                  25 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 11 from patent US 6300544.
ACCESSION   AR370671
VERSION     AR370671.1  GI:34607459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
  TITLE     Cytochrome P450 monooxygenases
  JOURNAL   Patent: US 6300544-A 11 09-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              :||||||||||||||||
Db         25 BAAAAAAAAAAAAAAA 9


RESULT 1657
AR431257/c
LOCUS       AR431257                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 11 from patent US 6649814.
ACCESSION   AR431257
VERSION     AR431257.1  GI:40193207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
  TITLE     Cytochrome P450 monooxygenases
  JOURNAL   Patent: US 6649814-A 11 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              :||||||||||||||||
Db         25 BAAAAAAAAAAAAAAA 9


RESULT 1658
BD057791/c
LOCUS       BD057791                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Cytochrome P450 Monooxygenases.
ACCESSION   BD057791
VERSION     BD057791.1  GI:22603397
KEYWORDS    JP 2001514515-A/6.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
  TITLE     Cytochrome P450 Monooxygenases
  JOURNAL   Patent: JP 2001514515-A 6 11-SEP-2001;
            NOVARTIS AG,ROYAL VETERINARY AND AGRICULTURE UNIV
COMMENT     PN   JP 2001514515-A/6
            PD   11-SEP-2001
            PF   05-MAR-1998 JP 1998539180
            PR   07-MAR-1997 EP   97810132.7,08-DEC-1997 EP   97810954.4 PI
            BARBARA ANN HALKIER,SOREN BAK,RACHEL ALICE KAHN,BIRGER  PI
            LINDBERG MOLLER
            PC   C12N9/02,C12N15/82//C12N15/53
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:4577"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAA 2801
              :||||||||||||||||
Db         25 BAAAAAAAAAAAAAAA 9


RESULT 1659
AX042981/c
LOCUS       AX042981                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 547 from Patent WO0065088.
ACCESSION   AX042981
VERSION     AX042981.1  GI:11341589
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 547 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2801
              | ||  ||||||||||||||||
Db         21 AGTTCCAAAAAAAAAAAAAA 1


RESULT 1660
AX115700
LOCUS       AX115700                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 823 from Patent WO0129262.
ACCESSION   AX115700
VERSION     AX115700.1  GI:14032642
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
```

```
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 1299 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        266 TCCGCCGGGCAGCACCTCTAC 286
              ||||||| ||||||| || ||
Db          1 TCCGCCGTGCAGCACGTCAAC 21


RESULT 1652
AR260368
LOCUS       AR260368                  24 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1299 from patent US 6489455.
ACCESSION   AR260368
VERSION     AR260368.1  GI:27310879
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6489455-A 1299 03-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        266 TCCGCCGGGCAGCACCTCTAC 286
              ||||||| ||||||| || ||
Db          1 TCCGCCGTGCAGCACGTCAAC 21


RESULT 1653
AX377075
LOCUS       AX377075                  24 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 33 from Patent WO0212557.
ACCESSION   AX377075
VERSION     AX377075.1  GI:19573369
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cailloux,F. and Gobron,S.
  TITLE     Method for detecting known mutations in tube
  JOURNAL   Patent: WO 0212557-A 33 14-FEB-2002;
            Nucleica (FR)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Amorce pour la detection de mutations responsables
                     de la mucoviscidose."

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTT 2176
              ||| |||| ||||| ||||||
Db          2 TTTCTTCTTCTTTTCTTTTT 22


RESULT 1654
BD064144
LOCUS       BD064144                  24 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Isolation of the biosynthesis genes for pseudo-oligosaccharides
            from Streptomyces glaucescens GLA.O and their use.
ACCESSION   BD064144
VERSION     BD064144.1  GI:22609747
KEYWORDS    JP 2001507923-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Decker,H.
  TITLE     Isolation of the biosynthesis genes for pseudo-oligosaccharides
            from Streptomyces glaucescens GLA.O and their use
  JOURNAL   Patent: JP 2001507923-A 2 19-JUN-2001;
            HOECHST AKTIENGESELLSCHAFT
COMMENT     PN   JP 2001507923-A/2
            PD   19-JUN-2001
            PF   30-MAY-1997 JP 1998501137
            PR   07-JUN-1996 DE 196 22 783.6
            PI   HEINRICH DECKER
            PC   C12N15/52,C12N9/00,C07K14/36,C12Q1/68,C12N15/63,C12N1/21, PC
            C12P19/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   exon            1. .24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGCCGTAAT 819
              ||::||||:::||:||||| |
Db          2 GGWVCTGGYVSGGSCCGTAGT 22


RESULT 1655
A85331/c
LOCUS       A85331                    25 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 11 from Patent WO9840470.
ACCESSION   A85331
VERSION     A85331.1  GI:6733935
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Halkier,B.A. and Kahn,R.A.
  TITLE     CYTOCHROME P450 MONOOXYGENASES
  JOURNAL   Patent: WO 9840470-A 11 17-SEP-1998;
            CIBA GEIGY AG (CH); HALKIER BARBARA ANN (DK)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 25;
  Best Local Similarity   94.1%;  Pred. No. 2.4e+03;
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FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Reverse PCR primer for amplifying a region around
                     the -403 polymorphism (Lui sequence)."

  Query Match              0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2261 TGCATATTTATTTCAGATGTT 2281
              ||| |||| ||| ||||||||
Db          1 TGCTTATTCATTACAGATGTT 21


RESULT 1647
AX457060/c
LOCUS       AX457060                  22 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 21 from Patent WO0231186.
ACCESSION   AX457060
VERSION     AX457060.1  GI:21715842
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K.
  TITLE     Method for the detection of cytosine methylations
  JOURNAL   Patent: WO 0231186-A 21 18-APR-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match              0.6%;  Score 16.2;  DB 1;  Length 22;
  Best Local Similarity   85.7%;  Pred. No. 1.8e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | | ||||||| |||||||||
Db         21 TAATAAAAAAATAAAAAAAAA 1


RESULT 1648
A93098
LOCUS       A93098                    24 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 2 from Patent WO9747748.
ACCESSION   A93098
VERSION     A93098.1  GI:6741496
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Decker,H.
  TITLE     ISOLATION OF THE BIOSYNTHESIS GENES FOR PSEUDO-OLIGOSACCHARIDES
            FROM STREPTOMYCES GLAUCESCENS GLA.O AND THEIR USE
  JOURNAL   Patent: WO 9747748-A 2 18-DEC-1997;
            HOECHST AG (DE); DECKER HEINRICH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     exon            1. .24

  Query Match              0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGCCGTAAT 819
              ||::||||:::||:||||| |
Db          2 GGWVCTGGYVSGGSCCGTAGT 22


RESULT 1649
AR091179
LOCUS       AR091179                  24 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1299 from patent US 5994076.
ACCESSION   AR091179
VERSION     AR091179.1  GI:10017934
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 1299 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   85.7%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        266 TCCGCCGGGCAGCACCTCTAC 286
              ||||||| ||||||| || ||
Db          1 TCCGCCGTGCAGCACGTCAAC 21


RESULT 1650
AR174054
LOCUS       AR174054                  24 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 2 from patent US 6306627.
ACCESSION   AR174054
VERSION     AR174054.1  GI:17914374
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Decker,H.
  TITLE     Isolation of the biosynthesis genes for pseudo-oligosaccharides
            from streptomyces glaucescens GLA.O, and their use
  JOURNAL   Patent: US 6306627-A 2 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 16.2;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 2.2e+03;
  Matches   14;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        799 GGAGCTGGTGGGGGCCGTAAT 819
              ||::||||:::||:||||| |
Db          2 GGWVCTGGYVSGGSCCGTAGT 22


RESULT 1651
AR198214
LOCUS       AR198214                  24 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 1299 from patent US 6352829.
ACCESSION   AR198214
VERSION     AR198214.1  GI:20248063
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

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  JOURNAL   Patent: JP 2002531145-A 2 24-SEP-2002;
            THE VICTORIA UNIVERSITY OF MANCHESTER
COMMENT     OS   Artificial Sequence
            PN   JP 2002531145-A/2
            PD   24-SEP-2002
            PF   09-DEC-1999 JP 2000586949
            PR   10-DEC-1998 GB    9827032.5,29-SEP-1999 GB    9922984.1 PI
            ALI HAJEER,WILLIAM OLLIER
            PC   C12Q1/68,A61K45/00,A61P11/06,A61P29/00,A61P31/18,A61P43/00//
            PC   C12N15/09,
            PC   C12N15/09,C12N15/00,C12N15/00
            CC   Description of Artificial Sequence: Reverse PCR primer for  CC
                      amplifying a
            CC   region around the -403 polymorphism (Lui sequence). FH   Key
                      Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2261 TGCATATTTATTTCAGATGTT 2281
              ||| |||| ||| ||||||||
Db          1 TGCTTATTCATTACAGATGTT 21


RESULT 1643
E28097
LOCUS       E28097                    21 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28097
VERSION     E28097.1  GI:13018322
KEYWORDS    JP 1999196874-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hideki,K. and Senshu,U.
  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 8 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/8
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTT 2181
              | |  ||||||||||||||||
Db          1 TGTGGTTTTTTTTTTTTTTT 21


RESULT 1644
AR241776/c
LOCUS       AR241776                  21 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 64 from patent US 6472154.
ACCESSION   AR241776
VERSION     AR241776.1  GI:27287588
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 64 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1938 AGGTAATGGTTGGTTTTTGTG 1958
              ||| |||||| ||||||| ||
Db         21 AGGGAATGGTGGGTTTTTCTG 1


RESULT 1645
AR296425
LOCUS       AR296425                  21 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 8160 from patent US 6537751.
ACCESSION   AR296425
VERSION     AR296425.1  GI:31683709
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 8160 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1567 AAAAATCCTTCTCCACCGCAC 1587
              || |||| |||||||| ||||
Db          1 AATAATCTTTCTCCACTGCAC 21


RESULT 1646
AX026215
LOCUS       AX026215                  21 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 2 from Patent WO0034516.
ACCESSION   AX026215
VERSION     AX026215.1  GI:10187625
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hajeer,A. and Ollier,W.
  TITLE     Detection of rantes gene promotor polymorphisms
  JOURNAL   Patent: WO 0034516-A 2 15-JUN-2000;
            HAJEER ALI (GB) ; OLLIER WILLIAM (GB) ; UNIV MANCHESTER (GB)
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  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              | ||||||||||||||||
Db         18 TCAAAAAAAAAAAAAAAA 1


RESULT 1638
A63569/c
LOCUS       A63569                    26 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 10 from Patent WO9720924.
ACCESSION   A63569
VERSION     A63569.1  GI:3717224
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
            AGENTS
  JOURNAL   Patent: WO 9720924-A 10 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 26;
  Best Local Similarity   76.9%;  Pred. No. 2.5e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   | |||||||| ||||||||
Db         26 AAAAAAAACAAAAAAAACAAAAAAAA 1


RESULT 1639
AX351711
LOCUS       AX351711                  30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 7 from Patent WO0193902.
ACCESSION   AX351711
VERSION     AX351711.1  GI:18616994
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 7 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     DNA/RNA oligonucleotide~Synthetic DNA/RNA oligonucleotide"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 30;
  Best Local Similarity   76.9%;  Pred. No. 3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   |||||||  ||||||||||
Db          1 AAAAAAAAAAAAAACGAAAAAAAAAA 26


RESULT 1640
A63566/c
LOCUS       A63566                    35 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 7 from Patent WO9720924.
ACCESSION   A63566
VERSION     A63566.1  GI:3717221
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
            AGENTS
  JOURNAL   Patent: WO 9720924-A 7 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 35;
  Best Local Similarity   76.9%;  Pred. No. 3.3e+03;
  Matches   20;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||| ||||||| |||
Db         32 AAAAAACAAAAAAACAAAAAAACAAA 7


RESULT 1641
AR142678
LOCUS       AR142678                  21 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 8 from patent US 6203988.
ACCESSION   AR142678
VERSION     AR142678.1  GI:15103964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kambara,H. and Uematsu,C.
  TITLE     DNA fragment preparation method for gene expression profiling
  JOURNAL   Patent: US 6203988-A 8 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.2;  DB 1;  Length 21;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTT 2181
              | |  ||||||||||||||||
Db          1 TGTGGTTTTTTTTTTTTTTT 21


RESULT 1642
BD246728
LOCUS       BD246728                  21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Detection of RANTES gene promoter polymorphism.
ACCESSION   BD246728
VERSION     BD246728.1  GI:33056498
KEYWORDS    JP 2002531145-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hajeer,A. and Ollier,W.
  TITLE     Detection of RANTES gene promoter polymorphism
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VERSION     AX498245.1  GI:23343164
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 1 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||
Db         23 GAGAAAAAAAAAAAAAA 6


RESULT 1634
AX692820
LOCUS       AX692820                25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5552 from Patent EP1281758.
ACCESSION   AX692820
VERSION     AX692820.1  GI:29415783
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5552 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2180
              | |||||||||||||||
Db          8 TTCTTTTTTTTTTTTTT 25


RESULT 1635
AX692820/c
LOCUS       AX692820                25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5552 from Patent EP1281758.
ACCESSION   AX692820
VERSION     AX692820.1  GI:29415783
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5552 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||| ||
Db         25 AAAAAAAAAAAAAAAGAA 8


RESULT 1636
AX692830
LOCUS       AX692830                25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5562 from Patent EP1281758.
ACCESSION   AX692830
VERSION     AX692830.1  GI:29415793
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5562 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTGA 18


RESULT 1637
AX692830/c
LOCUS       AX692830                25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5562 from Patent EP1281758.
ACCESSION   AX692830
VERSION     AX692830.1  GI:29415793
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5562 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
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           Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAA 2797
              ||||| ||||||||||||
Db         18 GAATTTAAAAAAAAAAAAA 1


RESULT 1629
AX043367
LOCUS       AX043367                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 933 from Patent WO0065088.
ACCESSION   AX043367
VERSION     AX043367.1  GI:11341975
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 933 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAAC 2189
              |||||||||||||| ||||
Db          1 TTTTTTTTTTTTTGTAAC 18


RESULT 1630
AX043374
LOCUS       AX043374                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 940 from Patent WO0065088.
ACCESSION   AX043374
VERSION     AX043374.1  GI:11341982
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 940 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTAA 2188
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTGTTTAA 18


RESULT 1631
AX043481
LOCUS       AX043481                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1047 from Patent WO0065088.
ACCESSION   AX043481
VERSION     AX043481.1  GI:11342089
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1047 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB345 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTGAACCCC 1788
              |||||||||||||| ||
Db          2 TTTTTTTTTTGAACTCC 19


RESULT 1632
AX043747
LOCUS       AX043747                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1313 from Patent WO0065088.
ACCESSION   AX043747
VERSION     AX043747.1  GI:11342362
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1313 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAAC 2189
              |||||||||||||| ||||
Db          1 TTTTTTTTTTTTTATAAC 18


RESULT 1633
AX498245/c
LOCUS       AX498245                  25 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1 from Patent WO0218951.
ACCESSION   AX498245
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  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAAC 2189
              ||||||||||||| ||||
Db          1 TTTTTTTTTTTTTGTAAC 18


RESULT 1624
AX042714/c
LOCUS       AX042714                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 280 from Patent WO0065088.
ACCESSION   AX042714
VERSION     AX042714.1  GI:11341322
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 280 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-A Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2799
              ||||| ||||||||||||
Db         18 ATTGACAAAAAAAAAAA 1


RESULT 1625
AX042891
LOCUS       AX042891                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 457 from Patent WO0065088.
ACCESSION   AX042891
VERSION     AX042891.1  GI:11341499
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 457 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAAC 2189
              ||||||||||||| ||||
Db          1 TTTTTTTTTTTTTATAAC 18


RESULT 1626
AX043076/c
LOCUS       AX043076                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 642 from Patent WO0065088.
ACCESSION   AX043076
VERSION     AX043076.1  GI:11341684
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 642 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAA 2797
              || ||||||||||||||||
Db         18 GAGTTGAAAAAAAAAAAA 1


RESULT 1627
AX043184
LOCUS       AX043184                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 750 from Patent WO0065088.
ACCESSION   AX043184
VERSION     AX043184.1  GI:11341792
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 750 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAACT 2190
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTGTAACT 18


RESULT 1628
AX043287/c
LOCUS       AX043287                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 853 from Patent WO0065088.
ACCESSION   AX043287
VERSION     AX043287.1  GI:11341895
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 853 02-NOV-2000;
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AX043114
LOCUS       AX043114                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 680 from Patent WO0065088.
ACCESSION   AX043114
VERSION     AX043114.1  GI:11341722
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 680 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTGTA 18


RESULT 1620
AX042547
LOCUS       AX042547                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 113 from Patent WO0065088.
ACCESSION   AX042547
VERSION     AX042547.1  GI:11341155
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 113 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Homozygote primer sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACT 2190
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTGTAACT 18


RESULT 1621
AX042585/c
LOCUS       AX042585                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 151 from Patent WO0065088.
ACCESSION   AX042585
VERSION     AX042585.1  GI:11341193
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 151 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAA 2797
              ||||| ||||||||||
Db         18 GAATTTAAAAAAAAAAA 1


RESULT 1622
AX042614/c
LOCUS       AX042614                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 180 from Patent WO0065088.
ACCESSION   AX042614
VERSION     AX042614.1  GI:11341222
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 180 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1973 ACCTTGAAAAAAAGAAAA 1990
              ||||||||||||| ||||
Db         18 ACCTTGAAAAAAAAAAAA 1


RESULT 1623
AX042616
LOCUS       AX042616                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 182 from Patent WO0065088.
ACCESSION   AX042616
VERSION     AX042616.1  GI:11341224
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 182 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
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  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 978 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB345 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              || |||||||||||||||
Db         18 AAGAAAAAAAAAAAAAA 1


RESULT 1615
AX043581/c
LOCUS       AX043581                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1147 from Patent WO0065088.
ACCESSION   AX043581
VERSION     AX043581.1  GI:11342189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1147 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAA 2798
              || |||||||||||||||
Db         18 AAGTGAAAAAAAAAAAA 1


RESULT 1616
AX042984/c
LOCUS       AX042984                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 550 from Patent WO0065088.
ACCESSION   AX042984
VERSION     AX042984.1  GI:11341592
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 550 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2799
              | |||||||||||||||
Db         18 ACTGAAAAAAAAAAAAA 1


RESULT 1617
AX043693/c
LOCUS       AX043693                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1259 from Patent WO0065088.
ACCESSION   AX043693
VERSION     AX043693.1  GI:11342308
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1259 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2799
              | |||||||||||||||
Db         18 AGTGAAAAAAAAAAAAA 1


RESULT 1618
AX692829/c
LOCUS       AX692829                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5561 from Patent EP1281758.
ACCESSION   AX692829
VERSION     AX692829.1  GI:29415792
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5561 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2801
              | |||||||||||||||
Db         19 TCAAAAAAAAAAAAAAA 2


RESULT 1619
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  JOURNAL   Patent: US 6486130-A 66 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1760 ATTCATTAAGCTTTTTTT 1777
              ||||||||||| |||||||
Db          4 ATTCATTAAGGTTTTTTT 21


RESULT 1610
AR279815/c
LOCUS       AR279815                 24 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 10 from patent US 6518018.
ACCESSION   AR279815
VERSION     AR279815.1  GI:29714960
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 10 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              |||||||||||| |||||
Db         23 GAAAAAAAAAAATAAAAA 6


RESULT 1611
AX043291
LOCUS       AX043291                 24 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 857 from Patent WO0065088.
ACCESSION   AX043291
VERSION     AX043291.1  GI:11341899
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 857 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTAACTCT 18


RESULT 1612
AX498250/c
LOCUS       AX498250                 24 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 6 from Patent WO0218951.
ACCESSION   AX498250
VERSION     AX498250.1  GI:23343169
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dubertret,B., Calame,M. and Libchaber,A.
  TITLE     Methods employing fluorescence quenching by metal surfaces
  JOURNAL   Patent: WO 0218951-A 6 07-MAR-2002;
            THE ROCKEFELLER UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||
Db         23 GAGAAAAAAAAAAAAAAA 6


RESULT 1613
AX043077
LOCUS       AX043077                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 643 from Patent WO0065088.
ACCESSION   AX043077
VERSION     AX043077.1  GI:11341685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 643 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 25;
  Best Local Similarity   94.4%;  Pred. No. 2.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTAACT 2190
              ||||||||||||||| |||
Db          1 TTTTTTTTTTTTTCACT 18


RESULT 1614
AX043412/c
LOCUS       AX043412                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 978 from Patent WO0065088.
ACCESSION   AX043412
VERSION     AX043412.1  GI:11342020
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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RESULT 1605
AX053002
LOCUS       AX053002                23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 18 from Patent WO0071749.
ACCESSION   AX053002
VERSION     AX053002.1  GI:12227104
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 18 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Komponente (b)-5"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTGTA 18


RESULT 1606
AR162082/c
LOCUS       AR162082                24 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 10 from patent US 6258558.
ACCESSION   AR162082
VERSION     AR162082.1  GI:16229146
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Method for selection of proteins using RNA-protein fusions
  JOURNAL   Patent: US 6258558-A 10 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              ||||||||||||| |||||
Db         23 GAAAAAAAAAAATAAAAA 6


RESULT 1607
AR166607/c
LOCUS       AR166607                24 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 10 from patent US 6281344.
ACCESSION   AR166607
VERSION     AR166607.1  GI:16241999
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Nucleic acid-protein fusion molecules and libraries
  JOURNAL   Patent: US 6281344-A 10 28-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              ||||||||||||| |||||
Db         23 GAAAAAAAAAAATAAAAA 6


RESULT 1608
BD238389/c
LOCUS       BD238389                24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238389
VERSION     BD238389.1  GI:33048159
KEYWORDS    JP 2002536025-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 7 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/7
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US    09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 24;
  Best Local Similarity   94.4%;  Pred. No. 2.1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              ||||||||||||| |||||
Db         23 GAAAAAAAAAAATAAAAA 6


RESULT 1609
AR257304
LOCUS       AR257304                24 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 66 from patent US 6486130.
ACCESSION   AR257304
VERSION     AR257304.1  GI:27307146
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Livey,I., Crowe,B. and Dorner,F.
  TITLE     Immunogenic formulation of OSPC antigen vaccines for the prevention
            and treatment of lyme disease and recombinant methods for the
            preparation of such antigens
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            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 24 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/24
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
     source             1. .23
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||
Db          6 ACAAAAAAAAAAAAAAA 23


RESULT 1602
BD245242
LOCUS       BD245242                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245242
VERSION     BD245242.1  GI:33055012
KEYWORDS    JP 2002532386-A/28.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 28 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/28
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
     source             1. .23
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||
Db          6 ATAAAAAAAAAAAAAAA 23


RESULT 1603
AX052992
LOCUS       AX052992                  23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 8 from Patent WO0071749.
ACCESSION   AX052992
VERSION     AX052992.1  GI:12227094
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 8 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES                Location/Qualifiers
     source             1. .23
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Komponente (b)-1"

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAC 2189
              |||||||||||||||| |
Db          1 TTTTTTTTTTTTTTAGC 18


RESULT 1604
AX052993
LOCUS       AX052993                  23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 9 from Patent WO0071749.
ACCESSION   AX052993
VERSION     AX052993.1  GI:12227095
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 9 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES                Location/Qualifiers
     source             1. .23
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Komponente (b)-2"

  Query Match              0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTGTA 18
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Qy       2533 ATACAGGGTATTAAGAAT 2550
              |||||||||||| |||||
Db          3 ATACAGGGTATTTAGAAT 20


RESULT 1597
AR003288
LOCUS       AR003288                  22 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 10 from patent US 5744300.
ACCESSION   AR003288
VERSION     AR003288.1  GI:3964547
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Linskens,M.H.K., Hirsch,K.S., Villeponteau,B., Feng,J., Funk,W. and
            West,M.David.
  TITLE     Methods and reagents for the identification and regulation of
            senescence-related genes
  JOURNAL   Patent: US 5744300-A 10 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 22;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGAA 1784
              |||||||||||||||| ||
Db          5 AAGCTTTTTTTTTTTTAA 22


RESULT 1598
I30199
LOCUS       I30199                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 28 from patent US 5580726.
ACCESSION   I30199
VERSION     I30199.1  GI:1820990
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Linskens,M.H.K.
  TITLE     Method and Kit for enhanced differential display
  JOURNAL   Patent: US 5580726-A 28 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 22;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGAA 1784
              |||||||||||||||| ||
Db          5 AAGCTTTTTTTTTTTTAA 22


RESULT 1599
BD206201
LOCUS       BD206201                  22 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Process for producing polypeptide in mold variant cell.
ACCESSION   BD206201
VERSION     BD206201.1  GI:33015971
KEYWORDS    JP 2002515252-A/14.
SOURCE      Aspergillus oryzae
  ORGANISM  Aspergillus oryzae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
            Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Wahleithner,J. and Christensen,T.
  TITLE     Process for producing polypeptide in mold variant cell
  JOURNAL   Patent: JP 2002515252-A 14 28-MAY-2002;
            NOVO NORDISK BIOTECH INC,NOVO NORDISK AS
COMMENT     OS   Aspergillus oryzae
            PN   JP 2002515252-A/14
            PD   28-MAY-2002
            PF   14-MAY-1999 JP 2000549742
            PR   15-MAY-1998 US    09/079601,15-MAY-1998 US    09/079344 PI
            JILL WAHLEITHNER,TOVE CHRISTENSEN
            PC   C12N15/09,C07K14/38,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/
            PC   00,C12N9/30,
            PC   C12P21/00,C12P21/02//(C12N1/15,C12R1:685),(C12N1/15,C12R1:69),
            PC   (C12N1/21,C12R1:19),(C12N9/30,C12R1:19),C12N15/00,C12N5/00 CC
             Process for producing polypeptide in mold variant cell. FH   Key
                    Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Aspergillus oryzae'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Aspergillus oryzae"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:5062"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 22;
  Best Local Similarity   94.4%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1767 AAGCTTTTTTTTTTTGAA 1784
              |||||||||||||||| ||
Db          5 AAGCTTTTTTTTTTTTAA 22


RESULT 1600
AR123791
LOCUS       AR123791                  23 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 7 from patent US 6171803.
ACCESSION   AR123791
VERSION     AR123791.1  GI:14109152
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kinet,J.Pierre.
  TITLE     Isolation, characterization, and use of the human .beta. subunit of
            the high affinity receptor for immunoglobulin E
  JOURNAL   Patent: US 6171803-A 7 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 23;
  Best Local Similarity   94.4%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||| ||||||||||||||
Db          4 AAAACAAAAAAAAAAAA 21


RESULT 1601
BD245238
LOCUS       BD245238                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245238
VERSION     BD245238.1  GI:33055008
KEYWORDS    JP 2002532386-A/24.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6451968-A 49 17-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   89.5%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              ||||||| |||| ||||||
Db          1 CTTTTTTCTTTTNTTTTT 19


RESULT 1593
AX048436
LOCUS       AX048436                 20 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 35 from Patent WO0071747.
ACCESSION   AX048436
VERSION     AX048436.1  GI:12225600
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 35 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Erkennungssystem"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTT 2191
              ||||||||||||||| ||
Db          1 TTTTTTTTTTTTTAAGTT 18


RESULT 1594
AX326966
LOCUS       AX326966                 20 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 162 from Patent WO0178894.
ACCESSION   AX326966
VERSION     AX326966.1  GI:18097677
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Keith,T.
  TITLE     Novel human gene relating to respiratory diseases, obesity, and
            inflammatory bowel disease
  JOURNAL   Patent: WO 0178894-A 162 25-OCT-2001;
            Genome Therapeutics Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1558 CAGGACTGCAAAAATCCT 1575
              |||||||||||| |||||
Db          1 CAGGACTGCAAACATCCT 18


RESULT 1595
AX356851
LOCUS       AX356851                 21 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 9 from Patent WO0206490.
ACCESSION   AX356851
VERSION     AX356851.1  GI:18674099
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dudler,R., Schaffrath,U. and Lawton,K.A.
  TITLE     Lipoxygenase genes, promoters, transit peptides and proteins
            thereof
  JOURNAL   Patent: WO 0206490-A 9 24-JAN-2002;
            Syngenta Participations AG (CH) ; Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTT 2180
              | ||||||||||||||||
Db          3 TGCTTTTTTTTTTTTTT 20


RESULT 1596
AX838805
LOCUS       AX838805                 21 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 10 from Patent WO03076667.
ACCESSION   AX838805
VERSION     AX838805.1  GI:39922360
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Jeney,C. and Takacs,T.
  TITLE     Amplification-hybridisation method for detecting and typing
            humanpapillomavirus
  JOURNAL   Patent: WO 03076667-A 10 18-SEP-2003;
            Jeney, Csaba (HU) ; Takacs, Tibor (HU)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer (L1CR16)"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2786 AAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||||
Db         18 ACAAAAAAAAAAAAAAAAA 1


RESULT 1588
AX085251/c
LOCUS       AX085251                  18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 5 from Patent WO0112855.
ACCESSION   AX085251
VERSION     AX085251.1  GI:13275309
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 5 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              | |||||||||||||||||
Db         18 GCAAAAAAAAAAAAAAAA 1


RESULT 1589
AX085252
LOCUS       AX085252                  18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 6 from Patent WO0112855.
ACCESSION   AX085252
VERSION     AX085252.1  GI:13275310
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 6 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTGT 18


RESULT 1590
AX085252/c
LOCUS       AX085252                  18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 6 from Patent WO0112855.
ACCESSION   AX085252
VERSION     AX085252.1  GI:13275310
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 6 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||||
Db         18 ACAAAAAAAAAAAAAAAAA 1


RESULT 1591
E59328
LOCUS       E59328                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for purifying oligonucleotide.
ACCESSION   E59328
VERSION     E59328.1  GI:18622505
KEYWORDS    JP 2000342265-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hirose,K. and Yoshida,T.
  TITLE     Method for purifying oligonucleotide
  JOURNAL   Patent: JP 2000342265-A 9 12-DEC-2000;
            TOAGOSEI CHEM IND CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000342265-A/9
            PD   12-DEC-2000
            PF   02-JUN-1999 JP 1999154974
            PR
            PI   KUNIHIKO HIROSE,TADAO YOSHIDA
            PC   C12N15/09,B01D15/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 1.3e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              ||||||||| ||||||||
Db          2 AAAAAAAAAGAAAAAAA 19


RESULT 1592
AR231312
LOCUS       AR231312                  20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 49 from patent US 6451968.
ACCESSION   AR231312
VERSION     AR231312.1  GI:27272243
KEYWORDS    .
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Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTCA 18


RESULT 1583
AX085253
LOCUS       AX085253                 18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 7 from Patent WO0112855.
ACCESSION   AX085253
VERSION     AX085253.1  GI:13275311
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 7 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTCA 18


RESULT 1584
A14689
LOCUS       A14689                   18 bp    DNA     linear   PAT 28-MAR-1994
DEFINITION  Nucleotide sequence 9 from patent number WO8303623.
ACCESSION   A14689
VERSION     A14689.1  GI:513760
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   .
  TITLE     CODING DNA FRAGMENTS FOR POLYPEPTIDES CONTAINING AT LEAST ONE
            ANTIGENIC DETERMINANT OF THE PAPILLOMAVIRUS PARTICULARLY OF THE 1a
            HPV TYPE AND CORRESPONDING POLYPEPTIDES
  JOURNAL   Patent: WO 8303623-A 9 27-OCT-1983;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db          1 GCAAAAAAAAAAAAAAA 18


RESULT 1585
AR208425/c
LOCUS       AR208425                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6383754.
ACCESSION   AR208425
VERSION     AR208425.1  GI:21509576
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 5 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||
Db         18 GCAAAAAAAAAAAAAAA 1


RESULT 1586
AR208426
LOCUS       AR208426                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6383754.
ACCESSION   AR208426
VERSION     AR208426.1  GI:21509577
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 6 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||  |
Db          1 TTTTTTTTTTTTTTTTGT 18


RESULT 1587
AR208426/c
LOCUS       AR208426                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6383754.
ACCESSION   AR208426
VERSION     AR208426.1  GI:21509577
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 6 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

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FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="530A11"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .25
                     /note="T-DNA flanking sequence
                     right border"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTA 2187
              |||| ||| ||||| | ||||||
Db          3 CTTTGTTTGTTTTTGTCTTTTA 25


RESULT 1580
AB068802/c
LOCUS       AB068802                  25 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, forward primer for human STS sts-WI-21093
            at 1p36.
ACCESSION   AB068802
VERSION     AB068802.1  GI:15129606
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 25)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .25
                     /note="forward primer for human STS sts-WI-21093 at 1p36
                     sts-WI-21093 obtained from clones B127J4, B284O17, B45I3,
                     Human BAC library RPCI-11"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2589 CTATTTAATTGAAACTCTCTGTT 2611
              | |||| |||||||| ||||||
Db         25 CGATTTTATTGAAACCTTCTGTT 3


RESULT 1581
E04206/c
LOCUS       E04206                    29 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  single strand DNA sequence of Type C hepatitis virus.
ACCESSION   E04206
VERSION     E04206.1  GI:2172416
KEYWORDS    JP 1993001099-A/34.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Morita,K., Hasegawa,M., Yokoo,Y., Sato,M., Sekine,S., Sugimoto,S.,
            Koda,H., Mori,H. and Arima,T.
  TITLE     FUSED ANTIGENIC POLYPEPTIDE
  JOURNAL   Patent: JP 1993001099-A 34 08-JAN-1993;
            KYOWA HAKKO KOGYO CO LTD
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1993001099-A/34
            PD   08-JAN-1993
            PF   25-JUN-1991 JP 1991153031
            PI   MORITA KAZUKI, HASEGAWA MAMORU, YOKOO YOSHIHARU, SATO
            MORIYUKI, PI   SEKINE SUSUMU, SUGIMOTO SEIJI, KODA HAJIME, MORI
            HIDEJI, PI   ARIMA TERUMASA
            PC   C07K7/10,C07K13/00,C12N1/21,C12N15/62,C12N15/70,C12P21/02, PC
             C12Q1/68,
            PC
            G01N33/569,G01N33/576//A61K39/00,C12N15/51,(C12N1/21,C12R1:19), PC
             (C12P21/02,
            PC   C12R1:19),C07K99:00;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 29;
  Best Local Similarity   82.6%;  Pred. No. 2.8e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
              | ||  |||||||| ||||||||
Db         29 AAAAACGAAAAAAAGAAAAAAAA 7


RESULT 1582
AR208427
LOCUS       AR208427                  18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 7 from patent US 6383754.
ACCESSION   AR208427
VERSION     AR208427.1  GI:21509578
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 7 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.4;  DB 1;  Length 18;
  Best Local Similarity   94.4%;  Pred. No. 1e+03;
  Matches   17;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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            PC   G01N33/564,G01N33/569,C12N15/00,C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'DNA (synthetic)'
            CC   /note = 'page 11'
            FH   Key             Location/Qualifiers
            FT   misc_feature    1. .25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1951 TTTTTGTGTCCGCTAAATATTTA 1973
              |||||| |||| || | ||||||
Db          1 TTTTTGAGTCCCCTTAGTATTTA 23


RESULT 1577
BD074392
LOCUS       BD074392                 25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method of diagnosis and treatment of autoimmune disease such as
            insulin-dependent diabetes mellitus containing retroviral
            superantigen.
ACCESSION   BD074392
VERSION     BD074392.1  GI:22619995
KEYWORDS    JP 2001511363-A/24.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Conra,B. and Matthew,B.
  TITLE     Method of diagnosis and treatment of autoimmune disease such as
            insulin-dependent diabetes mellitus containing retroviral
  JOURNAL   Patent: JP 2001511363-A 24 14-AUG-2001;
            NOVIMMUNE SA
COMMENT     OS   Unidentified
            PN   JP 2001511363-A/24
            PD   14-AUG-2001
            PF   22-JUL-1998 JP 2000504461
            PR   22-JUL-1997 EP   97112482.1,23-JUL-1997 EP   97401773.3 PI
            BERNARD CONRA,BERNARD MATTHEW
            PC   C12N15/09,A01K67/027,A61K31/7088,A61K31/7115,A61K39/21,A61P3/
            PC   10,A61P37/00,
            PC   C07K7/00,C07K14/08,C12N5/10,C12N7/00,C12P21/02,C12Q1/02,C12Q1/
            PC   68,
            PC   G01N33/564,G01N33/569,C12N15/00,C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   /desc = 'SYNTHETIC DNA'
            CC   /note = 'page 52'
            FH   Key             Location/Qualifiers
            FT   misc_feature    1. .25.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1951 TTTTTGTGTCCGCTAAATATTTA 1973
              |||||| |||| || | ||||||
Db          1 TTTTTGAGTCCCCTTAGTATTTA 23


RESULT 1578
BD088021/c
LOCUS       BD088021                 25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD088021
VERSION     BD088021.1  GI:22633631
KEYWORDS    JP 2001321190-A/265.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 265 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/265
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2589 CTATTTAATTGAAACTCTCTGTT 2611
              | |||| |||||||| ||||||
Db         25 CGATTTTATTGAAACCTTCTGTT 3


RESULT 1579
AJ588309
LOCUS       AJ588309                 25 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            530A11.
ACCESSION   AJ588309
VERSION     AJ588309.1  GI:37937933
KEYWORDS    right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 25)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
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```
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 878 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||| |||  | ||
Db          1 TTTTTTTTTTTTATCTTGCAGAG 23


RESULT 1573
AX043616
LOCUS       AX043616                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1182 from Patent WO0065088.
ACCESSION   AX043616
VERSION     AX043616.1  GI:11342224
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1182 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATTCT 1793
              ||||||||||||  ||| || ||
Db          2 TTTTTTTTTTTGGTCCCAATACT 24


RESULT 1574
AX043642/c
LOCUS       AX043642                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1208 from Patent WO0065088.
ACCESSION   AX043642
VERSION     AX043642.1  GI:11342257
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1208 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2801
              |||   | ||||||||||||||||
Db         23 AGACAGGGAAAAAAAAAAAAAAA 1


RESULT 1575
AX104992
LOCUS       AX104992                  25 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 37 from Patent WO0123568.
ACCESSION   AX104992
VERSION     AX104992.1  GI:13921189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Duckett,C. and Mir,S.S.
  TITLE     Members of the iap gene family
  JOURNAL   Patent: WO 0123568-A 37 05-APR-2001;
            THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        996 CCTTGCGGGAGAAGTTGGACAAG 1018
              ||| ||| || ||| ||||||||
Db          1 CCTGGCGCGAAAAGGTGGACAAG 23


RESULT 1576
BD074369
LOCUS       BD074369                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method of diagnosis and treatment of autoimmune disease such as
            insulin-dependent diabetes mellitus containing retroviral
            superantigen.
ACCESSION   BD074369
VERSION     BD074369.1  GI:22619972
KEYWORDS    JP 2001511363-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Conra,B. and Matthew,B.
  TITLE     Method of diagnosis and treatment of autoimmune disease such as
            insulin-dependent diabetes mellitus containing retroviral
  JOURNAL   Patent: JP 2001511363-A 1 14-AUG-2001;
            NOVIMMUNE SA
COMMENT     OS   Unidentified
            PN   JP 2001511363-A/1
            PD   14-AUG-2001
            PF   22-JUL-1998 JP 2000504461
            PR   22-JUL-1997 EP   97112482.1,23-JUL-1997 EP   97401773.3 PI
            BERNARD CONRA,BERNARD MATTHEW
            PC   C12N15/09,A01K67/027,A61K31/7088,A61K31/7115,A61K39/21,A61P3/
            PC   10,A61P37/00,
            PC   C07K7/00,C07K14/08,C12N5/10,C12N7/00,C12P21/02,C12Q1/02,C12Q1/
            PC   68,
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FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
              || ||| || | ||||||||||
Db         24 ATAGAACAACAGAAAAAAAAAAA 2


RESULT 1568
AX043216/c
LOCUS       AX043216                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 782 from Patent WO0065088.
ACCESSION   AX043216
VERSION     AX043216.1  GI:11341824
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 782 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAA 2801
              || | || || ||||||||||||
Db         23 AGTACTGGAACAAAAAAAAAAAA 1


RESULT 1569
AX043257
LOCUS       AX043257                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 823 from Patent WO0065088.
ACCESSION   AX043257
VERSION     AX043257.1  GI:11341865
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 823 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATTCT 1793
              ||||||||||||||   ||| ||
Db          2 TTTTTTTTTTTGAAGGACATCCT 24


RESULT 1570
AX043259/c
LOCUS       AX043259                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 825 from Patent WO0065088.
ACCESSION   AX043259
VERSION     AX043259.1  GI:11341867
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 825 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2802
              | | || || ||||||||||||||
Db         23 GTACTGGAACAAAAAAAAAAAAA 1


RESULT 1571
AX043286
LOCUS       AX043286                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 852 from Patent WO0065088.
ACCESSION   AX043286
VERSION     AX043286.1  GI:11341894
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 852 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAA 2195
              ||||||||||||||  || | |||
Db          1 TTTTTTTTTTTTTCCACATAGAA 23


RESULT 1572
AX043312
LOCUS       AX043312                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 878 from Patent WO0065088.
ACCESSION   AX043312
VERSION     AX043312.1  GI:11341920
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  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||| |||  | ||
Db          1 TTTTTTTTTTTTATCTTGCAGAG 23


RESULT 1563
AX042904
LOCUS       AX042904                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 470 from Patent WO0065088.
ACCESSION   AX042904
VERSION     AX042904.1  GI:11341512
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 470 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTGAACCCCATTCT 1793
              ||||||||||||   ||||||| |
Db          3 TTTTTTTTTTACCCCCCATTGT 25


RESULT 1564
AX042952/c
LOCUS       AX042952                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 518 from Patent WO0065088.
ACCESSION   AX042952
VERSION     AX042952.1  GI:11341560
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 518 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAAA 2799
              || |  ||| ||||||||||||||
Db         23 TTCGGGTTGTAAAAAAAAAAAAA 1


RESULT 1565
AX042955/c
LOCUS       AX042955                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 521 from Patent WO0065088.
ACCESSION   AX042955
VERSION     AX042955.1  GI:11341563
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 521 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAA 2800
              | |||||  | ||||||||||||
Db         23 TGGAATTCCACAAAAAAAAAAAA 1


RESULT 1566
AX042962
LOCUS       AX042962                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 528 from Patent WO0065088.
ACCESSION   AX042962
VERSION     AX042962.1  GI:11341570
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 528 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2176 TTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||| ||||||  | |
Db          1 TTTTTTTTTTTTCCTTTGATACT 23


RESULT 1567
AX043108/c
LOCUS       AX043108                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 674 from Patent WO0065088.
ACCESSION   AX043108
VERSION     AX043108.1  GI:11341716
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 674 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
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RESULT 1558
AR435048
LOCUS       AR435048                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1471 from patent US 6656700.
ACCESSION   AR435048
VERSION     AR435048.1  GI:40197891
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1471 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        444 CGGCGCCCACAGGCAGCCAGCAG 466
              ||||   |||||| |||||||||
Db          2 CGGCCAGCACAGGTAGCCAGCAG 24


RESULT 1559
AR435049
LOCUS       AR435049                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1472 from patent US 6656700.
ACCESSION   AR435049
VERSION     AR435049.1  GI:40197892
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1472 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        444 CGGCGCCCACAGGCAGCCAGCAG 466
              ||||   |||||| |||||||||
Db          1 CGGCCAGCACAGGTAGCCAGCAG 23


RESULT 1560
AX000308
LOCUS       AX000308                  25 bp    DNA     linear   PAT 10-MAR-2000
DEFINITION  Sequence 1 from Patent WO9905527.
ACCESSION   AX000308
VERSION     AX000308.1  GI:7240723
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Conrad,B. and Mach,B.
  TITLE     METHODS FOR DIAGNOSIS AND THERAPY OF AUTOIMMUNE DISEASE, SUCH AS
            INSULIN DEPENDENT DIABETES MELLITUS, INVOLVING RETROVIRAL
            SUPERANTIGENS
  JOURNAL   Patent: WO 9905527-A 1 04-FEB-1999;
            MEDIGEN S A (CH); CONRAD BERNARD (CH)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1951 TTTTTGTGTCCGCTAAATATTTA 1973
              |||||| |||| || | ||||||
Db          1 TTTTTGAGTCCCCTTAGTATTTA 23


RESULT 1561
AX000331
LOCUS       AX000331                  25 bp    DNA     linear   PAT 10-MAR-2000
DEFINITION  Sequence 24 from Patent WO9905527.
ACCESSION   AX000331
VERSION     AX000331.1  GI:7240746
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Conrad,B. and Mach,B.
  TITLE     METHODS FOR DIAGNOSIS AND THERAPY OF AUTOIMMUNE DISEASE, SUCH AS
            INSULIN DEPENDENT DIABETES MELLITUS, INVOLVING RETROVIRAL
            SUPERANTIGENS
  JOURNAL   Patent: WO 9905527-A 24 04-FEB-1999;
            MEDIGEN S A (CH); CONRAD BERNARD (CH)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1951 TTTTTGTGTCCGCTAAATATTTA 1973
              |||||| |||| || | ||||||
Db          1 TTTTTGAGTCCCCTTAGTATTTA 23


RESULT 1562
AX042593
LOCUS       AX042593                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 159 from Patent WO0065088.
ACCESSION   AX042593
VERSION     AX042593.1  GI:11341201
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 159 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Miyata,S., Ohshima,A., Inouye,S. and Inouye,M.
  TITLE     Eukaryotes expressing single stranded hybrid molecules
  JOURNAL   Patent: US 5849563-A 7 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2531 ATATACAGGGTATTAAGAATTAA 2553
              || || |||||||||| ||| ||
Db         24 ATCTAGAGGGTATTAATAATGAA 2


RESULT 1554
AR146859
LOCUS       AR146859                  25 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from patent US 6218598.
ACCESSION   AR146859
VERSION     AR146859.1  GI:15110048
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ishige,F., Nishikawa,S. and Oeda,K.
  TITLE     Plant promoter
  JOURNAL   Patent: US 6218598-A 9 17-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1896 CCCTAGATCAACAGATCAACAAT 1918
              | ||||||||||  |||||| |
Db          2 CTCTAGATCAACACCTCAACATT 24


RESULT 1555
E55072
LOCUS       E55072                    25 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Plant promoter.
ACCESSION   E55072
VERSION     E55072.1  GI:18625258
KEYWORDS    JP 2000083679-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ishige,I., Nishikawa,S. and Oeda,K.
  TITLE     Plant promoter
  JOURNAL   Patent: JP 2000083679-A 9 28-MAR-2000;
            SUMITOMO CHEM CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000083679-A/9
            PD   28-MAR-2000
            PF   12-JUL-1999 JP 1999197240
            PR
            PI   IKUHARU ISHIGE,SATOMI NISHIKAWA,KENJI OEDA
            PC   C12N15/09,A01H5/00,C12N1/21,C12N5/10//(C12N15/09,C12R1:91), PC
              (C12N5/10,C12R1:91),C12N15/00,C12N5/00,(C12N15/00,C12R1:91), PC
             (C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1896 CCCTAGATCAACAGATCAACAAT 1918
              | ||||||||||  |||||| |
Db          2 CTCTAGATCAACACCTCAACATT 24


RESULT 1556
I42108
LOCUS       I42108                    25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 3 from patent US 5629147.
ACCESSION   I42108
VERSION     I42108.1  GI:2467603
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Asgari,M., Blick,M., Bresser,J., Cubbage,M.L. and Prashad,N.
  TITLE     Enriching and identifying fetal cells in maternal blood for in situ
            hybridization
  JOURNAL   Patent: US 5629147-A 3 13-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGACGC 73
              ||||||| ||||||||| |  ||
Db          3 GCGGCGGCGGCGGCGGCGGCGGC 25


RESULT 1557
AR435047
LOCUS       AR435047                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1470 from patent US 6656700.
ACCESSION   AR435047
VERSION     AR435047.1  GI:40197890
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1470 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        444 CGGCGCCCACAGGCAGCCAGCAG 466
              ||||   |||||| |||||||||
Db          3 CGGCCAGCACAGGTAGCCAGCAG 25
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            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTTGAACCCCATTCT 1793
              ||||||||||   ||||||| |
Db          3 TTTTTTTTTTTTCCCCCATTGT 25


RESULT 1549
AX320851/c
LOCUS       AX320851                  25 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 21 from Patent WO0183736.
ACCESSION   AX320851
VERSION     AX320851.1  GI:17902402
KEYWORDS    .
SOURCE      Hepatitis C virus
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1
  AUTHORS   Pellerin,C. and Kukolj,G.
  TITLE     Internal de novo initiation sites of the hcv ns5b polymerase and
            use thereof
  JOURNAL   Patent: WO 0183736-A 21 08-NOV-2001;
            BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Hepatitis C virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11103"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2801
              ||||   || ||||||||||||||
Db         23 AGAAGGAAAGAAAAAAAAAAAAA 1


RESULT 1550
AX042831
LOCUS       AX042831                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 397 from Patent WO0065088.
ACCESSION   AX042831
VERSION     AX042831.1  GI:11341439
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 397 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||| ||||  | ||
Db          1 TTTTTTTTTTTTCTTTTCCACCT 23


RESULT 1551
AR028113
LOCUS       AR028113                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5858649.
ACCESSION   AR028113
VERSION     AR028113.1  GI:5940086
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Asgari,M., Blick,M., Bresser,J., Cubbage,M.Lee. and Prashad,N.
  TITLE     Amplification of mRNA for distinguishing fetal cells in maternal
            blood
  JOURNAL   Patent: US 5858649-A 3 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGACGC 73
              ||||||| ||||||||| |  ||
Db          3 GCGGCGGCGGCGGCGGCGGC 25


RESULT 1552
AR030289
LOCUS       AR030289                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5861253.
ACCESSION   AR030289
VERSION     AR030289.1  GI:5943503
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Asgari,M., Blick,M., Bresser,J., Cubbage,M.Lee. and Prashad,N.
  TITLE     Intracellular antigens for identifying fetal cells in maternal
            blood
  JOURNAL   Patent: US 5861253-A 3 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         51 GCGGCGGGGGCGGCGGCAGACGC 73
              ||||||| ||||||||| |  ||
Db          3 GCGGCGGCGGCGGCGGCGGC 25


RESULT 1553
AR065818/c
LOCUS       AR065818                  25 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 7 from patent US 5849563.
ACCESSION   AR065818
VERSION     AR065818.1  GI:5996034
KEYWORDS    .
SOURCE      Unknown.
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Cantor,C.R., Ito,T. and Smith,C.L.
  TITLE     DNA purification by triplex-affinity capture and affinity capture
            electrophoresis
  JOURNAL   Patent: US 5482836-A 4 09-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTT 2177
              || |||||| |||| ||||| ||
Db          2 TTCTTTTCTTCTTTCTTTTTCTT 24


RESULT 1545
AX093547
LOCUS       AX093547                 24 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 77 from Patent WO0118198.
ACCESSION   AX093547
VERSION     AX093547.1  GI:13509985
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weissenbach,J. and Hazan,J.
  TITLE     Cloning, expression and characterisation of the spg4 gene
            responsible for the most frequent form of autosomal spastic
            paraplegia
  JOURNAL   Patent: WO 0118198-A 77 15-MAR-2001;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Site accepteur d' pissage du g ne SPG4."

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1789 ATTCTTTCCTTCTCTGAAAGTGG 1811
              | | |||||||| || ||||||||
Db          1 ACTTTTTCCTTGTCAGAAAGTGG 23


RESULT 1546
BD143588/c
LOCUS       BD143588                 24 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of anticipating efficacy of interferon and primer and probe
            to be used therein.
ACCESSION   BD143588
VERSION     BD143588.1  GI:27849346
KEYWORDS    JP 2002125683-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Yatsuhashi,H., Katsume,A., Inoue,K., Obara,K. and Obar,M.
  TITLE     Method of anticipating efficacy of interferon and primer and probe
            to be used therein
  JOURNAL   Patent: JP 2002125683-A 10 08-MAY-2002;
            TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, HIROSHI
            YATSUHASHI, CHUGAI PHARMACEUTICAL CO LTD,SRL INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002125683-A/10
            PD   08-MAY-2002
            PF   27-OCT-2000 JP 2000329615
            PI   HIROSHI YATSUHASHI,ASAO KATSUME,KAZUAKI INOUE,KYOKO OBARA, PI
             MICHINORI OBARA
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Reverse primer for CIS3
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 24;
  Best Local Similarity   82.6%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        656 AACCTGGGGCTCCACGACATGCC 678
              || |||| || |||| |||||||
Db         24 AAGCTGGTGCACCACTACATGCC 2


RESULT 1547
AX043064
LOCUS       AX043064                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 630 from Patent WO0065088.
ACCESSION   AX043064
VERSION     AX043064.1  GI:11341672
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 630 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.6;  DB 1;  Length 25;
  Best Local Similarity   82.6%;  Pred. No. 2.1e+03;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||||| |   |||
Db          1 TTTTTTTTTTTTTTTCAGTCTTG 23


RESULT 1548
AX043082
LOCUS       AX043082                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 648 from Patent WO0065088.
ACCESSION   AX043082
VERSION     AX043082.1  GI:11341690
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 648 02-NOV-2000;
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FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match              0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1922 TTTTTTTTCAGTGTTAAGGT 1941
              |||||||||||| ||| |||
Db          5 TTTTTTTTCAGTCTTATGGT 24


RESULT 1540
AX043318
LOCUS       AX043318                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 884 from Patent WO0065088.
ACCESSION   AX043318
VERSION     AX043318.1  GI:11341926
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 884 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQB1 Heterozygote Primer Sequence"

  Query Match              0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGA 2194
              |||||||||||||||  ||
Db          1 TTTTTTTTTTTTAACTACGA 20


RESULT 1541
AX043413/c
LOCUS       AX043413                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 979 from Patent WO0065088.
ACCESSION   AX043413
VERSION     AX043413.1  GI:11342021
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 979 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB345 Heterozygote Primer Sequence"

  Query Match              0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAA 2799
              |||  ||||||||||||||||
Db         20 GAAGAGAAAAAAAAAAAAAA 1


RESULT 1542
AX744661
LOCUS       AX744661                  25 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 626 from Patent WO03031621.
ACCESSION   AX744661
VERSION     AX744661.1  GI:30723328
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 626 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match              0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGG 2124
              |||| |||||||||  |||||
Db          6 GGGGACCTTCTGGTCTTAGG 25


RESULT 1543
AX744667
LOCUS       AX744667                  25 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 632 from Patent WO03031621.
ACCESSION   AX744667
VERSION     AX744667.1  GI:30723334
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 632 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match              0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2106 GGGGCCTTCTGGTTTTAGGA 2125
              ||| |||||||| ||||||
Db          1 GGGACCTTCTGGTCTTAGGA 20


RESULT 1544
I16929
LOCUS       I16929                    24 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 4 from patent US 5482836.
ACCESSION   I16929
VERSION     I16929.1  GI:1251837
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  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||| | ||
Db          1 TTTTTTTTTTTTAACCTGGA 20


RESULT 1535
AX043284/c
LOCUS       AX043284                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 850 from Patent WO0065088.
ACCESSION   AX043284
VERSION     AX043284.1  GI:11341892
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 850 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAA 2797
              | | ||||||||||||||||
Db         20 TGGGATTGAAAAAAAAAAAA 1


RESULT 1536
AX043295/c
LOCUS       AX043295                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 861 from Patent WO0065088.
ACCESSION   AX043295
VERSION     AX043295.1  GI:11341903
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 861 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAA 2798
              || | ||||||||||||||||
Db         20 AGGAATGAAAAAAAAAAAA 1


RESULT 1537
AX043297
LOCUS       AX043297                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 863 from Patent WO0065088.
ACCESSION   AX043297
VERSION     AX043297.1  GI:11341905
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 863 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTT 2192
              |||||||||||| ||||| |
Db          1 TTTTTTTTTTTTATAACTCT 20


RESULT 1538
AX043310
LOCUS       AX043310                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 876 from Patent WO0065088.
ACCESSION   AX043310
VERSION     AX043310.1  GI:11341918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 876 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1922 TTTTTTTTCAGTGTTAAGGT 1941
              |||||||||||| ||| |||
Db          5 TTTTTTTTCAGTCTTACGGT 24


RESULT 1539
AX043311
LOCUS       AX043311                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 877 from Patent WO0065088.
ACCESSION   AX043311
VERSION     AX043311.1  GI:11341919
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 877 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
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LOCUS       AX042933                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 499 from Patent WO0065088.
ACCESSION   AX042933
VERSION     AX042933.1  GI:11341541
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 499 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||| | |||
Db          1 TTTTTTTTTTTTTAGCCTTG 20


RESULT 1531
AX043112
LOCUS       AX043112                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 678 from Patent WO0065088.
ACCESSION   AX043112
VERSION     AX043112.1  GI:11341720
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 678 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAACTT 2191
              |||||||||||| | |||||
Db          1 TTTTTTTTTTTTGTCAACTT 20


RESULT 1532
AX043114/c
LOCUS       AX043114                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 680 from Patent WO0065088.
ACCESSION   AX043114
VERSION     AX043114.1  GI:11341722
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 680 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              || | ||||||||||||||||
Db         20 TGTACAAAAAAAAAAAAAAA 1


RESULT 1533
AX043119
LOCUS       AX043119                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 685 from Patent WO0065088.
ACCESSION   AX043119
VERSION     AX043119.1  GI:11341727
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 685 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||| ||| ||
Db          1 TTTTTTTTTTTTTGTTTGTA 20


RESULT 1534
AX043218
LOCUS       AX043218                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 784 from Patent WO0065088.
ACCESSION   AX043218
VERSION     AX043218.1  GI:11341826
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 784 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
```

```
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 93 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAACTT 2191
              ||||||||||||  | |||||
Db          1 TTTTTTTTTTTTGTCAACTT 20


RESULT 1526
AX042543
LOCUS       AX042543                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 109 from Patent WO0065088.
ACCESSION   AX042543
VERSION     AX042543.1  GI:11341151
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 109 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Homozygote primer sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||||  ||
Db          1 TTTTTTTTTTTTAACTACGA 20


RESULT 1527
AX042569/c
LOCUS       AX042569                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 135 from Patent WO0065088.
ACCESSION   AX042569
VERSION     AX042569.1  GI:11341177
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 135 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAA 2797
              || | ||||||||||||||||
Db         20 TAAACTTGAAAAAAAAAAAAA 1


RESULT 1528
AX042831/c
LOCUS       AX042831                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 397 from Patent WO0065088.
ACCESSION   AX042831
VERSION     AX042831.1  GI:11341439
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 397 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              | ||||| ||||||||||||
Db         20 TGGAAAAGAAAAAAAAAAAA 1


RESULT 1529
AX042902
LOCUS       AX042902                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 468 from Patent WO0065088.
ACCESSION   AX042902
VERSION     AX042902.1  GI:11341510
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 468 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1771 TTTTTTTTTTGAACCCCAT 1790
              |||||||||||| ||||| |
Db          4 TTTTTTTTTTGCACCCCTT 23


RESULT 1530
AX042933
```

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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||  ||
Db         22 CCTTTTTTTTTTTTTTCCTT 3


RESULT 1521
AX803836
LOCUS       AX803836                 24 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 4 from Patent WO03060160.
ACCESSION   AX803836
VERSION     AX803836.1  GI:38520971
KEYWORDS    .
SOURCE      Salmo salar (Atlantic salmon)
  ORGANISM  Salmo salar
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 4 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Salmo salar"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8030"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 24;
  Best Local Similarity   90.0%;  Pred. No. 1.8e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2800
              ||||| |||||| |||||||
Db          2 AATTGGAAAAAACAAAAAAA 21


RESULT 1522
AX692828/c
LOCUS       AX692828                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5560 from Patent EP1281758.
ACCESSION   AX692828
VERSION     AX692828.1  GI:29415791
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5560 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2803
              | |||||||||||||||| |
Db         20 TCAAAAAAAAAAAAAAAGA 1


RESULT 1523
I45922
LOCUS       I45922                   25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 10 from patent US 5639595.
ACCESSION   I45922
VERSION     I45922.1  GI:2469887
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Mirabelli,C.K., Ecker,D.J., Vickers,T.A. and Robertson,D.L.
  TITLE     Identification of novel drugs and reagents
  JOURNAL   Patent: US 5639595-A 10 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2184
              |||  ||||||||||||||||
Db          6 CTTGGTTTTTTTTTTTTTT 25


RESULT 1524
AR435374
LOCUS       AR435374                 25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1797 from patent US 6656700.
ACCESSION   AR435374
VERSION     AR435374.1  GI:40198217
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1797 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 25;
  Best Local Similarity   90.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTG 2329
              |||| | ||||||||||||||
Db          6 AAGCCAGTTGTTGCTGCTTG 25


RESULT 1525
AX042527
LOCUS       AX042527                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 93 from Patent WO0065088.
ACCESSION   AX042527
VERSION     AX042527.1  GI:11341135
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
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  JOURNAL   Patent: JP 2002532386-A 23 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/23
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTT 2183
              ||  ||||||||||||||||
Db          4 CCAGTTTTTTTTTTTTTTTT 23


RESULT 1517
AX053001
LOCUS       AX053001                  23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 17 from Patent WO0071749.
ACCESSION   AX053001
VERSION     AX053001.1  GI:12227103
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 17 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Komponente (b)-4"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||| || |
Db          1 TTTTTTTTTTTTTTTCTTGT 20


RESULT 1518
AX053001/c
LOCUS       AX053001                  23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 17 from Patent WO0071749.
ACCESSION   AX053001
VERSION     AX053001.1  GI:12227103
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 17 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Komponente (b)-4"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              || || ||||||||||||||
Db         21 GACAAGAAAAAAAAAAAAAA 2


RESULT 1519
AX115478
LOCUS       AX115478                  23 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 601 from Patent WO0129262.
ACCESSION   AX115478
VERSION     AX115478.1  GI:14032420
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 601 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Primer"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              ||||  ||||||||||||||
Db          1 TGAAGGAAAAAAAAAAAAAA 20


RESULT 1520
AX115478/c
LOCUS       AX115478                  23 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 601 from Patent WO0129262.
ACCESSION   AX115478
VERSION     AX115478.1  GI:14032420
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 601 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .23
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  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTG 808
              |||| | ||||||||||||||
Db          1 CCTGCCTGAAGGAGCTGGTG 20


RESULT 1513
AR066407
LOCUS       AR066407                 22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 31 from patent US 5849995.
ACCESSION   AR066407
VERSION     AR066407.1  GI:5996623
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hayden,M., Lin,B. and Nasir,J.
  TITLE     Mouse model for Huntington's Disease and related DNA sequences
  JOURNAL   Patent: US 5849995-A 31 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 22;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2182
              ||||| |||||||| |||||
Db          1 TCCTTCTTTTTTTTATTTTT 20


RESULT 1514
HUMO204RA/c
LOCUS       HUMO204RA                22 bp    DNA     linear   STS 29-MAY-2002
DEFINITION  A PCR primer for D21S16 locus STS, location 21q11.2, sequence
            tagged site.
ACCESSION   D50257
VERSION     D50257.1  GI:801798
KEYWORDS    STS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Tanahashi,H., Ito,T., Hattori,M., Ohira,M., Ohki,M., Tashiro,K. and
            Sakaki,Y.
  TITLE     Sixty new STSs (sequence-tagged sites) of human chromosome 21
  JOURNAL   DNA Res. 1 (2), 85-89 (1994)
  MEDLINE   96051984
   PUBMED   7584032
REFERENCE   2  (bases 1 to 22)
  AUTHORS   Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-APR-1995) Yoshiyuki Sakaki, Institute of Medical
            Science, University of Tokyo, Human Genome Center; 4-6-1
            Shirokanedai Minato-ku, Tokyo 108, Japan
            (E-mail:sakaki@hgc.ims.u-tokyo.ac.jp, Tel:03-5449-5362,
            Fax:03-5449-5445)
COMMENT     Submitted (28-Apr-1995) to DDBJ by:
            Yoshiyuki Sakaki
            Human Genome Center
            Institute of Medical Science
            University of Tokyo
            4-6-1 Shirokanedai Minato-ku
            Tokyo, 108
            Japan
            Phone: 03-5449-5362
            Fax  : 03-5449-5445.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="21"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 22;
  Best Local Similarity   90.0%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2374 GCGTTGAGTGTACAGATTTT 2393
              || || ||||||||||||||
Db         22 GCTTTCAGTGTACAGATTTT 3


RESULT 1515
BD245233
LOCUS       BD245233                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245233
VERSION     BD245233.1  GI:33055003
KEYWORDS    JP 2002532386-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 19 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/19
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 23;
  Best Local Similarity   90.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTT 2183
              ||  ||||||||||||||||
Db          4 CCAATTTTTTTTTTTTTTTT 23


RESULT 1516
BD245237
LOCUS       BD245237                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245237
VERSION     BD245237.1  GI:33055007
KEYWORDS    JP 2002532386-A/23.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
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  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: US 6596490-A 16 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||| | |||||||||
Db         20 TTTTTTTCACATTTTTTTTT 1


RESULT 1509
AR371269/c
LOCUS       AR371269                  20 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 5 from patent US 6395474.
ACCESSION   AR371269
VERSION     AR371269.1  GI:34608201
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 5 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTT 2183
              |||||||||||||| || ||
Db         20 CCTTTTTTTTTTTTCTTCTT 1


RESULT 1510
AX067205
LOCUS       AX067205                  20 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 57 from Patent WO0100669.
ACCESSION   AX067205
VERSION     AX067205.1  GI:12544870
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Barry,C., Bougueleret,L., Chumakov,I. and Cohen-Akenine,A.
  TITLE     A bap28 gene and protein
  JOURNAL   Patent: WO 0100669-A 57 04-JAN-2001;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide BAP28polyTcourt"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||| | ||
Db          1 TTTTTTTTTTTTTTTGTATA 20


RESULT 1511
AX441512/c
LOCUS       AX441512                  20 bp    DNA     linear   PAT 02-JUL-2002
DEFINITION  Sequence 16 from Patent WO0206531.
ACCESSION   AX441512
VERSION     AX441512.1  GI:21690473
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Dattagupta,N.
  TITLE     Nucleic acid hairpin probes and uses thereof
  JOURNAL   Patent: WO 0206531-A 16 24-JAN-2002;
            Applied Gene Technologies, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligo AGT02023"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||| | |||||||||
Db         20 TTTTTTTCACATTTTTTTTT 1


RESULT 1512
BD196314
LOCUS       BD196314                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Vertebrate telomerase genes and proteins and uses thereof.
ACCESSION   BD196314
VERSION     BD196314.1  GI:33006084
KEYWORDS    JP 2002514928-A/48.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kilian,A. and Bowtell,D.
  TITLE     Vertebrate telomerase genes and proteins and uses thereof
  JOURNAL   Patent: JP 2002514928-A 48 21-MAY-2002;
            CAMBIA BIOSYSTEMS LLC,PETER MACCALLUM CANCER INSTITUTE
COMMENT     OS   Artificial Sequence
            PN   JP 2002514928-A/48
            PD   21-MAY-2002
            PF   01-JUL-1998 JP 1999508771
            PR   01-JUL-1997 US    60/051410,21-JUL-1997 US    60/053018 PR
            21-JUL-1997 US    60/053329,04-AUG-1997 US    60/054642 PR
            09-SEP-1997 US    60/058287
            PI   ANDRZEJ KILIAN,DAVID BOWTELL
            PC   C12N15/54,C12N9/12,A61K38/45,C07K16/40,C12Q1/68,C12Q1/48, PC
            C12N15/11,
            PC   A61K31/70
            CC   Description of Artificial Sequence:Synthesized Amplification
            CC           Primer Design
            CC   based on EST Sequence GenBank Accession Number AA281296 FH
            Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
```

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              ||||||||||||  ||||||
Db          1 ATATTTATTTCATTTGTTTC 20


RESULT 1504
AR163839
LOCUS       AR163839                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 37 from patent US 6271030.
ACCESSION   AR163839
VERSION     AR163839.1  GI:16234618
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Butler,M.M. and Wyatt,J.
  TITLE     Antisense inhibition of C/EBP beta expression
  JOURNAL   Patent: US 6271030-A 37 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         47 GCGCGCGGCGGGGGCGGCGG 66
              ||| ||||||| ||||||||
Db          1 GCGGGCGGCGGCGGCGGCGG 20


RESULT 1505
E12411
LOCUS       E12411                   20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide.
ACCESSION   E12411
VERSION     E12411.1  GI:3251244
KEYWORDS    JP 1996332100-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okano,K. and Kanbara,H.
  TITLE     PRIMER FOR DNA POLYMERASE REACTION AND DETERMINATION OF
            POLYNUCLEOTIDE SEQUENCE USING THE SAME
  JOURNAL   Patent: JP 1996332100-A 1 17-DEC-1996;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996332100-A/1
            PD   17-DEC-1996
            PF   06-JUN-1995 JP 1995139051
            PI   OKANO KAZUNOBU, KANBARA HIDEKI
            PC   C12Q1/68,C07H21/04//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||| ||| |
Db          1 TTTTTTTTTTTTTAGCTTGG 20


RESULT 1506
AR359565
LOCUS       AR359565                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 158 from patent US 6593305.
ACCESSION   AR359565
VERSION     AR359565.1  GI:33766288
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A.
  TITLE     Antitumor antisense sequences directed against R1 and R2 components
            of ribonucleotide reductase
  JOURNAL   Patent: US 6593305-A 158 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2182
              ||| |||||||||| |||||
Db          1 TCCGTTTTTTTTTCTTTTT 20


RESULT 1507
AR360401/c
LOCUS       AR360401                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 16 from patent US 6596489.
ACCESSION   AR360401
VERSION     AR360401.1  GI:33767431
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N. and Tseng,T.-C.
  TITLE     Methods and compositions for analyzing nucleotide sequence
            mismatches using RNase H
  JOURNAL   Patent: US 6596489-A 16 22-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTT 2174
              |||||||| | |||||||||
Db         20 TTTTTTTCACATTTTTTTTT 1


RESULT 1508
AR360428/c
LOCUS       AR360428                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 16 from patent US 6596490.
ACCESSION   AR360428
VERSION     AR360428.1  GI:33767458
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dattagupta,N.
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  Query Match             0.6%;  Score 17;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 1499
AR068450/c
LOCUS       AR068450                  28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5853991.
ACCESSION   AR068450
VERSION     AR068450.1  GI:6000657
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA subtractive cloning method
  JOURNAL   Patent: US 5853991-A 14 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 1500
AR162868/c
LOCUS       AR162868                  29 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6258943.
ACCESSION   AR162868
VERSION     AR162868.1  GI:16230214
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Fong,T.Ming., Huang,R.-R.C. and Strader,C.D.
  TITLE     Human neurokinin-3 receptor
  JOURNAL   Patent: US 6258943-A 8 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAA 13


RESULT 1501
AR194018/c
LOCUS       AR194018                  29 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 8 from patent US 6349330.
ACCESSION   AR194018
VERSION     AR194018.1  GI:20240610
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Fong,T.Ming., Huang,R.-R.C. and Strader,C.D.
  TITLE     Method for measuring human neurokinin-3 receptor ligand binding
  JOURNAL   Patent: US 6348330-A 8 19-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAA 13


RESULT 1502
AR093063
LOCUS       AR093063                  20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 158 from patent US 5998383.
ACCESSION   AR093063
VERSION     AR093063.1  GI:10019815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A. and Young,A.H.
  TITLE     Antitumor antisense sequences directed against ribonucleotide
            reductase
  JOURNAL   Patent: US 5998383-A 158 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2182
              ||| |||||||||| |||||
Db          1 TCCGTTTTTTTTTCTTTTT 20


RESULT 1503
AR107647
LOCUS       AR107647                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 87 from patent US 6110664.
ACCESSION   AR107647
VERSION     AR107647.1  GI:12823134
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M.
  TITLE     Antisense inhibition of G-alpha-S1 expression
  JOURNAL   Patent: US 6110664-A 87 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 16.8;  DB 1;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.1e+03;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2264 ATATTTATTTCAGATGTTTC 2283
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REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 3537 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTAAC 2189
              ||||||| ||||  ||| ||| |||
Db         26 CTTTTTGTTTTGATTTGTTTCAAC 2


RESULT 1495
BD169479/c
LOCUS       BD169479                 26 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel guanosine triphosphate (GTP)-binding protein-coupled receptor
            protein, BG7.
ACCESSION   BD169479
VERSION     BD169479.1  GI:27875291
KEYWORDS    WO 0240669-A/30.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Maruyama,T., Nakamura,T., Itadani,H. and Tanaka,K.
  TITLE     Novel guanosine triphosphate (GTP)-binding protein-coupled receptor
            protein, BG7
  JOURNAL   Patent: WO 0240669-A 30 23-MAY-2002;
            BANYU PHARMACEUTICAL CO LTD,TAKAHARU MARUYAMA,TAKAO NAKAMURA,
            HIRAKU ITADANI,KENICHI TANAKA
COMMENT     OS   Artificial Sequence
            PN   WO 0240669-A/30
            PD   23-MAY-2002
            PF   30-OCT-2001 WO 2001JP009512
            PR   17-NOV-2000 JP 00P   351741,15-FEB-2001 JP 01P   038619 PR
            16-MAR-2001 JP 01P   077000
            PI   TAKAHARU MARUYAMA,TAKAO NAKAMURA,HIRAKU ITADANI,KENICHI TANAKA
            PC   C12N15/12,C12N1/21,C12N5/10,C07K14/705,C07K16/28,C12P21/02, PC
              C12Q1/02,
            PC   A61K45/00,A61P1/00,A61P7/00,A61P9/00,A61P11/00,A61P13/00, PC
            A61P21/00,
            PC   A61P29/00,A61P43/00,G01N33/15,G01N33/50,G01N33/53 CC
            Description of Artificial Sequence:Artificially Synthesized CC
            Primer Sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        354 CCTACCAGCAGCTGGCCTACTCCCA 378
              ||||| |  |||||| |||||| ||
Db         25 CCTACTACTAGCTGGGCTACTCACA 1


RESULT 1496
AR055108/c
LOCUS       AR055108                 28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5837468.
ACCESSION   AR055108
VERSION     AR055108.1  GI:5980685
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA substractive cloning method
  JOURNAL   Patent: US 5837468-A 13 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 1497
AR055109/c
LOCUS       AR055109                 28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5837468.
ACCESSION   AR055109
VERSION     AR055109.1  GI:5980686
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA substractive cloning method
  JOURNAL   Patent: US 5837468-A 14 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAA 11


RESULT 1498
AR068449/c
LOCUS       AR068449                 28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5853991.
ACCESSION   AR068449
VERSION     AR068449.1  GI:6000656
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA subtractive cloning method
  JOURNAL   Patent: US 5853991-A 13 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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VERSION     I18346.1  GI:1598701
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.
  TITLE     Genetically engineering cotton plants for altered fiber
  JOURNAL   Patent: US 5495070-A 1 27-FEB-1996;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         10 CCTTTTTTTTTTTTTT 26


RESULT 1490
I21333
LOCUS       I21333                    26 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5521078.
ACCESSION   I21333
VERSION     I21333.1  GI:1601687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.
  TITLE     Genetically engineering cotton plants for altered fiber
  JOURNAL   Patent: US 5521078-A 1 28-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         10 CCTTTTTTTTTTTTTT 26


RESULT 1491
I35739
LOCUS       I35739                    26 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5602321.
ACCESSION   I35739
VERSION     I35739.1  GI:2087590
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.
  TITLE     Transgenic cotton plants producing heterologous polyhydroxy(e)
            butyrate bioplastic
  JOURNAL   Patent: US 5602321-A 1 11-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         10 CCTTTTTTTTTTTTTT 26


RESULT 1492
I36757
LOCUS       I36757                    26 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5608148.
ACCESSION   I36757
VERSION     I36757.1  GI:2086582
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.E.
  TITLE     Transgenic cotton plants producing heterologous peroxidase
  JOURNAL   Patent: US 5608148-A 1 04-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         10 CCTTTTTTTTTTTTTT 26


RESULT 1493
I40322
LOCUS       I40322                    26 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5620882.
ACCESSION   I40322
VERSION     I40322.1  GI:2082614
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.
  TITLE     Genetically engineering cotton plants for altered fiber
  JOURNAL   Patent: US 5620882-A 1 15-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         10 CCTTTTTTTTTTTTTT 26


RESULT 1494
AX118414/c
LOCUS       AX118414                  26 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 3537 from Patent WO0129262.
ACCESSION   AX118414
VERSION     AX118414.1  GI:14035365
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
```

```
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="exon No. 2 - 3' end of the exon-intron boundary of
                     human MLT gene"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTA 17


RESULT 1485
AR034927
LOCUS       AR034927                  26 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5869720.
ACCESSION   AR034927
VERSION     AR034927.1  GI:5950532
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.E.
  TITLE     Transgenic cotton plants producing heterologous peroxidase
  JOURNAL   Patent: US 5869720-A 1 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db         10 CCTTTTTTTTTTTTTTT 26


RESULT 1486
AR078461/c
LOCUS       AR078461                  26 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5962664.
ACCESSION   AR078461
VERSION     AR078461.1  GI:10005207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Friedhoff,A.J., Basham,D.A. and Miller,J.C.
  TITLE     Psychosis protecting nucleic acid, peptides, compositions and
            method of use
  JOURNAL   Patent: US 5962664-A 1 05-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 1487
AR145386
LOCUS       AR145386                  26 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 10 from patent US 6211430.
ACCESSION   AR145386
VERSION     AR145386.1  GI:15107253
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   John,M.E.
  TITLE     FbLate promoter
  JOURNAL   Patent: US 6211430-A 10 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db         10 CCTTTTTTTTTTTTTTT 26


RESULT 1488
E31574/c
LOCUS       E31574                    26 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for preparing DNA sample and reagent.
ACCESSION   E31574
VERSION     E31574.1  GI:13018517
KEYWORDS    JP 1999341986-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kazunori,O., Hideki,K., Tim,C.R. and Michal,A.L.
  TITLE     Method for preparing DNA sample and reagent
  JOURNAL   Patent: JP 1999341986-A 10 14-DEC-1999;
            HITACHI LTD,NYCOMED AMERSHAM PLC
COMMENT     OS   Unidentified
            PN   JP 1999341986-A/10
            PD   14-DEC-1999
            PF   02-JUN-1998 JP 1998152598
            PR
            PI   KAZUNORI OKANO,HIDEKI KAMIBARA,TIM C RICHADSON,MICHAL A LIBU
            PC   C12N15/09,C12Q1/68,G01N33/50,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              |||||||||||||||||
Db         22 TGAAAAAAAAAAAAAAA 6


RESULT 1489
I18346
LOCUS       I18346                    26 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5495070.
ACCESSION   I18346
```

```
     misc_feature    1. .25
                     /note="T-DNA flanking sequence
                     left border"

  Query Match              0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         22 GAAAAAAAAAAAAAAAA 6


RESULT 1480
AR010003/c
LOCUS       AR010003                  26 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 15 from patent US 5756684.
ACCESSION   AR010003
VERSION     AR010003.1  GI:3968808
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Johnson,E.M. and Bergemann,A.D.
  TITLE     Cloning and expression of PUR protein
  JOURNAL   Patent: US 5756684-A 15 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAA 10


RESULT 1481
AR034738/c
LOCUS       AR034738                  26 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5869622.
ACCESSION   AR034738
VERSION     AR034738.1  GI:5950343
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Johnson,E.M. and Bergemann,A.D.
  TITLE     Monoclonal antibodies to the pur protein
  JOURNAL   Patent: US 5869622-A 15 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAA 10


RESULT 1482
I24758/c
LOCUS       I24758                    26 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 21 from patent US 5545551.
ACCESSION   I24758
VERSION     I24758.1  GI:1604628
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Johnson,E.M. and Bergmann,A.D.
  TITLE     Cloning and expression of pur protein
  JOURNAL   Patent: US 5545551-A 21 13-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAA 10


RESULT 1483
AR050239/c
LOCUS       AR050239                  26 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5827518.
ACCESSION   AR050239
VERSION     AR050239.1  GI:5972964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Webb,B.Allen. and Cui,L.
  TITLE     Viral and insect genes that inhibit the immune system and methods
            of use thereof
  JOURNAL   Patent: US 5827518-A 8 27-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAA 10


RESULT 1484
AX055876
LOCUS       AX055876                  26 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 12 from Patent WO0073500.
ACCESSION   AX055876
VERSION     AX055876.1  GI:12228983
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baens,M., Marynen,P. and Dierlamm,J.
  TITLE     Molecular characterisation of chromosome translocation
            t(11;18)(q21;q21) and its correlation to carcinogenesis
  JOURNAL   Patent: WO 0073500-A 12 07-DEC-2000;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Homo sapiens"
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5560 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          2 CTTTTTTTTTTTTTTT 18


RESULT 1477
AX692829
LOCUS       AX692829                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5561 from Patent EP1281758.
ACCESSION   AX692829
VERSION     AX692829.1  GI:29415792
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5561 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTT 2181
              ||||||||||||||||
Db          1 CTTTTTTTTTTTTTTT 17


RESULT 1478
BD075857/c
LOCUS       BD075857                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Standardized nucleic acid library and method of constructing the
            same.
ACCESSION   BD075857
VERSION     BD075857.1  GI:22621460
KEYWORDS    JP 2001517460-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Li,W.B., Jessee,J. and Nisson,P.E.
  TITLE     Standardized nucleic acid library and method of constructing the
  JOURNAL   Patent: JP 2001517460-A 2 09-OCT-2001;
            LIFE TECHNOLOGIES INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001517460-A/2
            PD   09-OCT-2001
            PF   24-SEP-1998 JP 2000512989
            PR   24-SEP-1997 US    60/059817,23-SEP-1998 US    09/159496 PI
            WU BO LI,JOEL JESSEE,PAUL E NISSON
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P19/34 PC
            ,C12Q1/68,C12N15/00,
            PC   C12N5/00
            CC   Description of artificial sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTT 2180
              ||||||||||||||||
Db         17 CCTTTTTTTTTTTTTT 1


RESULT 1479
AJ595474/c
LOCUS       AJ595474                  25 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            417E08.
ACCESSION   AJ595474
VERSION     AJ595474.1  GI:37945102
KEYWORDS    left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 25)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="417E08"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
```

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  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAA 2798
              ||| | | ||||  ||||||||||
Db          1 TTGATCGCATTGTCAAAAAAAAAAA 25


RESULT 1472
AX494261
LOCUS       AX494261                  25 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 26 from Patent WO02059256.
ACCESSION   AX494261
VERSION     AX494261.1  GI:23339871
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 26 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAA 2798
              ||| | | ||||  ||||||||||
Db          1 TTGATCGCATTGTCAAAAAAAAAAA 25


RESULT 1473
AX494264
LOCUS       AX494264                  25 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 29 from Patent WO02059256.
ACCESSION   AX494264
VERSION     AX494264.1  GI:23339874
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 29 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAA 2798
              ||| | | ||||  ||||||||||
Db          1 TTGATCGCATTGTCAAAAAAAAAAA 25


RESULT 1474
AX547804
LOCUS       AX547804                  25 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 943 from Patent WO02053141.
ACCESSION   AX547804
VERSION     AX547804.1  GI:25812948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 943 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          9 TTTTTTTTTTTTTTTTT 25


RESULT 1475
AX547804/c
LOCUS       AX547804                  25 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 943 from Patent WO02053141.
ACCESSION   AX547804
VERSION     AX547804.1  GI:25812948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 943 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAA 9


RESULT 1476
AX692828
LOCUS       AX692828                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5560 from Patent EP1281758.
ACCESSION   AX692828
VERSION     AX692828.1  GI:29415791
KEYWORDS    .
SOURCE      Homo sapiens (human)
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DEFINITION  Sequence 943 from Patent WO0122972.
ACCESSION   AX104751
VERSION     AX104751.1  GI:13920948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 943 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAA 9


RESULT 1468
AX117632/c
LOCUS       AX117632                25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 2755 from Patent WO0129262.
ACCESSION   AX117632
VERSION     AX117632.1  GI:14034583
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 2755 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||
Db         24 TTTTTTTTTTTTTTTAA 8


RESULT 1469
AX166683/c
LOCUS       AX166683                25 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 174 from Patent WO0138503.
ACCESSION   AX166683
VERSION     AX166683.1  GI:14546958
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
            Flanagan,P. and Clary,D.S.
  TITLE     Novel human protein kinases and protein kinase-like enzymes
  JOURNAL   Patent: WO 0138503-A 174 31-MAY-2001;
            Sugen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1786 CCCATTCTTTCCTTCTC 1802
              |||||||||||||||||
Db         19 CCCATTCTTTCCTTCTC 3


RESULT 1470
AX320851
LOCUS       AX320851                25 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 21 from Patent WO0183736.
ACCESSION   AX320851
VERSION     AX320851.1  GI:17902402
KEYWORDS    .
SOURCE      Hepatitis C virus
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1
  AUTHORS   Pellerin,C. and Kukolj,G.
  TITLE     Internal de novo initiation sites of the hcv ns5b polymerase and
            use thereof
  JOURNAL   Patent: WO 0183736-A 21 08-NOV-2001;
            BOEHRINGER INGELHEIM (CANADA) LTD. (CA)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Hepatitis C virus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:11103"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACTTT 2192
              |||||||||||| |||    ||||
Db          1 TTTTTTTTTTTTTCTTTCCTTCTTT 25


RESULT 1471
AX494260
LOCUS       AX494260                25 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 25 from Patent WO02059256.
ACCESSION   AX494260
VERSION     AX494260.1  GI:23339870
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 25 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1217 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||||||||  | | ||  |||
Db          1 TTTTTTTTTTTTTCAATCTGTGAGT 25


RESULT 1463
AX043651/c
LOCUS       AX043651                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1217 from Patent WO0065088.
ACCESSION   AX043651
VERSION     AX043651.1  GI:11342266
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1217 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2798
              |||||||||||||||||
Db         17 ATTGAAAAAAAAAAAAA 1


RESULT 1464
AX043680/c
LOCUS       AX043680                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1246 from Patent WO0065088.
ACCESSION   AX043680
VERSION     AX043680.1  GI:11342295
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1246 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAA 2797
              |||  | | | |||||||||||||
Db         25 CTTCATCGCAGTGAAAAAAAAAAAA 1


RESULT 1465
AX043693
LOCUS       AX043693                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1259 from Patent WO0065088.
ACCESSION   AX043693
VERSION     AX043693.1  GI:11342308
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1259 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              |||||||||||||| |||  |  ||
Db          1 TTTTTTTTTTTTTTCACTCGGTCAG 25


RESULT 1466
AX104751
LOCUS       AX104751                  25 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 943 from Patent WO0122972.
ACCESSION   AX104751
VERSION     AX104751.1  GI:13920948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 943 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          9 TTTTTTTTTTTTTTTTT 25


RESULT 1467
AX104751/c
LOCUS       AX104751                  25 bp    DNA     linear   PAT 30-APR-2001
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  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAA 2797
              ||  | ||| || ||||||||||||
Db         25 CTGATGAGATTTAAAAAAAAAAAAA 1


RESULT 1458
AX043296/c
LOCUS       AX043296                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 862 from Patent WO0065088.
ACCESSION   AX043296
VERSION     AX043296.1  GI:11341904
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 862 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              ||||  ||  || ||||||||||||
Db         25 AGAAGGGAGGAAGAAAAAAAAAAAA 1


RESULT 1459
AX043461/c
LOCUS       AX043461                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1027 from Patent WO0065088.
ACCESSION   AX043461
VERSION     AX043461.1  GI:11342069
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1027 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB345 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAA 2797
              |||||||||||||||||
Db         17 AATTGAAAAAAAAAAAA 1


RESULT 1460
AX043487
LOCUS       AX043487                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1053 from Patent WO0065088.
ACCESSION   AX043487
VERSION     AX043487.1  GI:11342095
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1053 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||||||||| | | ||  |||
Db          1 TTTTTTTTTTTTTCAGTCTGTGAGT 25


RESULT 1461
AX043647
LOCUS       AX043647                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1213 from Patent WO0065088.
ACCESSION   AX043647
VERSION     AX043647.1  GI:11342262
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1213 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAGTT 2199
              |||||||||||||  | || ||| |
Db          1 TTTTTTTTTTTTACTTCTGGAAGGT 25


RESULT 1462
AX043651
LOCUS       AX043651                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1217 from Patent WO0065088.
ACCESSION   AX043651
VERSION     AX043651.1  GI:11342266
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
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RESULT 1453
AX043060
LOCUS       AX043060                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 626 from Patent WO0065088.
ACCESSION   AX043060
VERSION     AX043060.1  GI:11341668
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 626 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||  |  | ||||||
Db          1 TTTTTTTTTTTTTCGAGATGTGAAAG 25


RESULT 1454
AX043082/c
LOCUS       AX043082                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 648 from Patent WO0065088.
ACCESSION   AX043082
VERSION     AX043082.1  GI:11341690
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 648 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              | ||| |   ||||||||||||||||
Db         25 ACAATGGGGGAAAAAAAAAAAAAAA 1


RESULT 1455
AX043206
LOCUS       AX043206                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 772 from Patent WO0065088.
ACCESSION   AX043206
VERSION     AX043206.1  GI:11341814
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 772 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACT 2190
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTAACT 17


RESULT 1456
AX043237/c
LOCUS       AX043237                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 803 from Patent WO0065088.
ACCESSION   AX043237
VERSION     AX043237.1  GI:11341845
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 803 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAA 2797
              ||| || ||   ||||||||||||
Db         25 CTTCTTGGAGGGGAAAAAAAAAAAA 1


RESULT 1457
AX043292/c
LOCUS       AX043292                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 858 from Patent WO0065088.
ACCESSION   AX043292
VERSION     AX043292.1  GI:11341900
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 858 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"
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  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 600 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTAAC 17


RESULT 1449
AX043034/c
LOCUS       AX043034                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 600 from Patent WO0065088.
ACCESSION   AX043034
VERSION     AX043034.1  GI:11341642
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 600 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAA 2798
              ||||  |  ||  ||||||||||||
Db         25 TTGTATGTGTTAAAAAAAAAAAAA 1


RESULT 1450
AX043035
LOCUS       AX043035                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 601 from Patent WO0065088.
ACCESSION   AX043035
VERSION     AX043035.1  GI:11341643
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 601 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||| || | || | |
Db          1 TTTTTTTTTTTTGTTGTGAAATGT 25


RESULT 1451
AX043035/c
LOCUS       AX043035                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 601 from Patent WO0065088.
ACCESSION   AX043035
VERSION     AX043035.1  GI:11341643
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 601 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2803
              | |  || | ||  ||||||||||||||
Db         25 ACATTTCACAACAAAAAAAAAAAAA 1


RESULT 1452
AX043045
LOCUS       AX043045                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 611 from Patent WO0065088.
ACCESSION   AX043045
VERSION     AX043045.1  GI:11341653
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 611 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTAAC 17
```

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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-A Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAA 2798
              |||||||||||||||||
Db         17 ATTGAAAAAAAAAAAAA 1


RESULT 1444
AX042825/c
LOCUS       AX042825                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 391 from Patent WO0065088.
ACCESSION   AX042825
VERSION     AX042825.1  GI:11341433
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 391 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAA 2800
              | | || | | |||||||||||||||
Db         25 GGTGGACTGGGAAAAAAAAAAAAAA 1


RESULT 1445
AX042938
LOCUS       AX042938                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 504 from Patent WO0065088.
ACCESSION   AX042938
VERSION     AX042938.1  GI:11341546
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 504 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAGTT 2199
              ||||||||||||  |||| | || |
Db          1 TTTTTTTTTTTTGGCTTTCAGAGAT 25


RESULT 1446
AX042984
LOCUS       AX042984                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 550 from Patent WO0065088.
ACCESSION   AX042984
VERSION     AX042984.1  GI:11341592
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 550 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              |||||||||||||| | |  | |||
Db          1 TTTTTTTTTTTTTTCAGTGAGGAAG 25


RESULT 1447
AX043019
LOCUS       AX043019                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 585 from Patent WO0065088.
ACCESSION   AX043019
VERSION     AX043019.1  GI:11341627
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 585 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTT 2191
              |||||||||||||||||
Db          1 TTTTTTTTTTTTAACTT 17


RESULT 1448
AX043034
LOCUS       AX043034                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 600 from Patent WO0065088.
ACCESSION   AX043034
VERSION     AX043034.1  GI:11341642
KEYWORDS    .
SOURCE      synthetic construct
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Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAA 2797
              ||  | ||| || ||||||||||||
Db         25 CTGATGAGATTTAAAAAAAAAAAAA 1


RESULT 1439
AX042652
LOCUS       AX042652                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 218 from Patent WO0065088.
ACCESSION   AX042652
VERSION     AX042652.1  GI:11341260
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 218 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB1 Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||||||  | |||  ||
Db          1 TTTTTTTTTTTTTACGTCTGAGTGT 25


RESULT 1440
AX042684
LOCUS       AX042684                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 250 from Patent WO0065088.
ACCESSION   AX042684
VERSION     AX042684.1  GI:11341292
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 250 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-A Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||||| | | ||  |||
Db          1 TTTTTTTTTTTTTCAGTCTGTGAGT 25


RESULT 1441
AX042691/c
LOCUS       AX042691                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 257 from Patent WO0065088.
ACCESSION   AX042691
VERSION     AX042691.1  GI:11341299
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 257 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-A Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              ||  || | ||| ||||||||||||
Db         25 GATGTGGAGAAATAAAAAAAAAAAA 1


RESULT 1442
AX042718
LOCUS       AX042718                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 284 from Patent WO0065088.
ACCESSION   AX042718
VERSION     AX042718.1  GI:11341326
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 284 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-A Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||||| | | ||  |||
Db          1 TTTTTTTTTTTTTCAATCTGTGAGT 25


RESULT 1443
AX042718/c
LOCUS       AX042718                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 284 from Patent WO0065088.
ACCESSION   AX042718
VERSION     AX042718.1  GI:11341326
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 284 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
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  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db          9 CCTTTTTTTTTTTTTTT 25


RESULT 1434
AR211579/c
LOCUS       AR211579                  25 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 2 from patent US 6399334.
ACCESSION   AR211579
VERSION     AR211579.1  GI:21514938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Li,W.-B., Nisson,P.E. and Jessee,J.
  TITLE     Normalized nucleic acid libraries and methods of production thereof
  JOURNAL   Patent: US 6399334-A 2 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db         17 CCTTTTTTTTTTTTTTT 1


RESULT 1435
AR434873/c
LOCUS       AR434873                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1296 from patent US 6656700.
ACCESSION   AR434873
VERSION     AR434873.1  GI:40197716
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1296 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1770 CTTTTTTTTTTGAACCCCATTCTT 1794
              |||| |||||||   |||| |||||
Db         25 CTTTCTTTTTTTTCCCCCCTTCTT 1


RESULT 1436
AR435380
LOCUS       AR435380                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1803 from patent US 6656700.
ACCESSION   AR435380
VERSION     AR435380.1  GI:40198223
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1803 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2311 AGCAATTTGTTGCTGCTTGTCACCC 2335
              ||| | |||||||||||||||   ||
Db          1 AGCCAGTTGTTGCTGCTTGTGTTCC 25


RESULT 1437
AR435381
LOCUS       AR435381                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1804 from patent US 6656700.
ACCESSION   AR435381
VERSION     AR435381.1  GI:40198224
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1804 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2312 GCAATTTGTTGCTGCTTGTCACCCC 2336
              || | |||||||||||||   |||
Db          1 GCCAGTTGTTGCTGCTTGTGTTCCC 25


RESULT 1438
AX042591/c
LOCUS       AX042591                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 157 from Patent WO0065088.
ACCESSION   AX042591
VERSION     AX042591.1  GI:11341199
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 157 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
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Db          3 TNGNAAAAAAAAAAAAAAA 21


RESULT 1429
AX496104/c
LOCUS       AX496104                  23 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1869 from Patent WO02059256.
ACCESSION   AX496104
VERSION     AX496104.1  GI:23341714
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 1869 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTT 2180
              |||||||||||||||||
Db         23 CCTTTTTTTTTTTTTTT 7


RESULT 1430
I33155
LOCUS       I33155                    24 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 9 from patent US 5589622.
ACCESSION   I33155
VERSION     I33155.1  GI:1823946
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Gurr,S.J., McPherson,M.J., Atkinson,H.J. and Bowles,D.J.
  TITLE     Plant parasitic nematode control
  JOURNAL   Patent: US 5589622-A 9 31-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTT 2181
              |||||||||||||||||
Db          8 CTTTTTTTTTTTTTTTT 24


RESULT 1431
AX043282/c
LOCUS       AX043282                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 848 from Patent WO0065088.
ACCESSION   AX043282
VERSION     AX043282.1  GI:11341890
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 848 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAA 2800
              | |  |||  ||||||||||||||||
Db         25 GGTCAAATCTAAAAAAAAAAAAAAA 1


RESULT 1432
AX043152
LOCUS       AX043152                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 718 from Patent WO0065088.
ACCESSION   AX043152
VERSION     AX043152.1  GI:11341760
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 718 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              |||||||||||||||| | |   ||
Db          1 TTTTTTTTTTTTTTAAGTGTACCAG 25


RESULT 1433
I56670
LOCUS       I56670                    25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5650279.
ACCESSION   I56670
VERSION     I56670.1  GI:2477083
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Nagpal,S. and Chandraratna,R.A.
  TITLE     Gene sequence induced in skin by retinoids
  JOURNAL   Patent: US 5650279-A 1 22-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 25;
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          PR   02-JUN-2000 JP 00P   170436
          PI   MASAKO MIZUTANI,KEIKO SAKAKIBARA,YOSHIKAZU TANAKA,TAKAAKI  PI
           KUSUMI,
          PI   EIICHIRO ONO
          PC   C12N15/09,C12N15/29,C12N15/54,C12N1/15,C12N1/19,C12N1/21 PC
          ,C12N5/10,C12N9/10,
          PC   A01H5/00
          CC   Primer
          FH   Key             Location/Qualifiers
          FT   source          1. .23
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 1426
BD245234
LOCUS       BD245234                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245234
VERSION     BD245234.1  GI:33055004
KEYWORDS    JP 2002532386-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 20 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/20
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db          7 GAAAAAAAAAAAAAAAA 23


RESULT 1427
BD245241
LOCUS       BD245241                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245241
VERSION     BD245241.1  GI:33055011
KEYWORDS    JP 2002532386-A/27.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 27 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/27
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTT 2181
              |||||||||||||||||
Db          7 CTTTTTTTTTTTTTTTT 23


RESULT 1428
AX496104
LOCUS       AX496104                  23 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1869 from Patent WO02059256.
ACCESSION   AX496104
VERSION     AX496104.1  GI:23341714
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 1869 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              | | |||||||||||||||
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DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245245
VERSION     BD245245.1  GI:33055015
KEYWORDS    JP 2002532386-A/31.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 31 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/31
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .23
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 1422
AR084981/c
LOCUS       AR084981                  23 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 15 from patent US 5981251.
ACCESSION   AR084981
VERSION     AR084981.1  GI:10011752
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Ullrich,A. and Vogel,W.
  TITLE     PTP 1D: a novel protein tyrosine phosphatase
  JOURNAL   Patent: US 5981251-A 15 09-NOV-1999;
FEATURES            Location/Qualifiers
     source         1. .23
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 1423
I32906/c
LOCUS       I32906                    23 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 15 from patent US 5589375.
ACCESSION   I32906
VERSION     I32906.1  GI:1823697
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Ullrich,A. and Vogel,W.
  TITLE     PTP 1D: a novel protein tyrosine phosphatase
  JOURNAL   Patent: US 5589375-A 15 31-DEC-1996;
FEATURES            Location/Qualifiers
     source         1. .23
                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 1424
AR306617/c
LOCUS       AR306617                  23 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 15 from patent US 6548641.
ACCESSION   AR306617
VERSION     AR306617.1  GI:31696809
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Ullrich,A. and Vogel,W.
  TITLE     PTP 1D: a novel protein tyrosine phosphatase
  JOURNAL   Patent: US 6548641-A 15 15-APR-2003;
FEATURES            Location/Qualifiers
     source         1. .23
                    /organism="unknown"
                    /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAA 7


RESULT 1425
BD105197/c
LOCUS       BD105197                  23 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel glucosyltransferase gene.
ACCESSION   BD105197
VERSION     BD105197.1  GI:22650771
KEYWORDS    WO 0192509-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Mizutani,M., Sakakibara,K., Tanaka,Y., Kusumi,T. and Ono,E.
  TITLE     Novel glucosyltransferase gene
  JOURNAL   Patent: WO 0192509-A 3 06-DEC-2001;
            INTERNATIONAL FLOWER DEVELOPMENTS PROPRIETARY LTD,MASAKO MIZUTANI,
            KEIKO SAKAKIBARA,YOSHIKAZU TANAKA,TAKAAKI KUSUMI,EIICHIRO ONO
COMMENT     OS   Artificial Sequence
            PN   WO 0192509-A/3
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004675
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  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          4 TTTTTTTTTTTTTTTT 20


RESULT 1418
BD161924/c
LOCUS       BD161924                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate.
ACCESSION   BD161924
VERSION     BD161924.1  GI:27867682
KEYWORDS    JP 2002191369-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
  TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate
  JOURNAL   Patent: JP 2002191369-A 1 09-JUL-2002;
            TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   JP 2002191369-A/1
            PD   09-JUL-2002
            PF   27-DEC-2000 JP 2000399573
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
            C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC   Method for
            carrying out thermal cycle of PCR using DNA- CC
            immobilized
            CC   substrate
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAA 2802
              ||||||||||||||||
Db         20 AAAAAAAAAAAAAAAA 4


RESULT 1419
BD244863/c
LOCUS       BD244863                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
ACCESSION   BD244863
VERSION     BD244863.1  GI:33054633
KEYWORDS    JP 2002532063-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 8 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/8
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            CC   N = 3-Nitropyrrole
            CC   N = 3-Nitropyrrole
            FH   Key             Location/Qualifiers
            FT   modified_base   (8)
            FT   modified_base   (18).
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||| |||
Db         23 AAAAANAAAAAAAAANAAA 5


RESULT 1420
BD244865/c
LOCUS       BD244865                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
ACCESSION   BD244865
VERSION     BD244865.1  GI:33054635
KEYWORDS    JP 2002532063-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 10 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/10
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            CC   N - inosine
            CC   N = inosine
            FH   Key             Location/Qualifiers
            FT   modified_base   (8)
            FT   modified_base   (18).
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 23;
  Best Local Similarity   89.5%;  Pred. No. 1.5e+03;
  Matches   17;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||| |||
Db         23 AAAAANAAAAAAAAANAAA 5


RESULT 1421
BD245245/c
LOCUS       BD245245                  23 bp    DNA     linear   PAT 17-JUL-2003
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```
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 18 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Double-stranded
                     product DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 1414
AR030917/c
LOCUS       AR030917                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 20 from patent US 5861487.
ACCESSION   AR030917
VERSION     AR030917.1  GI:5944131
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Holton,T.Albert., Cornish,E.Cecily., Kovacic,F., Tanaka,Y. and
            Lester,D.Ruth.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: US 5861487-A 20 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1415
I28309/c
LOCUS       I28309                    20 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 20 from patent US 5569832.
ACCESSION   I28309
VERSION     I28309.1  GI:1819085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: US 5569832-A 20 29-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1416
I47310/c
LOCUS       I47310                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 11 from patent US 5639870.
ACCESSION   I47310
VERSION     I47310.1  GI:2471275
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Holton,T.Albert., Cornish,E.Cecily. and Tanaka,Y.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: US 5639870-A 11 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1417
BD161924
LOCUS       BD161924                  20 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate.
ACCESSION   BD161924
VERSION     BD161924.1  GI:27867682
KEYWORDS    JP 2002191369-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
  TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate
  JOURNAL   Patent: JP 2002191369-A 1 09-JUL-2002;
            TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   JP 2002191369-A/1
            PD   09-JUL-2002
            PF   27-DEC-2000 JP 2000399573
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
            C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC   Method for
            carrying out thermal cycle of PCR using DNA- CC
            immobilized
            CC   substrate
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
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VERSION     E32458.1  GI:13018694
KEYWORDS    JP 2000037190-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 18 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/18
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAA 2800
              |||||||||||||||||
Db         18 TGAAAAAAAAAAAAAAA 2


RESULT 1410
AX028845
LOCUS       AX028845                 18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 29 from Patent WO9732023.
ACCESSION   AX028845
VERSION     AX028845.1  GI:10189948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 29 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Oligonucleotide"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 1411
AX028845/c
LOCUS       AX028845                 18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 29 from Patent WO9732023.
ACCESSION   AX028845
VERSION     AX028845.1  GI:10189948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 29 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Oligonucleotide"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1412
AX361600/c
LOCUS       AX361600                 18 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 18 from Patent WO0208461.
ACCESSION   AX361600
VERSION     AX361600.1  GI:18694219
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
  TITLE     A method and an algorithm for mrna expression analysis
  JOURNAL   Patent: WO 0208461-A 18 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES              Location/Qualifiers
     source           1. .18
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Double-stranded product DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 1413
AX814932/c
LOCUS       AX814932                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 18 from Patent WO03064691.
ACCESSION   AX814932
VERSION     AX814932.1  GI:39104070
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 27 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1406
AX028844
LOCUS       AX028844                 18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 28 from Patent WO9732023.
ACCESSION   AX028844
VERSION     AX028844.1  GI:10189947
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 28 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTT 17


RESULT 1407
BD190553/c
LOCUS       BD190553                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Secretory proteins and polynucleotides encoding the same.
ACCESSION   BD190553
VERSION     BD190553.1  GI:33000292
KEYWORDS    JP 2002515753-A/12.
SOURCE      Rattus
  ORGANISM  Rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secretory proteins and polynucleotides encoding the same
  JOURNAL   Patent: JP 2002515753-A 12 28-MAY-2002;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2002515753-A/12
            PD   28-MAY-2002
            PF   31-OCT-1997 JP 1998521609
            PR   01-NOV-1996 US     08/724973
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
              DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
            Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Rattus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10114"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTT 2182
              ||||||||||||||||
Db         18 TTTTTTTTTTTTTTTT 2


RESULT 1408
E32456
LOCUS       E32456                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32456
VERSION     E32456.1  GI:13018692
KEYWORDS    JP 2000037190-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jun,N., Yusuke,N. and Toshihiro,T.
  TITLE     Mammal-derived tissue specific physiologically active protein
  JOURNAL   Patent: JP 2000037190-A 16 08-FEB-2000;
            JAPAN TOBACCO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000037190-A/16
            PD   08-FEB-2000
            PF   23-JUL-1998 JP 1998225228
            PR
            PI   JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
            PC   C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
            C12N15/02,
            PC   C12P21/02,C12P21/08//(C12N5/10,C12R1:91),(C12P21/08,C12R1:91),
            PC   C12N15/00,
            PC   C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   primer_bind     (1). .(18).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 7.8e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAA 2188
              ||||||||||||||||
Db          2 TTTTTTTTTTTTTTAA 18


RESULT 1409
E32458/c
LOCUS       E32458                   18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Mammal-derived tissue specific physiologically active protein.
ACCESSION   E32458
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Qy       1767 AAGCTTTTTTTTTTTGA 1783
              |||||||||||||||||
Db          1 AAGCTTTTTTTTTTTGA 17


RESULT 1401
AX361606/c
LOCUS       AX361606                  17 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 24 from Patent WO0208461.
ACCESSION   AX361606
VERSION     AX361606.1  GI:18694225
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
  TITLE     A method and an algorithm for mrna expression analysis
  JOURNAL   Patent: WO 0208461-A 24 31-JAN-2002;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Double-stranded product DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 1402
AX692525
LOCUS       AX692525                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5257 from Patent EP1281758.
ACCESSION   AX692525
VERSION     AX692525.1  GI:29415483
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5257 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTT 2181
              |||||||||||||||||
Db          1 CTTTTTTTTTTTTTTTT 17


RESULT 1403
AX762112
LOCUS       AX762112                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 5433 from Patent WO03040369.
ACCESSION   AX762112
VERSION     AX762112.1  GI:32256728
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 5433 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2460 GATCCAATTTTAATATT 2476
              |||||||||||||||||
Db          1 GATCCAATTTTAATATT 17


RESULT 1404
AX814938/c
LOCUS       AX814938                  17 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 24 from Patent WO03064691.
ACCESSION   AX814938
VERSION     AX814938.1  GI:39104076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 24 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Double-stranded
                     product DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 1405
AX028843/c
LOCUS       AX028843                  18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 27 from Patent WO9732023.
ACCESSION   AX028843
VERSION     AX028843.1  GI:10189946
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
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                  ||||||||||||||||||
Db          17 TTTTTTTTTTTTTTTTT 1


RESULT 1396
AR236087
LOCUS       AR236087                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6462184.
ACCESSION   AR236087
VERSION     AR236087.1  GI:27279786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6462184-A 5 08-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
                  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 1397
AR236087/c
LOCUS       AR236087                  17 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6462184.
ACCESSION   AR236087
VERSION     AR236087.1  GI:27279786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6462184-A 5 08-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
                  ||||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1398
AR323672
LOCUS       AR323672                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1074 from patent US 6566127.
ACCESSION   AR323672
VERSION     AR323672.1  GI:33709480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTT 2181
                  ||||||||||||||||||
Db          1 CTTTTTTTTTTTTTTTT 17


RESULT 1399
AR323673/c
LOCUS       AR323673                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1075 from patent US 6566127.
ACCESSION   AR323673
VERSION     AR323673.1  GI:33709481
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 1075 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
                  ||||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 1400
AX146682
LOCUS       AX146682                  17 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 24 from Patent WO0134834.
ACCESSION   AX146682
VERSION     AX146682.1  GI:14285075
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Leffers,H., Jorgensen,M. and skakkeb K,N.E.
  TITLE     Endogenous gene expression assay
  JOURNAL   Patent: WO 0134834-A 24 17-MAY-2001;
            Rigshospitalet (DK)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer sequence"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 1391
AR175846/c
LOCUS       AR175846                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 132 from patent US 6309867.
ACCESSION   AR175846
VERSION     AR175846.1  GI:17917145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Cech,T.R. and Nakamura,T.
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 132 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1392
AR187062
LOCUS       AR187062                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2550 from patent US 6346398.
ACCESSION   AR187062
VERSION     AR187062.1  GI:20233027
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2550 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTT 2181
              |||||||||||||||||
Db          1 CTTTTTTTTTTTTTTTT 17


RESULT 1393
AR187063/c
LOCUS       AR187063                  17 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 2551 from patent US 6346398.
ACCESSION   AR187063
VERSION     AR187063.1  GI:20233028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6346398-A 2551 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2801
              |||||||||||||||||
Db         17 GAAAAAAAAAAAAAAAA 1


RESULT 1394
AR222463
LOCUS       AR222463                  17 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 23 from patent US 6429300.
ACCESSION   AR222463
VERSION     AR222463.1  GI:23329994
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 23 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 17


RESULT 1395
AR222463/c
LOCUS       AR222463                  17 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 23 from patent US 6429300.
ACCESSION   AR222463
VERSION     AR222463.1  GI:23329994
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 23 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1386
AR104585
LOCUS       AR104585                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 132 from patent US 6093809.
ACCESSION   AR104585
VERSION     AR104585.1  GI:12817293
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE     Telomerase
  JOURNAL   Patent: US 6093809-A 132 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 1387
AR104585/c
LOCUS       AR104585                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 132 from patent US 6093809.
ACCESSION   AR104585
VERSION     AR104585.1  GI:12817293
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Cech,T.R. and Lingner,J.
  TITLE     Telomerase
  JOURNAL   Patent: US 6093809-A 132 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1388
AR141074
LOCUS       AR141074                  17 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 5 from patent US 6207819.
ACCESSION   AR141074
VERSION     AR141074.1  GI:14483570
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6207819-A 5 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 1389
AR141074/c
LOCUS       AR141074                  17 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 5 from patent US 6207819.
ACCESSION   AR141074
VERSION     AR141074.1  GI:14483570
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6207819-A 5 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||
Db         17 AAAAAAAAAAAAAAAAA 1


RESULT 1390
AR175846
LOCUS       AR175846                  17 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 132 from patent US 6309867.
ACCESSION   AR175846
VERSION     AR175846.1  GI:17917145
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Cech,T.R. and Nakamura,T.
  TITLE     Telomerase
  JOURNAL   Patent: US 6309867-A 132 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
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  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAA 11


RESULT 1381
AR340907/c
LOCUS       AR340907                  28 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6573075.
ACCESSION   AR340907
VERSION     AR340907.1  GI:33732850
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 6573075-A 9 03-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAA 11


RESULT 1382
AX029525/c
LOCUS       AX029525                  28 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 9 from Patent EP0981953.
ACCESSION   AX029525
VERSION     AX029525.1  GI:10190261
KEYWORDS    .
SOURCE      Exophiala spinifera
  ORGANISM  Exophiala spinifera
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Chaetothyriomycetes;
            Chaetothyriales; Herpotrichiellaceae; mitosporic
            Herpotrichiellaceae; Exophiala.
REFERENCE   1
  AUTHORS   Duvick,J., Maddox,J.R., Rood,T.A. and Wang,X.
  TITLE     Transgenic plants transformed with fumonisin detoxifying enzymes
  JOURNAL   Patent: EP 0981953-A 9 01-MAR-2000;
            PIONEER HI BRED INT (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Exophiala spinifera"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:91928"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAA 11


RESULT 1383
I35032/c
LOCUS       I35032                    35 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 118 from patent US 5599704.
ACCESSION   I35032
VERSION     I35032.1  GI:2088000
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Thompson,J.D. and Draper,K.G.
  TITLE     ErbB2/neu targeted ribozymes
  JOURNAL   Patent: US 5599704-A 118 04-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 35;
  Best Local Similarity   86.4%;  Pred. No. 3e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2804
              || |||||| |||| ||||||||
Db         33 TTAAAAAAACAAAACAAAAAAA 12


RESULT 1384
A28997
LOCUS       A28997                    17 bp    DNA     linear   PAT 30-JUN-1995
DEFINITION  primer sequence 4 from patent EP0522880.
ACCESSION   A28997
VERSION     A28997.1  GI:1248848
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: EP 0522880-A 16 13-JAN-1993;
            INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2182
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 17


RESULT 1385
A28997/c
LOCUS       A28997                    17 bp    DNA     linear   PAT 30-JUN-1995
DEFINITION  primer sequence 4 from patent EP0522880.
ACCESSION   A28997
VERSION     A28997.1  GI:1248848
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: EP 0522880-A 16 13-JAN-1993;
            INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
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FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAAA 11


RESULT 1376
AR150988/c
LOCUS       AR150988                  28 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from patent US 6229071.
ACCESSION   AR150988
VERSION     AR150988.1  GI:15115579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J., Maddox,J.R., Rood,T.A. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 6229071-A 9 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAAA 11


RESULT 1377
AR156058/c
LOCUS       AR156058                  28 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from patent US 6239330.
ACCESSION   AR156058
VERSION     AR156058.1  GI:15124111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J., Maddox,J.R. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 6239330-A 9 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAAA 11


RESULT 1378
AR172065/c
LOCUS       AR172065                  28 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 19 from patent US 6297425.
ACCESSION   AR172065
VERSION     AR172065.1  GI:17911015
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6297425-A 19 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAAA 11


RESULT 1379
AR173356/c
LOCUS       AR173356                  28 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 19 from patent US 6303846.
ACCESSION   AR173356
VERSION     AR173356.1  GI:17912847
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6303846-A 19 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 28;
  Best Local Similarity   94.4%;  Pred. No. 2.2e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db         28 BAAAAAAAAAAAAAAAAA 11


RESULT 1380
I87998/c
LOCUS       I87998                    28 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 9 from patent US 5716820.
ACCESSION   I87998
VERSION     I87998.1  GI:3407938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J., Rood,T. and Wang,X.
  TITLE     Fumonisin detoxification enzymes
  JOURNAL   Patent: US 5716820-A 9 10-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 28;
```

```
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 604 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
             ||||||||||||  ||| |||
Db          1 TTTTTTTTTTTTTCCAACCTTG 22


RESULT 1372
AX043067
LOCUS       AX043067                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 633 from Patent WO0065088.
ACCESSION   AX043067
VERSION     AX043067.1  GI:11341675
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 633 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTG 2193
             ||||||||||||||  | | |||
Db          1 TTTTTTTTTTTTTCACCCTTG 22


RESULT 1373
AX055876/c
LOCUS       AX055876                 26 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 12 from Patent WO0073500.
ACCESSION   AX055876
VERSION     AX055876.1  GI:12228983
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baens,M., Marynen,P. and Dierlamm,J.
  TITLE     Molecular characterisation of chromosome translocation
            t(11;18)(q21;q21) and its correlation to carcinogenesis
  JOURNAL   Patent: WO 0073500-A 12 07-DEC-2000;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="exon No. 2 - 3' end of the exon-intron boundary of
                     human MLT gene"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 26;
  Best Local Similarity   86.4%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2803
             |||   |||||||||||||||
Db         22 ATTCCTAAAAAAAAAAAAAAA 1


RESULT 1374
BD082357
LOCUS       BD082357                 26 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
            corresponding polynucleotide molecules.
ACCESSION   BD082357
VERSION     BD082357.1  GI:22627967
KEYWORDS    JP 2001523954-A/64.
SOURCE      Mastadenovirus
  ORGANISM  Mastadenovirus
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kleanthous,H., Lissolo,L., Tomb,J.F., Miller,C. and Garawi,A.A.
  TITLE     76 kDa, 32 kDa, and 50 kDa helicobacter polypeptides and
            corresponding polynucleotide molecules
  JOURNAL   Patent: JP 2001523954-A 64 27-NOV-2001;
            MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
            VACCINS SECRETARY OF THE DEPARTMENT OF HEALTH HUMAN SERVICES SA,
            HUMAN GENOME SCIENCES INC
COMMENT     PN   JP 2001523954-A/64
            PD   27-NOV-2001
            PF   31-MAR-1998 JP 1998541962
            PI   HAROLD KLEANTHOUS,LING LISSOLO,JEAN FRANCOIS TOMB,CHARLES  PI
             MILLER,
            PI   AMAL AL GARAWI
            PC   A01N43/04,A01N59/16,A61K9/48,A61K31/70,A61K31/715,A61K39/02,
            PC   A61K39/40,
            PC   G01N33/554,G01N33/569
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mastadenovirus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10509"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 26;
  Best Local Similarity   86.4%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAA 2801
             |||||  |||||||  |||||||
Db          3 GAATTCAAAAAAACGAAAAAAA 24


RESULT 1375
AR022650/c
LOCUS       AR022650                 28 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 9 from patent US 5792931.
ACCESSION   AR022650
VERSION     AR022650.1  GI:3976712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J., Rood,T., Maddox,J.R. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 5792931-A 9 11-AUG-1998;
```

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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2804
              || |||||| ||||| ||||||
Db          1 TTAAAAAAACAAAAAGAAAAAA 22


RESULT 1367
AX042923/c
LOCUS       AX042923                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 489 from Patent WO0065088.
ACCESSION   AX042923
VERSION     AX042923.1  GI:11341531
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 489 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
              ||  || |||||||||||||||
Db         22 AGCGTTTAAAAAAAAAAAAAAA 1


RESULT 1368
AX042823/c
LOCUS       AX042823                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 389 from Patent WO0065088.
ACCESSION   AX042823
VERSION     AX042823.1  GI:11341431
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 389 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-B Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAA 2801
              | ||||  ||||||||||||||||
Db         22 GGATTGGGAAAAAAAAAAAAAA 1


RESULT 1369
AX042978/c
LOCUS       AX042978                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 544 from Patent WO0065088.
ACCESSION   AX042978
VERSION     AX042978.1  GI:11341586
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 544 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAA 2798
              | || | ||||||||||||||||
Db         22 TGAGGACTGAAAAAAAAAAAAA 1


RESULT 1370
AX042992
LOCUS       AX042992                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 558 from Patent WO0065088.
ACCESSION   AX042992
VERSION     AX042992.1  GI:11341600
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 558 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match              0.6%;  Score 17.2;  DB 1;  Length 25;
  Best Local Similarity   86.4%;  Pred. No. 1.7e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||  ||||| |
Db          1 TTTTTTTTTTTTTCCAACTTCG 22


RESULT 1371
AX043038
LOCUS       AX043038                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 604 from Patent WO0065088.
ACCESSION   AX043038
VERSION     AX043038.1  GI:11341646
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Komponente (b)-3"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAA 2800
              || ||  ||||||||||||||||
Db         22 AGCATCCAAAAAAAAAAAAAAA 1


RESULT 1363
AX119432/c
LOCUS       AX119432                 23 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 89 from Patent WO0129251.
ACCESSION   AX119432
VERSION     AX119432.1  GI:14036351
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Messiaen,L. and Callens,T.
  TITLE     Improved mutation analysis of the nf1 gene
  JOURNAL   Patent: WO 0129251-A 89 26-APR-2001;
            UNIVERSITEIT GENT (BE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2750 GATACGTGTATAATAAAAGTAT 2771
              |||||||| ||| || ||||||
Db         23 GATACGTGCATATTACAAGTAT 2


RESULT 1364
AX921569/c
LOCUS       AX921569                 23 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 562 from Patent WO02068652.
ACCESSION   AX921569
VERSION     AX921569.1  GI:40215190
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   .
  TITLE     Nov-x proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 02068652-A 562 06-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: oligonucleotide
                     primer"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        731 GATCAGACAGTCATTCGCAAAG 752
              |||| |||||||||| || ||
Db         22 GATCCGACAGTCATTCTCAGAG 1


RESULT 1365
BD187389
LOCUS       BD187389                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method for testing anti-osteoporosis agent.
ACCESSION   BD187389
VERSION     BD187389.1  GI:32997128
KEYWORDS    JP 2003009871-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Furukawa,H., Matsui,H., Kawaida,R. and Otsuka,T.
  TITLE     Method for testing anti-osteoporosis agent
  JOURNAL   Patent: JP 2003009871-A 6 14-JAN-2003;
            Sankyo Company Limited
COMMENT     OS   Artificial Sequence
            PN   JP 2003009871-A/6
            PD   14-JAN-2003
            PF   14-JUN-2001 JP 2001180142
            PI   hidehiko furukawa,hideki matsui,remi kawaida,toshiaki otsuka
            CC   Description of Artificial Sequence: PCR primer DAPG1 FH   Key
                      Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
              |||   ||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTT 22


RESULT 1366
BD244864
LOCUS       BD244864                 25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
ACCESSION   BD244864
VERSION     BD244864.1  GI:33054634
KEYWORDS    JP 2002532063-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 9 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/9
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
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                    /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACT 2190
                ||||||||||||||||| |  ||
Db         23 TTTTTTTTTTTTTTTTTCTGGCT 2


RESULT 1359
BD245238/c
LOCUS       BD245238                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245238
VERSION     BD245238.1  GI:33055008
KEYWORDS    JP 2002532386-A/24.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 24 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/24
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACT 2190
                ||||||||||||||||| |  ||
Db         23 TTTTTTTTTTTTTTTTTGTGGCT 2


RESULT 1360
BD245242/c
LOCUS       BD245242                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245242
VERSION     BD245242.1  GI:33055012
KEYWORDS    JP 2002532386-A/28.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 28 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/28
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACT 2190
                ||||||||||||||||| |  ||
Db         23 TTTTTTTTTTTTTTTTTATGGCT 2


RESULT 1361
I79499
LOCUS       I79499                   23 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 6 from patent US 5707807.
ACCESSION   I79499
VERSION     I79499.1  GI:3207789
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 6 13-JAN-1998;
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
                |||   ||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTT 22


RESULT 1362
AX053000/c
LOCUS       AX053000                 23 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 16 from Patent WO0071749.
ACCESSION   AX053000
VERSION     AX053000.1  GI:12227102
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 16 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
```

```
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Takagi,S. and Kamioka,S.
  TITLE     DETERMINATION OF CDNA
  JOURNAL   Patent: JP 1994303997-A 4 01-NOV-1994;
            NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994303997-A/4
            PD   01-NOV-1994
            PF   16-APR-1993 JP 1993112515
            PI   TAKAGI SHIGERU, KAMIOKA SUKEYUKI
            PC   C12Q1/68,C12N15/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .21
            FT                   /organism='Artificial sequences'.
FEATURES                Location/Qualifiers
     source             1. .21
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTV 18


RESULT 1356
E08333/c
LOCUS       E08333                    21 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Reverse transcription primer.
ACCESSION   E08333
VERSION     E08333.1  GI:2176450
KEYWORDS    JP 1994303997-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Takagi,S. and Kamioka,S.
  TITLE     DETERMINATION OF CDNA
  JOURNAL   Patent: JP 1994303997-A 4 01-NOV-1994;
            NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994303997-A/4
            PD   01-NOV-1994
            PF   16-APR-1993 JP 1993112515
            PI   TAKAGI SHIGERU, KAMIOKA SUKEYUKI
            PC   C12Q1/68,C12N15/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .21
            FT                   /organism='Artificial sequences'.
FEATURES                Location/Qualifiers
     source             1. .21
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 21;
  Best Local Similarity   94.4%;  Pred. No. 1.1e+03;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         18 BAAAAAAAAAAAAAAAA 1


RESULT 1357
AX457061/c
LOCUS       AX457061                  23 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 22 from Patent WO0231186.
ACCESSION   AX457061
VERSION     AX457061.1  GI:21715843
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K.
  TITLE     Method for the detection of cytosine methylations
  JOURNAL   Patent: WO 0231186-A 22 18-APR-2002;
            Epigenomics AG (DE)
FEATURES                Location/Qualifiers
     source             1. .23
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Primer"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 23;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2803
              ||| ||||| || |||||||||
Db         23 ATTAAAAAATAATAAAAAAAAA 2


RESULT 1358
BD245234/c
LOCUS       BD245234                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245234
VERSION     BD245234.1  GI:33055004
KEYWORDS    JP 2002532386-A/20.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 20 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/20
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                     Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
     source             1. .23
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
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RESULT 1352
E08331/c
LOCUS       E08331                    19 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Reverse transcription primer.
ACCESSION   E08331
VERSION     E08331.1  GI:2176448
KEYWORDS    JP 1994303997-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Takagi,S. and Kamioka,S.
  TITLE     DETERMINATION OF CDNA
  JOURNAL   Patent: JP 1994303997-A 2 01-NOV-1994;
            NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994303997-A/2
            PD   01-NOV-1994
            PF   16-APR-1993 JP 1993112515
            PI   TAKAGI SHIGERU, KAMIOKA SUKEYUKI
            PC   C12Q1/68,C12N15/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .19
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 8.4e+02;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         18 BAAAAAAAAAAAAAAAA 1


RESULT 1353
E08332
LOCUS       E08332                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Reverse transcription primer.
ACCESSION   E08332
VERSION     E08332.1  GI:2176449
KEYWORDS    JP 1994303997-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Takagi,S. and Kamioka,S.
  TITLE     DETERMINATION OF CDNA
  JOURNAL   Patent: JP 1994303997-A 3 01-NOV-1994;
            NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994303997-A/3
            PD   01-NOV-1994
            PF   16-APR-1993 JP 1993112515
            PI   TAKAGI SHIGERU, KAMIOKA SUKEYUKI
            PC   C12Q1/68,C12N15/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 9.7e+02;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTV 18


RESULT 1354
E08332/c
LOCUS       E08332                    20 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Reverse transcription primer.
ACCESSION   E08332
VERSION     E08332.1  GI:2176449
KEYWORDS    JP 1994303997-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Takagi,S. and Kamioka,S.
  TITLE     DETERMINATION OF CDNA
  JOURNAL   Patent: JP 1994303997-A 3 01-NOV-1994;
            NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994303997-A/3
            PD   01-NOV-1994
            PF   16-APR-1993 JP 1993112515
            PI   TAKAGI SHIGERU, KAMIOKA SUKEYUKI
            PC   C12Q1/68,C12N15/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 20;
  Best Local Similarity   94.4%;  Pred. No. 9.7e+02;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAA 2802
              :|||||||||||||||||
Db         18 BAAAAAAAAAAAAAAAA 1


RESULT 1355
E08333
LOCUS       E08333                    21 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Reverse transcription primer.
ACCESSION   E08333
VERSION     E08333.1  GI:2176450
KEYWORDS    JP 1994303997-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
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  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 109 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/109
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid,
            CC   and the base sequence was used as that of the probe. FH   Key
                   Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||| ||||||||
Db         30 AAAAAAAAAACAAAAAAA 12


RESULT 1349
AR163080
LOCUS       AR163080                  19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6270966.
ACCESSION   AR163080
VERSION     AR163080.1  GI:16233563
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weinstein,J.N. and Buolamwini,J.
  TITLE     Restriction display (RD-PCR) of differentially expressed mRNAs
  JOURNAL   Patent: US 6270966-A 1 07-AUG-2001;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 8.4e+02;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              :||||||||||||||||||
Db          2 BAAAAAAAAAAAAAAAAA 19


RESULT 1350
AR163080/c
LOCUS       AR163080                  19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6270966.
ACCESSION   AR163080
VERSION     AR163080.1  GI:16233563
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Weinstein,J.N. and Buolamwini,J.
  TITLE     Restriction display (RD-PCR) of differentially expressed mRNAs
  JOURNAL   Patent: US 6270966-A 1 07-AUG-2001;
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 8.4e+02;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||:
Db         19 TTTTTTTTTTTTTTTTV 2


RESULT 1351
E08331
LOCUS       E08331                    19 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Reverse transcription primer.
ACCESSION   E08331
VERSION     E08331.1  GI:2176448
KEYWORDS    JP 1994303997-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Takagi,S. and Kamioka,S.
  TITLE     DETERMINATION OF CDNA
  JOURNAL   Patent: JP 1994303997-A 2 01-NOV-1994;
            NIPPON TELEGR & TELEPH CORP <NTT>
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994303997-A/2
            PD   01-NOV-1994
            PF   16-APR-1993 JP 1993112515
            PI   TAKAGI SHIGERU, KAMIOKA SUKEYUKI
            PC   C12Q1/68,C12N15/10;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .19
            FT                   /organism='Artificial sequences'.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.2;  DB 1;  Length 19;
  Best Local Similarity   94.4%;  Pred. No. 8.4e+02;
  Matches   17;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTV 18
```

```
          CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
          CC   BODIBY FL/C6 upon the hybridization of the
          probe with a target
          CC             nucleic
          CC   acid.
          FH   Key             Location/Qualifiers
          FT   source          1. .30
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db         30 AAAAAAAAAAACAAAAAAA 12


RESULT 1346
BD166032/c
LOCUS       BD166032                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166032
VERSION     BD166032.1  GI:27871844
KEYWORDS    JP 2002191372-A/12.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 12 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/12
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1347
BD166033/c
LOCUS       BD166033                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166033
VERSION     BD166033.1  GI:27871845
KEYWORDS    JP 2002191372-A/13.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 13 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/13
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1348
BD166129/c
LOCUS       BD166129                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166129
VERSION     BD166129.1  GI:27871941
KEYWORDS    JP 2002191372-A/109.
SOURCE      unidentified
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RESULT 1343
BD166026/c
LOCUS       BD166026                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166026
VERSION     BD166026.1  GI:27871838
KEYWORDS    JP 2002191372-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 6 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/6
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||  |||||
Db         30 AAAAAAAAAAAAACAAAAA 12


RESULT 1344
BD166027/c
LOCUS       BD166027                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166027
VERSION     BD166027.1  GI:27871839
KEYWORDS    JP 2002191372-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 7 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/7
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||  |||||
Db         30 AAAAAAAAAAAAACAAAAA 12


RESULT 1345
BD166028/c
LOCUS       BD166028                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166028
VERSION     BD166028.1  GI:27871840
KEYWORDS    JP 2002191372-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 8 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/8
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
```

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            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/9
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||| ||||||||
Db         30 AAAAAAAAAACAAAAAAAA 12


RESULT 1341
BD145032/c
LOCUS       BD145032                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145032
VERSION     BD145032.1  GI:27850790
KEYWORDS    JP 2002119291-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 13 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/13
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||| ||||||||
Db         30 AAAAAAAAAAGAAAAAAAA 12


RESULT 1342
BD145033/c
LOCUS       BD145033                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145033
VERSION     BD145033.1  GI:27850791
KEYWORDS    JP 2002119291-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 14 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/14
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                    examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||| ||||||||
Db         30 AAAAAAAAAAGAAAAAAAA 12
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```
          CC   the probe with a target nucleic acid.
          FH   Key             Location/Qualifiers
          FT   source          1. .30
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||| |||||
Db         30 AAAAAAAAAAAAACAAAAA 12


RESULT 1338
BD145026/c
LOCUS       BD145026                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145026
VERSION     BD145026.1  GI:27850784
KEYWORDS    JP 2002119291-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 7 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/7
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||| ||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1339
BD145027/c
LOCUS       BD145027                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145027
VERSION     BD145027.1  GI:27850785
KEYWORDS    JP 2002119291-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 8 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/8
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||| |||||||
Db         30 AAAAAAAAAAACAAAAAAA 12


RESULT 1340
BD145028/c
LOCUS       BD145028                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145028
VERSION     BD145028.1  GI:27850786
KEYWORDS    JP 2002119291-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 9 23-APR-2002;
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  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||  ||||||||
Db         30 AAAAAAAAAACAAAAAAAA 12


RESULT 1335
BD107500/c
LOCUS       BD107500                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107500
VERSION     BD107500.1  GI:23202318
KEYWORDS    JP 2002000275-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 9 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/9
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||  ||||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1336
BD107501/c
LOCUS       BD107501                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107501
VERSION     BD107501.1  GI:23202319
KEYWORDS    JP 2002000275-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 10 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/10
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||  ||||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1337
BD145025/c
LOCUS       BD145025                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145025
VERSION     BD145025.1  GI:27850783
KEYWORDS    JP 2002119291-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 6 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/6
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
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RESULT 1332
BD107494/c
LOCUS       BD107494                 30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107494
VERSION     BD107494.1  GI:23202312
KEYWORDS    JP 2002000275-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 3 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/3
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1333
BD107495/c
LOCUS       BD107495                 30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107495
VERSION     BD107495.1  GI:23202313
KEYWORDS    JP 2002000275-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 4 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/4
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1334
BD107496/c
LOCUS       BD107496                 30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107496
VERSION     BD107496.1  GI:23202314
KEYWORDS    JP 2002000275-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 5 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/5
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
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  JOURNAL   Patent: JP 2001286300-A 11 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/11
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                       labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
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                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||| |||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1330
BD072874/c
LOCUS       BD072874                30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072874
VERSION     BD072874.1  GI:22618477
KEYWORDS    JP 2001286300-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 12 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/12
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                       labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||| |||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1331
BD107493/c
LOCUS       BD107493                30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107493
VERSION     BD107493.1  GI:23202311
KEYWORDS    JP 2002000275-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 2 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/2
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                       labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                ||||||||||||| |||||
Db         30 AAAAAAAAAAAAACAAAAA 12
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           FH   Key             Location/Qualifiers
           FT   source          1. .30
           FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1327
BD072868/c
LOCUS       BD072868                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072868
VERSION     BD072868.1  GI:22618471
KEYWORDS    JP 2001286300-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 6 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/6
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC . acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1328
BD072869/c
LOCUS       BD072869                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072869
VERSION     BD072869.1  GI:22618472
KEYWORDS    JP 2001286300-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 7 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/7
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||| ||||||||
Db         30 AAAAAAAAAACAAAAAAA 12


RESULT 1329
BD072873/c
LOCUS       BD072873                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072873
VERSION     BD072873.1  GI:22618476
KEYWORDS    JP 2001286300-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
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REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 12 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||  |||||||
Db         30 AAAAAAAAAAAGAAAAAAA 12


RESULT 1324
AR264929/c
LOCUS       AR264929                30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 13 from patent US 6492121.
ACCESSION   AR264929
VERSION     AR264929.1  GI:29693316
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 13 10-DEC-2002;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||  ||||||||
Db         30 AAAAAAAAAAGAAAAAAAA 12


RESULT 1325
BD072866/c
LOCUS       BD072866                30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072866
VERSION     BD072866.1  GI:22618469
KEYWORDS    JP 2001286300-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 4 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/4
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| |||||
Db         30 AAAAAAAAAAAAACAAAAA 12


RESULT 1326
BD072867/c
LOCUS       BD072867                30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072867
VERSION     BD072867.1  GI:22618470
KEYWORDS    JP 2001286300-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 5 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/5
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAACAAAA 12


RESULT 1319
AR264921/c
LOCUS       AR264921                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6492121.
ACCESSION   AR264921
VERSION     AR264921.1  GI:29693308
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 5 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| |||||
Db         30 AAAAAAAAAAAAACAAAAA 12


RESULT 1320
AR264922/c
LOCUS       AR264922                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6492121.
ACCESSION   AR264922
VERSION     AR264922.1  GI:29693309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 6 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1321
AR264923/c
LOCUS       AR264923                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 7 from patent US 6492121.
ACCESSION   AR264923
VERSION     AR264923.1  GI:29693310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 7 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAACAAAAAA 12


RESULT 1322
AR264924/c
LOCUS       AR264924                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6492121.
ACCESSION   AR264924
VERSION     AR264924.1  GI:29693311
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 8 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||| |||||||
Db         30 AAAAAAAAAAACAAAAAAA 12


RESULT 1323
AR264928/c
LOCUS       AR264928                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 12 from patent US 6492121.
ACCESSION   AR264928
VERSION     AR264928.1  GI:29693315
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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ACCESSION   BD107492
VERSION     BD107492.1  GI:23202310
KEYWORDS    JP 2002000275-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 1 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/1
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAACAAAA 12


RESULT 1317
BD145024/c
LOCUS       BD145024                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145024
VERSION     BD145024.1  GI:27850782
KEYWORDS    JP 2002119291-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 5 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/5
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                 hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAACAAAA 12


RESULT 1318
BD166025/c
LOCUS       BD166025                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166025
VERSION     BD166025.1  GI:27871837
KEYWORDS    JP 2002191372-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 5 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/5
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
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BD166031/c
LOCUS       BD166031                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166031
VERSION     BD166031.1  GI:27871843
KEYWORDS    JP 2002191372-A/11.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 11 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/11
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||  ||||||
Db         30 AAAAAAAAAAAAGAAAAAA 12


RESULT 1314
AR264920/c
LOCUS       AR264920                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 4 from patent US 6492121.
ACCESSION   AR264920
VERSION     AR264920.1  GI:29693307
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 4 10-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||  ||||
Db         30 AAAAAAAAAAAAAACAAAA 12


RESULT 1315
BD072865/c
LOCUS       BD072865                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072865
VERSION     BD072865.1  GI:22618468
KEYWORDS    JP 2001286300-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 3 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/3
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
                ||||||||||||  ||||
Db         30 AAAAAAAAAAAAAACAAAA 12


RESULT 1316
BD107492/c
LOCUS       BD107492                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
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            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| |||||
Db         30 AAAAAAAAAAAAAGAAAAA 12


RESULT 1311
BD145031/c
LOCUS       BD145031                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145031
VERSION     BD145031.1  GI:27850789
KEYWORDS    JP 2002119291-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 12 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/12
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                    hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| |||||
Db         30 AAAAAAAAAAAAAGAAAAA 12


RESULT 1312
BD166030/c
LOCUS       BD166030                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166030
VERSION     BD166030.1  GI:27871842
KEYWORDS    JP 2002191372-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 10 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/10
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| |||||
Db         30 AAAAAAAAAAAAAGAAAAA 12


RESULT 1313
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                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAAGAAAAAA 12


RESULT 1308
BD107498/c
LOCUS       BD107498                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107498
VERSION     BD107498.1  GI:23202316
KEYWORDS    JP 2002000275-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 7 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/7
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| |||||
Db         30 AAAAAAAAAAAAGAAAAA 12


RESULT 1309
BD107499/c
LOCUS       BD107499                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107499
VERSION     BD107499.1  GI:23202317
KEYWORDS    JP 2002000275-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 8 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/8
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| |||||
Db         30 AAAAAAAAAAAAGAAAAA 12


RESULT 1310
BD145030/c
LOCUS       BD145030                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145030
VERSION     BD145030.1  GI:27850788
KEYWORDS    JP 2002119291-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 11 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/11
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VERSION     AR264926.1  GI:29693313
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 10 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| |||||
Db         30 AAAAAAAAAAAAAGAAAAA 12


RESULT 1305
AR264927/c
LOCUS       AR264927                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 11 from patent US 6492121.
ACCESSION   AR264927
VERSION     AR264927.1  GI:29693314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 11 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| ||||||
Db         30 AAAAAAAAAAAAGAAAAAA 12


RESULT 1306
BD072871/c
LOCUS       BD072871                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072871
VERSION     BD072871.1  GI:22618474
KEYWORDS    JP 2001286300-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 9 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/9
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||| |||||
Db         30 AAAAAAAAAAAAAGAAAAA 12


RESULT 1307
BD072872/c
LOCUS       BD072872                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072872
VERSION     BD072872.1  GI:22618475
KEYWORDS    JP 2001286300-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 10 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/10
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
```

PI RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA PI KURATA,
PI KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
PC C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.

FEATURES Location/Qualifiers
source 1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||||| ||||
Db 30 AAAAAAAAAAAAAAGAAAA 12

RESULT 1302
BD145029/c
LOCUS BD145029 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method.
ACCESSION BD145029
VERSION BD145029.1 GI:27850787
KEYWORDS JP 2002119291-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Method for assaying nucleic acid, nucleic acid probe used therefor, and method for analyzing data obtained by that method
JOURNAL Patent: JP 2002119291-A 10 23-APR-2002;
JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002119291-A/10
PD 23-APR-2002
PF 27-APR-2001 JP 2001133529
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC 53,
PC G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
PC G01N1/28,
PC G01N1/28
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of
CC a nucleic acid probe labeled with BODIBY FL/C6 upon the CC hybridization of
CC the probe with a target nucleic acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.

FEATURES Location/Qualifiers
source 1. .30
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||||| ||||
Db 30 AAAAAAAAAAAAAAGAAAA 12

RESULT 1303
BD166029/c
LOCUS BD166029 30 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method.
ACCESSION BD166029
VERSION BD166029.1 GI:27871841
KEYWORDS JP 2002191372-A/9.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S., Yamada,K. and Yokomaku,T.
TITLE Novel nucleic acid probes, method for determining concentrations of nucleic acid by using the probes, and method for analyzing data obtained by the method
JOURNAL Patent: JP 2002191372-A 9 09-JUL-2002;
NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT OS Artificial Sequence
PN JP 2002191372-A/9
PD 09-JUL-2002
PF 26-SEP-2001 JP 2001295145
PI RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI PI TORIMURA,
PI SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC C12N15/00
CC The base sequence was prepared synthetically on the aim of CC examining the
CC decrease in fluorescence emission of a nucleic acid probe CC labeled with
CC BODIBY FL/C6 upon the hybridization of the probe with a target
CC nucleic
CC acid.
FH Key Location/Qualifiers
FT source 1. .30
FT /organism='Artificial Sequence'.

FEATURES Location/Qualifiers
source 1. .30
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.6%; Score 17.4; DB 1; Length 30;
Best Local Similarity 94.7%; Pred. No. 2.4e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2804
||||||||||||||| ||||
Db 30 AAAAAAAAAAAAAAGAAAA 12

RESULT 1304
AR264926/c
LOCUS AR264926 30 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 10 from patent US 6492121.
ACCESSION AR264926

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  Query Match             0.6%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   94.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db          9 GCAAAAAAAAAAAAAAAAA 27


RESULT 1298
AR068458
LOCUS       AR068458                  28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 22 from patent US 5853991.
ACCESSION   AR068458
VERSION     AR068458.1  GI:6000665
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA subtractive cloning method
  JOURNAL   Patent: US 5853991-A 22 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 28;
  Best Local Similarity   94.7%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db          9 GCAAAAAAAAAAAAAAAAA 27


RESULT 1299
AR264925/c
LOCUS       AR264925                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6492121.
ACCESSION   AR264925
VERSION     AR264925.1  GI:29693312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 9 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAAGAAAA 12


RESULT 1300
BD072870/c
LOCUS       BD072870                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072870
VERSION     BD072870.1  GI:22618473
KEYWORDS    JP 2001286300-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 8 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/8
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,  PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 30;
  Best Local Similarity   94.7%;  Pred. No. 2.4e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||| ||||
Db         30 AAAAAAAAAAAAAAGAAAA 12


RESULT 1301
BD107497/c
LOCUS       BD107497                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107497
VERSION     BD107497.1  GI:23202315
KEYWORDS    JP 2002000275-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 6 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/6
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
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                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| ||
Db         25 AAAAAAAAAAAAAAAAGAA 7


RESULT 1294
AX692822
LOCUS       AX692822                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5554 from Patent EP1281758.
ACCESSION   AX692822
VERSION     AX692822.1  GI:29415785
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5554 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              | ||||||||||||||||||
Db          6 TTCTTTTTTTTTTTTTTTT 24


RESULT 1295
AX692822/c
LOCUS       AX692822                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5554 from Patent EP1281758.
ACCESSION   AX692822
VERSION     AX692822.1  GI:29415785
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5554 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||| ||
Db         24 AAAAAAAAAAAAAAAAGAA 6


RESULT 1296
BD006733/c
LOCUS       BD006733                  25 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel polypeptide.
ACCESSION   BD006733
VERSION     BD006733.1  GI:18635104
KEYWORDS    JP 2001029090-A/36.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ito,Y., Mogi,S., Tanaka,H., Okubo,S. and Ogi,K.
  TITLE     Novel polypeptide
  JOURNAL   Patent: JP 2001029090-A 36 06-FEB-2001;
            TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001029090-A/36
            PD   06-FEB-2001
            PF   19-MAY-2000 JP 2000147530
            PR
            PI   YASUAKI ITO,SHINICHI MOGI,HIDEYUKI TANAKA,SHOICHI OKUBO, PI
            KAZUHIRO OGI
            PC   C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00,
            PC   A61P1/00,
            PC   A61P5/00,A61P9/00,A61P11/00,A61P25/00,A61P25/18,A61P31/00, PC
             A61P35/00,
            PC   A61P37/00,C07K14/47,C07K16/18,C12P21/02,G01N33/15,G01N33/50,
            PC   G01N33/566//
            PC   C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12P21/08,(C12P21/02, PC
            C12R1:91),
            PC   (C12N5/10,C12R1:91),(C12P21/08,C12R1:91),C12N15/00,A61K37/02,
            PC   C12N5/00,
            PC   (C12N5/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        454 AGGCAGCCAGCAGCAGGCC 472
              | ||||||||||||||||||
Db         25 AAGCAGCCAGCAGCAGGCC 7


RESULT 1297
AR055117
LOCUS       AR055117                  28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 22 from patent US 5837468.
ACCESSION   AR055117
VERSION     AR055117.1  GI:5980694
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA substractive cloning method
  JOURNAL   Patent: US 5837468-A 22 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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RESULT 1289
AX043581
LOCUS       AX043581                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1147 from Patent WO0065088.
ACCESSION   AX043581
VERSION     AX043581.1  GI:11342189
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1147 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTT 2192
              ||||||||||||| |||||
Db          1 TTTTTTTTTTTTTCACTTT 19


RESULT 1290
AX117576
LOCUS       AX117576                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 2699 from Patent WO0129262.
ACCESSION   AX117576
VERSION     AX117576.1  GI:14034527
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 2699 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||| |||||||
Db          1 AAAAAAAAAAAGAAAAAAA 19


RESULT 1291
AX117576/c
LOCUS       AX117576                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 2699 from Patent WO0129262.
ACCESSION   AX117576
VERSION     AX117576.1  GI:14034527
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 2699 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||| ||||||||||
Db         19 TTTTTTTCTTTTTTTTTT 1


RESULT 1292
AX692821
LOCUS       AX692821                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5553 from Patent EP1281758.
ACCESSION   AX692821
VERSION     AX692821.1  GI:29415784
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5553 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              | ||||||||||||||||||
Db          7 TTCTTTTTTTTTTTTTTTT 25


RESULT 1293
AX692821/c
LOCUS       AX692821                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5553 from Patent EP1281758.
ACCESSION   AX692821
VERSION     AX692821.1  GI:29415784
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5553 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 2 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 24;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||| |||
Db         24 AAAAAAAAAAAAAAAATAAA 6


RESULT 1285
AX043130/c
LOCUS       AX043130                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 696 from Patent WO0065088.
ACCESSION   AX043130
VERSION     AX043130.1  GI:11341738
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 696 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAA 2799
              |||| ||||||||||||||
Db         19 AATTCAAAAAAAAAAAAAA 1


RESULT 1286
AX115988/c
LOCUS       AX115988                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 1111 from Patent WO0129262.
ACCESSION   AX115988
VERSION     AX115988.1  GI:14032930
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 1111 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              ||||||| ||||||||||||
Db         25 AAAAAAACAAAAAAAAAAA 7


RESULT 1287
AX042590
LOCUS       AX042590                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 156 from Patent WO0065088.
ACCESSION   AX042590
VERSION     AX042590.1  GI:11341198
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 156 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2174 TTTTTTTTTTTTTAACTTT 2192
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTAACTCT 19


RESULT 1288
AX043064/c
LOCUS       AX043064                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 630 from Patent WO0065088.
ACCESSION   AX043064
VERSION     AX043064.1  GI:11341672
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 630 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAA 2800
              | ||||||||||||||||||
Db         19 ACTGAAAAAAAAAAAAAA 1
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                /mod_base=OTHER
     modified_base  9
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
     modified_base  12
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
     modified_base  15
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
     modified_base  18
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 876
AX825150/c
LOCUS       AX825150                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 48 from Patent WO03072818.
ACCESSION   AX825150
VERSION     AX825150.1  GI:39750879
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 48 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 877
AX825158/c
LOCUS       AX825158                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 56 from Patent WO03072818.
ACCESSION   AX825158
VERSION     AX825158.1  GI:39750887
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 56 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 878
AR118155
LOCUS       AR118155                 21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6140489.
ACCESSION   AR118155
VERSION     AR118155.1  GI:14099061
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Brenner,S.
  TITLE     Compositions for sorting polynucleotides
  JOURNAL   Patent: US 6140489-A 23 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTTTTT 21


RESULT 879
AR118155/c
LOCUS       AR118155                  21 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6140489.
ACCESSION   AR118155
VERSION     AR118155.1  GI:14099061
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Brenner,S.
  TITLE     Compositions for sorting polynucleotides
  JOURNAL   Patent: US 6140489-A 23 31-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 880
I84433
LOCUS       I84433                    21 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 23 from patent US 5695934.
ACCESSION   I84433
VERSION     I84433.1  GI:3021953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Brenner,S.
  TITLE     Massively parallel sequencing of sorted polynucleotides
  JOURNAL   Patent: US 5695934-A 23 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          3 TTTTTTTTTTTTTTTTTTT 21


RESULT 881
I84433/c
LOCUS       I84433                    21 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 23 from patent US 5695934.
ACCESSION   I84433
VERSION     I84433.1  GI:3021953
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Brenner,S.
  TITLE     Massively parallel sequencing of sorted polynucleotides
  JOURNAL   Patent: US 5695934-A 23 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 882
AX825107
LOCUS       AX825107                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 5 from Patent WO03072818.
ACCESSION   AX825107
VERSION     AX825107.1  GI:39750836
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 5 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 883
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AX825108
LOCUS       AX825108                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 6 from Patent WO03072818.
ACCESSION   AX825108
VERSION     AX825108.1  GI:39750837
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 6 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 884
AX825110
LOCUS       AX825110                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 8 from Patent WO03072818.
ACCESSION   AX825110
VERSION     AX825110.1  GI:39750839
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 8 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 885
AX825112
LOCUS       AX825112                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 10 from Patent WO03072818.
ACCESSION   AX825112
VERSION     AX825112.1  GI:39750841
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 10 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 886
AX825116
LOCUS       AX825116                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 14 from Patent WO03072818.
ACCESSION   AX825116
VERSION     AX825116.1  GI:39750845
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 14 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 887
AX825140/c
LOCUS       AX825140                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 38 from Patent WO03072818.
ACCESSION   AX825140
VERSION     AX825140.1  GI:39750869
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 38 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 888
AX825141/c
LOCUS       AX825141                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 39 from Patent WO03072818.
ACCESSION   AX825141
VERSION     AX825141.1  GI:39750870
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 39 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
             ||||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 889
AX825142/c
LOCUS       AX825142                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 40 from Patent WO03072818.
ACCESSION   AX825142
VERSION     AX825142.1  GI:39750871
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 40 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
             ||||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 890
AX825144/c
LOCUS       AX825144                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 42 from Patent WO03072818.
ACCESSION   AX825144
VERSION     AX825144.1  GI:39750873
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 42 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
             ||||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 891
AX825145/c
LOCUS       AX825145                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 43 from Patent WO03072818.
ACCESSION   AX825145
VERSION     AX825145.1  GI:39750874
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 43 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
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                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 892
AX825146/c
LOCUS       AX825146                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 44 from Patent WO03072818.
ACCESSION   AX825146
VERSION     AX825146.1  GI:39750875
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 44 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 893
AX825148/c
LOCUS       AX825148                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 46 from Patent WO03072818.
ACCESSION   AX825148
VERSION     AX825148.1  GI:39750877
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 46 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 894
AX825149/c
LOCUS       AX825149                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 47 from Patent WO03072818.
ACCESSION   AX825149
VERSION     AX825149.1  GI:39750878
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
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  JOURNAL    Patent: WO 03072818-A 47 04-SEP-2003;
             Degussa Bioactives GmbH (DE)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Beschreibung der kuenstlichen
                      Sequenz:Capture-Oligonukleotid"
     misc_binding     1
                      /bound_moiety="Biotin"
     modified_base    3
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    6
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    9
                      /note="LNA-T (Locked Nucleic Acid)"
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     modified_base    12
                      /note="LNA-T (Locked Nucleic Acid)"
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     modified_base    15
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    18
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
             |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 895
AX825156
LOCUS       AX825156                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 54 from Patent WO03072818.
ACCESSION   AX825156
VERSION     AX825156.1  GI:39750885
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 54 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Beschreibung der kuenstlichen
                      Sequenz:Capture-Oligonukleotid"
     misc_binding     1
                      /bound_moiety="Biotin"
     modified_base    3
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    6
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    9
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    12
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    15
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    18
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 896
AX825156/c
LOCUS       AX825156                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 54 from Patent WO03072818.
ACCESSION   AX825156
VERSION     AX825156.1  GI:39750885
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 54 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES              Location/Qualifiers
     source           1. .21
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Beschreibung der kuenstlichen
                      Sequenz:Capture-Oligonukleotid"
     misc_binding     1
                      /bound_moiety="Biotin"
     modified_base    3
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    6
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    9
                      /note="LNA-T (Locked Nucleic Acid)"
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                      /mod_base=OTHER
     modified_base    15
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER
     modified_base    18
                      /note="LNA-T (Locked Nucleic Acid)"
                      /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 897
AX825157
LOCUS       AX825157                 21 bp    DNA     linear   PAT 11-DEC-2003
```

```
DEFINITION  Sequence 55 from Patent WO03072818.
ACCESSION   AX825157
VERSION     AX825157.1  GI:39750886
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 55 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

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  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 898
AX825157/c
LOCUS       AX825157                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 55 from Patent WO03072818.
ACCESSION   AX825157
VERSION     AX825157.1  GI:39750886
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 55 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

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  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 899
AR164336
LOCUS       AR164336                  22 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 19 from patent US 6271369.
ACCESSION   AR164336
VERSION     AR164336.1  GI:16235464
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
  TITLE     Chimeric molecules targeted to viral RNAs
  JOURNAL   Patent: US 6271369-A 19 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 900
I31828
LOCUS       I31828                    22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 19 from patent US 5583032.
ACCESSION   I31828
VERSION     I31828.1  GI:1822619
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA
  JOURNAL   Patent: US 5583032-A 19 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
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                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 901
I69425
LOCUS       I69425                   22 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 19 from patent US 5677289.
ACCESSION   I69425
VERSION     I69425.1  GI:2831547
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA and medical treatments
            thereby
  JOURNAL   Patent: US 5677289-A 19 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 6.2e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 902
BD244857/c
LOCUS       BD244857                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
ACCESSION   BD244857
VERSION     BD244857.1  GI:33054627
KEYWORDS    JP 2002532063-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 2 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/2
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAAA 5


RESULT 903
BD244863
LOCUS       BD244863                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
ACCESSION   BD244863
VERSION     BD244863.1  GI:33054633
KEYWORDS    JP 2002532063-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 8 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/8
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            CC   N = 3-Nitropyrrole
            CC   N = 3-Nitropyrrole
            FH   Key             Location/Qualifiers
            FT   modified_base   (8)
            FT   modified_base   (18).
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   90.5%;  Pred. No. 7e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2186
              ||||||| ||||||||| |||
Db          1 TTTTTTTNTTTTTTTTTNTTT 21


RESULT 904
BD244865
LOCUS       BD244865                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
ACCESSION   BD244865
VERSION     BD244865.1  GI:33054635
KEYWORDS    JP 2002532063-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 10 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
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            PN   JP 2002532063-A/10
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            CC   N - inosine
            CC   N = inosine
            FH   Key             Location/Qualifiers
            FT   modified_base   (8)
            FT   modified_base   (18).
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   90.5%;  Pred. No. 7e+02;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||| ||||||||| |||
Db          1 TTTTTTTNTTTTTTTTTNTTT 21


RESULT 905
I79497
LOCUS       I79497                  23 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 4 from patent US 5707807.
ACCESSION   I79497
VERSION     I79497.1  GI:3207787
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 4 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||||
Db          4 TCCTTTTTTTTTTTTTTTT 22


RESULT 906
BD133515
LOCUS       BD133515                23 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method for testing remedy or preventive for osteoporosis or
            articular rheumatism.
ACCESSION   BD133515
VERSION     BD133515.1  GI:23228460
KEYWORDS    JP 2002051782-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Okutsu,J., Kawaida,R., Otsuka,T. and Takahashi,W.
  TITLE     Method for testing remedy or preventive for osteoporosis or
            articular rheumatism
  JOURNAL   Patent: JP 2002051782-A 6 19-FEB-2002;
            SANKYO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002051782-A/6
            PD   19-FEB-2002
            PF   09-AUG-2000 JP 2000241413
            PI   JUNICHI OKUTSU,REMI KAWAIDA,TOSHIAKI OTSUKA,WATARU TAKAHASHI
            PC   C12N15/09,C07K14/47,C07K16/18,C12Q1/02,C12Q1/66,C12Q1/68, PC
            G01N33/15,
            PC   G01N33/50,G01N33/50,G01N33/53//C12P21/08,C12N15/00 CC
            Description of Artificial Sequence: PCR primer for molecular  CC
                indexing
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||||
Db          4 TCCTTTTTTTTTTTTTTTT 22


RESULT 907
AR431310/c
LOCUS       AR431310                24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6651008.
ACCESSION   AR431310
VERSION     AR431310.1  GI:40193278
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 4 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAA 6


RESULT 908
AX817782
LOCUS       AX817782                24 bp    DNA     linear   PAT 10-DEC-2003
DEFINITION  Sequence 18 from Patent WO02067861.
ACCESSION   AX817782
VERSION     AX817782.1  GI:39722977
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   .
  TITLE     Oncolytic adenoviral vectors
  JOURNAL   Patent: WO 02067861-A 18 06-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Viral vector sequence"
     misc_feature    1. .24
                     /note="Fig. 1C. SV40 early Poly(A) site"
     polyA_site      3. .24

  Query Match             0.7%;  Score 19;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          3 AAAAAAAAAAAAAAAAAAA 21


RESULT 909
AX838369
LOCUS       AX838369                  24 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 8 from Patent WO02068627.
ACCESSION   AX838369
VERSION     AX838369.1  GI:39922050
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   .
  TITLE     Vector constructs
  JOURNAL   Patent: WO 02068627-A 8 06-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Viral vector sequence"
     misc_feature    1. .24
                     /note="Fig. 1C. SV40 early Poly(A) site"
     polyA_site      3. .24

  Query Match             0.7%;  Score 19;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          3 AAAAAAAAAAAAAAAAAAA 21


RESULT 910
E13209
LOCUS       E13209                    24 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  DNA probe.
ACCESSION   E13209
VERSION     E13209.1  GI:3252014
KEYWORDS    JP 1997149799-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kanbara,H., Okano,K. and Uematsu,K.
  TITLE     ANALYSIS OR DETECTION OF NUCLEIC ACID AND ANALYSER OR INSPECTION
            DEVICE OF NUCLEIC ACID
  JOURNAL   Patent: JP 1997149799-A 1 10-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997149799-A/1
            PD   10-JUN-1997
            PF   30-NOV-1995 JP 1995311949
            PI   KANBARA HIDEKI, OKANO KAZUNOBU, UEMATSU KAZUMUNE PC
            C12Q1/68,C07H21/04,C12M1/00,C12N15/09,C12Q1/44,C12Q1/48, PC
            G01N27/447,
            PC   G01N27/447,G01N33/50;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .24
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 911
AX394507
LOCUS       AX394507                  25 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 52 from Patent WO0218638.
ACCESSION   AX394507
VERSION     AX394507.1  GI:21065645
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
  TITLE     Detection of cyp2d6 polymorphisms
  JOURNAL   Patent: WO 0218638-A 52 07-MAR-2002;
            Gemini Genomics PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          3 AAAAAAAAAAAAAAAAAAA 21


RESULT 912
AX394514/c
LOCUS       AX394514                  25 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 59 from Patent WO0218638.
ACCESSION   AX394514
VERSION     AX394514.1  GI:21065652
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
  TITLE     Detection of cyp2d6 polymorphisms
  JOURNAL   Patent: WO 0218638-A 59 07-MAR-2002;
            Gemini Genomics PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
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                /note="Synthetic oligonucleotide"

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAAA 5


RESULT 913
AX116188/c
LOCUS       AX116188                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 1311 from Patent WO0129262.
ACCESSION   AX116188
VERSION     AX116188.1  GI:14033130
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 1311 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAA 7


RESULT 914
A85331
LOCUS       A85331                    25 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 11 from Patent WO9840470.
ACCESSION   A85331
VERSION     A85331.1  GI:6733935
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Halkier,B.A. and Kahn,R.A.
  TITLE     CYTOCHROME P450 MONOOXYGENASES
  JOURNAL   Patent: WO 9840470-A 11 17-SEP-1998;
            CIBA GEIGY AG (CH); HALKIER BARBARA ANN (DK)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              |||||||||||||||||||
Db          6 TCCTTTTTTTTTTTTTTTT 24


RESULT 915
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```
AR370671
LOCUS       AR370671                  25 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 11 from patent US 6300544.
ACCESSION   AR370671
VERSION     AR370671.1  GI:34607459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
  TITLE     Cytochrome P450 monooxygenases
  JOURNAL   Patent: US 6300544-A 11 09-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              |||||||||||||||||||
Db          6 TCCTTTTTTTTTTTTTTTT 24


RESULT 916
AR431257
LOCUS       AR431257                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 11 from patent US 6649814.
ACCESSION   AR431257
VERSION     AR431257.1  GI:40193207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
  TITLE     Cytochrome P450 monooxygenases
  JOURNAL   Patent: US 6649814-A 11 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              |||||||||||||||||||
Db          6 TCCTTTTTTTTTTTTTTTT 24


RESULT 917
BD057791
LOCUS       BD057791                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Cytochrome P450 Monooxygenases.
ACCESSION   BD057791
VERSION     BD057791.1  GI:22603397
KEYWORDS    JP 2001514515-A/6.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Halkier,B.A., Bak,S., Kahn,R.A. and Moller,B.L.
  TITLE     Cytochrome P450 Monooxygenases
  JOURNAL   Patent: JP 2001514515-A 6 11-SEP-2001;
            NOVARTIS AG,ROYAL VETERINARY AND AGRICULTURE UNIV
COMMENT     PN   JP 2001514515-A/6
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            PD   11-SEP-2001
            PF   05-MAR-1998 JP 1998539180
            PR   07-MAR-1997 EP   97810132.7,08-DEC-1997 EP   97810954.4 PI
            BARBARA ANN HALKIER,SOREN BAK,RACHEL ALICE KAHN,BIRGER  PI
            LINDBERG MOLLER
            PC   C12N9/02,C12N15/82//C12N15/53
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .25
                        /organism="Zea mays"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:4577"

  Query Match             0.7%;  Score 19;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||
Db          6 TCCTTTTTTTTTTTTTTTT 24


RESULT 918
AX427136
LOCUS       AX427136                  28 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 36 from Patent WO0196559.
ACCESSION   AX427136
VERSION     AX427136.1  GI:21530519
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
            Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
  TITLE     Regulatable, catalytically active nucleic acids
  JOURNAL   Patent: WO 0196559-A 36 20-DEC-2001;
            Board of Regents, The University of Texas System (US)
FEATURES                Location/Qualifiers
     source             1. .28
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Primer"

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 919
I06459/c
LOCUS       I06459                    28 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 2 from Patent WO 9001065.
ACCESSION   I06459
VERSION     I06459.1  GI:589700
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Fry,K., Larrick,J. and Tam,A.
  TITLE     RNA AND DNA AMPLIFICATION TECHNIQUES
  JOURNAL   Patent: WO 9001065-A 2 08-FEB-1990;
FEATURES                Location/Qualifiers
     source             1. .28
                        /organism="unknown"
                        /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAAA 10


RESULT 920
AR371171
LOCUS       AR371171                  28 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 10 from patent US 6395306.
ACCESSION   AR371171
VERSION     AR371171.1  GI:34608085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Cui,X. and Lu,Y.
  TITLE     Bee venom protein and gene encoding same
  JOURNAL   Patent: US 6395306-A 10 28-MAY-2002;
FEATURES                Location/Qualifiers
     source             1. .28
                        /organism="unknown"
                        /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         10 CTTTTTTTTTTTTTTTTTT 28


RESULT 921
BD015304
LOCUS       BD015304                  28 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Primer single-stranded DNA, process for preparing double-stranded
            cDNA by using the same and process for amplifying one side
            single-stranded DNA.
ACCESSION   BD015304
VERSION     BD015304.1  GI:22556442
KEYWORDS    JP 2001204472-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Nakamura,T.
  TITLE     Primer single-stranded DNA, process for preparing double-stranded
            cDNA by using the same and process for amplifying one side
  JOURNAL   Patent: JP 2001204472-A 5 31-JUL-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001204472-A/5
            PD   31-JUL-2001
            PF   21-JAN-2000 JP 2000012535
            PI   TAKESHI NAKAMURA
            PC   C12N15/09,C12P19/34,G01N33/50//C12Q1/68,C12N15/00 CC   PCR
            primer
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .28
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         10 CTTTTTTTTTTTTTTTTT 28


RESULT 922
I65795/c
LOCUS       I65795                    29 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 13 from patent US 5668295.
ACCESSION   I65795
VERSION     I65795.1  GI:2482365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Wahab,S.Z. and Malik,V.S.
  TITLE     Protein involved in nicotine synthesis, DNA encoding, and use of
            sense and antisense DNAs corresponding thereto to affect nicotine
            content in transgenic tobacco cells and plants
  JOURNAL   Patent: US 5668295-A 13 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAAAA 11


RESULT 923
AR268128
LOCUS       AR268128                  29 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6498025.
ACCESSION   AR268128
VERSION     AR268128.1  GI:29698371
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Miller,J.E.
  TITLE     Methods and compositions for cDNA synthesis
  JOURNAL   Patent: US 6498025-A 5 24-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 924
AX079109/c
LOCUS       AX079109                  30 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 7 from Patent WO0106226.
ACCESSION   AX079109
VERSION     AX079109.1  GI:13158683
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mueller,O.
  TITLE     Methods for determining the proliferation activity of cells
  JOURNAL   Patent: WO 0106226-A 7 25-JAN-2001;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAAA 10


RESULT 925
AX196237
LOCUS       AX196237                  30 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 68 from Patent WO0151665.
ACCESSION   AX196237
VERSION     AX196237.1  GI:15386440
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0151665-A 68 19-JUL-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 926
AX440138
LOCUS       AX440138                  30 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 68 from Patent WO0173123.
ACCESSION   AX440138
VERSION     AX440138.1  GI:21664949
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0173123-A 68 04-OCT-2001;
            Nanosphere, Inc. (US)
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FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 927
AX465324
LOCUS       AX465324                 30 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 68 from Patent WO0218643.
ACCESSION   AX465324
VERSION     AX465324.1  GI:21899687
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0218643-A 68 07-MAR-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 928
AX556137
LOCUS       AX556137                 30 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 68 from Patent WO0246472.
ACCESSION   AX556137
VERSION     AX556137.1  GI:25899519
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 68 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 929
AX079108
LOCUS       AX079108                 30 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 6 from Patent WO0106226.
ACCESSION   AX079108
VERSION     AX079108.1  GI:13158682
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mueller,O.
  TITLE     Methods for determining the proliferation activity of cells
  JOURNAL   Patent: WO 0106226-A 6 25-JAN-2001;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"

  Query Match             0.7%;  Score 19;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          7 AAAAAAAAAAAAAAAAAAA 25


RESULT 930
AX080522/c
LOCUS       AX080522                 32 bp    DNA     linear   PAT 26-FEB-2001
DEFINITION  Sequence 10 from Patent WO0109291.
ACCESSION   AX080522
VERSION     AX080522.1  GI:13162176
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brownlee,G.G., Fodor,E.S. and Poon,L.S.
  TITLE     Attenuated influenza virus useful as vaccine
  JOURNAL   Patent: WO 0109291-A 10 08-FEB-2001;
            ISIS INNOVATION LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PRIMER"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAAA 14


RESULT 931
I32124/c
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LOCUS       I32124                    32 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 14 from patent US 5585242.
ACCESSION   I32124
VERSION     I32124.1  GI:1822915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Bouma,S.R., Khalil,O.S. and Pabich,E.K.
  TITLE     Method for detection of nucleic acid using total internal
            reflectance
  JOURNAL   Patent: US 5585242-A 14 17-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAAA 14


RESULT 932
AR274390
LOCUS       AR274390                  32 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 51 from patent US 6506564.
ACCESSION   AR274390
VERSION     AR274390.1  GI:29706836
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6506564-A 51 14-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 933
AR344932
LOCUS       AR344932                  32 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 51 from patent US 6582921.
ACCESSION   AR344932
VERSION     AR344932.1  GI:33741013
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            thereof
  JOURNAL   Patent: US 6582921-A 51 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 934
AR382308
LOCUS       AR382308                  32 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 51 from patent US 6610491.
ACCESSION   AR382308
VERSION     AR382308.1  GI:40090720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6610491-A 51 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 935
AR429649
LOCUS       AR429649                  32 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 51 from patent US 6645721.
ACCESSION   AR429649
VERSION     AR429649.1  GI:40189945
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6645721-A 51 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19
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RESULT 936
AX196220
LOCUS       AX196220                  32 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 51 from Patent WO0151665.
ACCESSION   AX196220
VERSION     AX196220.1  GI:15386423
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0151665-A 51 19-JUL-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 937
AX440121
LOCUS       AX440121                  32 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 51 from Patent WO0173123.
ACCESSION   AX440121
VERSION     AX440121.1  GI:21664932
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0173123-A 51 04-OCT-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 938
AX465307
LOCUS       AX465307                  32 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 51 from Patent WO0218643.
ACCESSION   AX465307
VERSION     AX465307.1  GI:21899670
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0218643-A 51 07-MAR-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 939
AX556120
LOCUS       AX556120                  32 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 51 from Patent WO0246472.
ACCESSION   AX556120
VERSION     AX556120.1  GI:25899502
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 51 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 940
AR174572/c
LOCUS       AR174572                  34 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 27 from patent US 6307024.
ACCESSION   AR174572
VERSION     AR174572.1  GI:17914892
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
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          Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 27 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         34 AAAAAAAAAAAAAAAAAAA 16


RESULT 941
BD248965/c
LOCUS       BD248965                34 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel cytokine ZALPHA11 ligand.
ACCESSION   BD248965
VERSION     BD248965.1  GI:33058735
KEYWORDS    JP 2002537839-A/26.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Novel cytokine ZALPHA11 ligand
  JOURNAL   Patent: JP 2002537839-A 26 12-NOV-2002;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002537839-A/26
            PD   12-NOV-2002
            PF   09-MAR-2000 JP 2000603382
            PR   09-MAR-1999 US    09/264908,11-MAR-1999 US    09/265992 PR
            01-JUL-1999 US    60/142013
            PI   JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C  PI
            FOSTER,
            PI   RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
            PI   STACEY R DILLON,ANGELA K HAMMOND
            PC   C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
            PC   C07K14/53,
            PC   C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
             A61K37/02
            CC   Oligonucleotide primer ZC18698
            FH   Key             Location/Qualifiers
            FT   source          1. .34
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         34 AAAAAAAAAAAAAAAAAAA 16


RESULT 942
AR374064/c
LOCUS       AR374064                34 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 27 from patent US 6605272.
ACCESSION   AR374064
VERSION     AR374064.1  GI:40076636
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Methods of using zalpha11 ligand
  JOURNAL   Patent: US 6605272-A 27 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         34 AAAAAAAAAAAAAAAAAAA 16


RESULT 943
AX179588/c
LOCUS       AX179588                34 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 11 from Patent WO0146422.
ACCESSION   AX179588
VERSION     AX179588.1  GI:15132019
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Presnell,S.R. and Kindsvogel,W.
  TITLE     Cytokine zcyto18
  JOURNAL   Patent: WO 0146422-A 11 28-JUN-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC18698"

  Query Match             0.7%;  Score 19;  DB 1;  Length 34;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         34 AAAAAAAAAAAAAAAAAAA 16


RESULT 944
AR029830/c
LOCUS       AR029830                35 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 19 from patent US 5861244.
ACCESSION   AR029830
VERSION     AR029830.1  GI:5943044
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 19 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .35
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                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19;  DB 1;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         35 GAAAAAAAAAAAAAAAAAA 17


RESULT 945
AX516913/c
LOCUS       AX516913                  41 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 3111 from Patent WO02052044.
ACCESSION   AX516913
VERSION     AX516913.1  GI:23565110
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  TITLE     Detection of genetic polymorphisms
  JOURNAL   Patent: WO 02052044-A 3111 04-JUL-2002;
            Riken (JP)
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.7%;  Score 19;  DB 1;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         40 AAAAAAAAAAAAAAAAAAA 22


RESULT 946
AX519424/c
LOCUS       AX519424                  41 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 5622 from Patent WO02052044.
ACCESSION   AX519424
VERSION     AX519424.1  GI:23569690
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  TITLE     Detection of genetic polymorphisms
  JOURNAL   Patent: WO 02052044-A 5622 04-JUL-2002;
            Riken (JP)
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match              0.7%;  Score 19;  DB 1;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||
Db         40 AAAAAAAAAAAAAAAAAAA 22


RESULT 947
BD085544/c
LOCUS       BD085544                  22 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Method of comparison and detection of RNA amount and DNA amount.
ACCESSION   BD085544
VERSION     BD085544.1  GI:22631154
KEYWORDS    JP 2001333800-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Shimada,K.
  TITLE     Method of comparison and detection of RNA amount and DNA amount
  JOURNAL   Patent: JP 2001333800-A 1 04-DEC-2001;
            UNITECH CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001333800-A/1
            PD   04-DEC-2001
            PF   30-MAY-2000 JP 2000160324
            PI   KAORI SHIMADA
            PC   C12Q1/68,C12N15/09,G01N33/50,C12N15/00
            CC   Method of comparison and detection of RNA amount and DNA  CC
                 amount
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match              0.7%;  Score 18.8;  DB 1;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 6.7e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| | |
Db         22 TTTTTTTTTTTTTTTTTTGATC 1


RESULT 948
BD245230/c
LOCUS       BD245230                  23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245230
VERSION     BD245230.1  GI:33055000
KEYWORDS    JP 2002532386-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 16 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/16
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
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FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 18.8;  DB 1;  Length 23;
  Best Local Similarity   90.9%;  Pred. No. 7.6e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||||  ||
Db         23 TTTTTTTTTTTTTTTTTTGGCT 2


RESULT 949
E12393
LOCUS       E12393                    23 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide primer.
ACCESSION   E12393
VERSION     E12393.1  GI:3251226
KEYWORDS    JP 1996322598-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Katou,K.
  TITLE     INDEXING METHOD OF DNA MOLECULE
  JOURNAL   Patent: JP 1996322598-A 3 10-DEC-1996;
            RES DEV CORP OF JAPAN
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996322598-A/3
            PD   10-DEC-1996
            PF   12-SEP-1995 JP 1995234122
            PR   28-MAR-1995 JP 95P    69695
            PI   KATOU KIKUYA
            PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .23
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 18.8;  DB 1;  Length 23;
  Best Local Similarity   90.9%;  Pred. No. 7.6e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTT 2183
              ||||  ||||||||||||||||
Db          1 CTCCAGTTTTTTTTTTTTTTT 22


RESULT 950
AX043130
LOCUS       AX043130                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 696 from Patent WO0065088.
ACCESSION   AX043130
VERSION     AX043130.1  GI:11341738
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 696 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match              0.7%;  Score 18.8;  DB 1;  Length 25;
  Best Local Similarity   90.9%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||  | |||||
Db          1 TTTTTTTTTTTTTTGAATTTGA 22


RESULT 951
AX043131
LOCUS       AX043131                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 697 from Patent WO0065088.
ACCESSION   AX043131
VERSION     AX043131.1  GI:11341739
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 697 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPA1 Heterozygote Primer Sequence"

  Query Match              0.7%;  Score 18.8;  DB 1;  Length 25;
  Best Local Similarity   90.9%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGA 2194
              ||||||||||||||  | |||||
Db          1 TTTTTTTTTTTTTTGAGTTTGA 22


RESULT 952
E30823/c
LOCUS       E30823                    26 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Modified antibody Fab fragment.
ACCESSION   E30823
VERSION     E30823.1  GI:13017253
KEYWORDS    JP 1999341980-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Takashi,S., Izumi,I. and Nobuhiko,M.
  TITLE     Modified antibody Fab fragment
  JOURNAL   Patent: JP 1999341980-A 6 14-DEC-1999;
            TOYOBO CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999341980-A/6
            PD   14-DEC-1999
            PF   02-JUN-1998 JP 1998152956
            PR
            PI   TAKASHI SAZU,IZUMI INOHARA,NOBUHIKO MAEKAWA
            PC   C12N1/21,C07K16/00,C07K17/08,C07K17/14,C12N15/09,G01N33/531,
            PC   G01N33/547//
            PC   C12P21/08,(C12N1/21,C12R1:19),C12N15/00
            CC   Strandedness: Single;
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            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 18.8;  DB 1;  Length 26;
  Best Local Similarity   90.9%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAAA 2804
              | ||||| ||||||||||||||
Db         24 TCGAAAATAAAAAAAAAAAAAA 3


RESULT 953
AX042549
LOCUS       AX042549                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 115 from Patent WO0065088.
ACCESSION   AX042549
VERSION     AX042549.1  GI:11341157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 115 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Homozygote primer sequence"

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              ||||||||||||||| ||||   ||
Db          1 TTTTTTTTTTTTTTACCTTTTCCAG 25


RESULT 954
AX042942
LOCUS       AX042942                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 508 from Patent WO0065088.
ACCESSION   AX042942
VERSION     AX042942.1  GI:11341550
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 508 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||||   ||||||| |
Db          1 TTTTTTTTTTTTGAGTTTTAACCT 25


RESULT 955
AX043077/c
LOCUS       AX043077                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 643 from Patent WO0065088.
ACCESSION   AX043077
VERSION     AX043077.1  GI:11341685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 643 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAAA 2799
              | | || | ||||||||||||||||
Db         25 TTTAAGCAGTGAAAAAAAAAAAAAA 1


RESULT 956
AX043230
LOCUS       AX043230                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 796 from Patent WO0065088.
ACCESSION   AX043230
VERSION     AX043230.1  GI:11341838
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 796 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 25;
  Best Local Similarity   84.0%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2173 TTTTTTTTTTTTTTAACTTTGAAAG 2197
              |||||||||||||| ||||   ||
Db          1 TTTTTTTTTTTTTTACCTTTTCCAG 25


RESULT 957
AR409915
LOCUS       AR409915                 27 bp    RNA     linear   PAT 18-DEC-2003
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DEFINITION  Sequence 28 from patent US 6635422.
ACCESSION   AR409915
VERSION     AR409915.1  GI:40161050
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 28 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 27;
  Best Local Similarity   84.0%;  Pred. No. 1.3e+03;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTTTTTTTT 2176
              | | |||||||||| ||||||| |||
Db          3 TTAATTTTTTCTCTTTTTTTCTTT 27


RESULT 958
AX052989
LOCUS       AX052989                 29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 5 from Patent WO0071749.
ACCESSION   AX052989
VERSION     AX052989.1  GI:12227091
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 5 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Puromycin-Linker"

  Query Match             0.7%;  Score 18.6;  DB 1;  Length 29;
  Best Local Similarity   80.8%;  Pred. No. 1.5e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   |||||||||| |||||||
Db          1 AAAAAAAAAAAAAAAAAAANAAAAAAA 26


RESULT 959
AR030917
LOCUS       AR030917                 20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 20 from patent US 5861487.
ACCESSION   AR030917
VERSION     AR030917.1  GI:5944131
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Holton,T.Albert., Cornish,E.Cecily., Kovacic,F., Tanaka,Y. and
            Lester,D.Ruth.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: US 5861487-A 20 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTAGC 20


RESULT 960
I28309
LOCUS       I28309                   20 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 20 from patent US 5569832.
ACCESSION   I28309
VERSION     I28309.1  GI:1819085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: US 5569832-A 20 29-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTAGC 20


RESULT 961
I47310
LOCUS       I47310                   20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 11 from patent US 5639870.
ACCESSION   I47310
VERSION     I47310.1  GI:2471275
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Holton,T.Albert., Cornish,E.Cecily. and Tanaka,Y.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: US 5639870-A 11 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTAGC 20
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RESULT 962
AR211367
LOCUS       AR211367                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6399305.
ACCESSION   AR211367
VERSION     AR211367.1  GI:21514670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Makino,Y., Abe,Y., Takagi,M., Takenaka,S., Yamashita,K. and
            Ogawa,M.
  TITLE     Protection of partial complementary nucleic acid fragment using a
            electroconductive chip and intercalator
  JOURNAL   Patent: US 6399305-A 5 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||  |||||||||
Db          1 TTTTTTTTTTATTTTTTTT 20


RESULT 963
AR371268/c
LOCUS       AR371268                  20 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 4 from patent US 6395474.
ACCESSION   AR371268
VERSION     AR371268.1  GI:34608200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 4 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||| |||||
Db         20 CTTTTTTTTTTTTTCTTTTT 1


RESULT 964
AX136903
LOCUS       AX136903                  20 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 5 from Patent EP1065278.
ACCESSION   AX136903
VERSION     AX136903.1  GI:14273252
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Makino,Y., Abe,Y., Ogawa,M., Takagi,M., Takenaka,S. and
            Yamashita,K.
  TITLE     Detection of partly complementary nucleic acid fragment
  JOURNAL   Patent: EP 1065278-A 5 03-JAN-2001;
            FUJI PHOTO FILM CO., LTD. (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sample nucleic acid fragment"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 20;
  Best Local Similarity   95.0%;  Pred. No. 6e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||  |||||||||
Db          1 TTTTTTTTTTATTTTTTTT 20


RESULT 965
AX825105/c
LOCUS       AX825105                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 3 from Patent WO03072818.
ACCESSION   AX825105
VERSION     AX825105.1  GI:39750834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 3 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||||
Db         20 TTAAAAAAAAAAAAAAAAAA 1


RESULT 966
AX825104/c
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LOCUS       AX825104                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 2 from Patent WO03072818.
ACCESSION   AX825104
VERSION     AX825104.1  GI:39750833
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 2 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              || |||||||||||||||||
Db         20 TTAAAAAAAAAAAAAAAAAA 1


RESULT 967
AX825136
LOCUS       AX825136                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 34 from Patent WO03072818.
ACCESSION   AX825136
VERSION     AX825136.1  GI:39750865
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 34 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTCA 20


RESULT 968
AX825138
LOCUS       AX825138                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 36 from Patent WO03072818.
ACCESSION   AX825138
VERSION     AX825138.1  GI:39750867
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 36 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
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  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTCA 20


RESULT 969
AX825113/c
LOCUS       AX825113                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 11 from Patent WO03072818.
ACCESSION   AX825113
VERSION     AX825113.1  GI:39750842
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 11 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         20 GTAAAAAAAAAAAAAAAAAA 1


RESULT 970
AX825114/c
LOCUS       AX825114                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 12 from Patent WO03072818.
ACCESSION   AX825114
VERSION     AX825114.1  GI:39750843
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 12 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         20 GTAAAAAAAAAAAAAAAAAA 1


RESULT 971
AX825117/c
LOCUS       AX825117                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 15 from Patent WO03072818.
ACCESSION   AX825117
VERSION     AX825117.1  GI:39750846
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 15 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
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                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||||
Db         21 GATAAAAAAAAAAAAAAAAA 2


RESULT 972
AX825121/c
LOCUS       AX825121                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 19 from Patent WO03072818.
ACCESSION   AX825121
VERSION     AX825121.1  GI:39750850
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 19 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         20 TCAAAAAAAAAAAAAAAAAA 1


RESULT 973
AX825112/c
LOCUS       AX825112                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 10 from Patent WO03072818.
ACCESSION   AX825112
VERSION     AX825112.1  GI:39750841
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 10 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         20 GTAAAAAAAAAAAAAAAAAA 1


RESULT 974
AX825148
LOCUS       AX825148                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 46 from Patent WO03072818.
ACCESSION   AX825148
VERSION     AX825148.1  GI:39750877
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 46 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
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     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTCT 20


RESULT 975
AX825149
LOCUS       AX825149                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 47 from Patent WO03072818.
ACCESSION   AX825149
VERSION     AX825149.1  GI:39750878
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 47 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTCT 20


RESULT 976
AX825120
LOCUS       AX825120                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 18 from Patent WO03072818.
ACCESSION   AX825120
VERSION     AX825120.1  GI:39750849
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 18 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
             ||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTGA 20


RESULT 977
AX825120/c
LOCUS       AX825120                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 18 from Patent WO03072818.
ACCESSION   AX825120
VERSION     AX825120.1  GI:39750849
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 18 04-SEP-2003;
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           Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         20 TCAAAAAAAAAAAAAAAAAA 1


RESULT 978
AX825122
LOCUS       AX825122                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 20 from Patent WO03072818.
ACCESSION   AX825122
VERSION     AX825122.1  GI:39750851
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 20 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTGA 20


RESULT 979
AX825122/c
LOCUS       AX825122                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 20 from Patent WO03072818.
ACCESSION   AX825122
VERSION     AX825122.1  GI:39750851
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 20 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         20 TCAAAAAAAAAAAAAAAAAA 1


RESULT 980
AX825128/c
LOCUS       AX825128                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 26 from Patent WO03072818.
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ACCESSION   AX825128
VERSION     AX825128.1  GI:39750857
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 26 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         20 GCAAAAAAAAAAAAAAAAAA 1


RESULT 981
AX825129/c
LOCUS       AX825129                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 27 from Patent WO03072818.
ACCESSION   AX825129
VERSION     AX825129.1  GI:39750858
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 27 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         20 GCAAAAAAAAAAAAAAAAAA 1


RESULT 982
AX825130/c
LOCUS       AX825130                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 28 from Patent WO03072818.
ACCESSION   AX825130
VERSION     AX825130.1  GI:39750859
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 28 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         20 GCAAAAAAAAAAAAAAAAAA 1


RESULT 983
AX825132
LOCUS       AX825132                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 30 from Patent WO03072818.
ACCESSION   AX825132
VERSION     AX825132.1  GI:39750861
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 30 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTGT 20


RESULT 984
AX825133
LOCUS       AX825133                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 31 from Patent WO03072818.
ACCESSION   AX825133
VERSION     AX825133.1  GI:39750862
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 31 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTGT 20


RESULT 985
AX825133/c
LOCUS       AX825133                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 31 from Patent WO03072818.
ACCESSION   AX825133
VERSION     AX825133.1  GI:39750862
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 31 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 21;
  Best Local Similarity   95.0%;  Pred. No. 6.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||
Db         21 GACAAAAAAAAAAAAAAAAA 2


RESULT 986
BD085544
LOCUS       BD085544                 22 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Method of comparison and detection of RNA amount and DNA amount.
ACCESSION   BD085544
VERSION     BD085544.1  GI:22631154
KEYWORDS    JP 2001333800-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Shimada,K.
  TITLE     Method of comparison and detection of RNA amount and DNA amount
  JOURNAL   Patent: JP 2001333800-A 1 04-DEC-2001;
            UNITECH CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001333800-A/1
            PD   04-DEC-2001
            PF   30-MAY-2000 JP 2000160324
            PI   KAORI SHIMADA
            PC   C12Q1/68,C12N15/09,G01N33/50,C12N15/00
            CC   Method of comparison and detection of RNA amount and DNA  CC
                 amount
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 7.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db          3 TCAAAAAAAAAAAAAAAAAA 22


RESULT 987
BD245245
LOCUS       BD245245                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245245
VERSION     BD245245.1  GI:33055015
KEYWORDS    JP 2002532386-A/31.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 31 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/31
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 23;
  Best Local Similarity   95.0%;  Pred. No. 8.9e+02;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTT 2183
              || ||||||||||||||||
Db          4 CCATTTTTTTTTTTTTTTT 23


RESULT 988
AR136778
LOCUS       AR136778                 26 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6162437.
ACCESSION   AR136778
VERSION     AR136778.1  GI:14478028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Pyun,K.-H., Choi,I., Kang,H.-S., Lee,J.-J. and Kim,Y.-H.
  TITLE     Method for inhibiting interleukin-6 production by administering
            extracts from root of Stephania tetrandra
  JOURNAL   Patent: US 6162437-A 1 19-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 26;
  Best Local Similarity   95.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTT 2183
              | ||||||||||||||||||
Db          7 CGTTTTTTTTTTTTTTTTT 26


RESULT 989
E64577
LOCUS       E64577                   26 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for obtaining DNA fragment in plant and utilization thereof.
ACCESSION   E64577
VERSION     E64577.1  GI:18628519
KEYWORDS    JP 2000157277-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Hibino,T. and Koshiyama,J.
  TITLE     Method for obtaining DNA fragment in plant and utilization thereof
  JOURNAL   Patent: JP 2000157277-A 1 13-JUN-2000;
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            NETSUTAIRIN SAISEI GIJUTSU KENKYU KUMIAI
COMMENT     OS   Artificial Sequence
            PN   JP 2000157277-A/1
            PD   13-JUN-2000
            PF   25-NOV-1998 JP 1998333469
            PR
            PI   TAKASHI HIBINO,JUNKO KOSHIYAMA
            PC   C12N15/09,A01H1/00,A01H5/00,C12N5/10//(C12N15/09,C12R1:91), PC
              C12N15/00,
            PC   C12N5/00,(C12N15/00,C12R1:91)
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 26;
  Best Local Similarity   95.0%;  Pred. No. 1.2e+03;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTT 2181
              | ||||||||||||||||||
Db          7 CCCCTTTTTTTTTTTTTTT 26


RESULT 990
AX394616/c
LOCUS       AX394616                 28 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 14 from Patent EP1186673.
ACCESSION   AX394616
VERSION     AX394616.1  GI:21065729
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 14 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 28;
  Best Local Similarity   78.6%;  Pred. No. 1.5e+03;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTT 2183
              ||||      ||||||||||||||||||
Db         28 TTTTGGGAGATTTTTTTTTTTTTTTT 1


RESULT 991
AX394617/c
LOCUS       AX394617                 28 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 15 from Patent EP1186673.
ACCESSION   AX394617
VERSION     AX394617.1  GI:21065730
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 15 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 28;
  Best Local Similarity   78.6%;  Pred. No. 1.5e+03;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTT 2183
              ||||      ||||||||||||||||||
Db         28 TTTTGGGAGATTTTTTTTTTTTTTTT 1


RESULT 992
AX394618/c
LOCUS       AX394618                 28 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 16 from Patent EP1186673.
ACCESSION   AX394618
VERSION     AX394618.1  GI:21065731
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 16 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.7%;  Score 18.4;  DB 1;  Length 28;
  Best Local Similarity   78.6%;  Pred. No. 1.5e+03;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTT 2182
              ||||||      ||||||||||||||||
Db         28 TTTTTTGGGAGATTTTTTTTTTTTTTT 1


RESULT 993
AR102020
LOCUS       AR102020                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 18 from patent US 6083731.
ACCESSION   AR102020
VERSION     AR102020.1  GI:12812818
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
  TITLE     Recombinant materials and methods for the production of limonene
            hydroxylases
  JOURNAL   Patent: US 6083731-A 18 04-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 5.6e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTH 19


RESULT 994
AR102020/c
LOCUS       AR102020                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 18 from patent US 6083731.
ACCESSION   AR102020
VERSION     AR102020.1  GI:12812818
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
  TITLE     Recombinant materials and methods for the production of limonene
            hydroxylases
  JOURNAL   Patent: US 6083731-A 18 04-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 5.6e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 DAAAAAAAAAAAAAAAAAA 1


RESULT 995
AR134802
LOCUS       AR134802                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 18 from patent US 6194185.
ACCESSION   AR134802
VERSION     AR134802.1  GI:14123707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
  TITLE     Recombinant materials and methods for production of limonene
            hydroxylases
  JOURNAL   Patent: US 6194185-A 18 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 5.6e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTH 19


RESULT 996
AR134802/c
LOCUS       AR134802                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 18 from patent US 6194185.
ACCESSION   AR134802
VERSION     AR134802.1  GI:14123707
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
  TITLE     Recombinant materials and methods for production of limonene
            hydroxylases
  JOURNAL   Patent: US 6194185-A 18 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 19;
  Best Local Similarity   94.7%;  Pred. No. 5.6e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 DAAAAAAAAAAAAAAAAAA 1


RESULT 997
E28098
LOCUS       E28098                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28098
VERSION     E28098.1  GI:13018323
KEYWORDS    JP 1999196874-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hideki,K. and Senshu,U.
  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 9 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/9
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 6.5e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTV 19


RESULT 998
E28098/c
LOCUS       E28098                    20 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for analyzing DNA fragment.
ACCESSION   E28098
VERSION     E28098.1  GI:13018323
KEYWORDS    JP 1999196874-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hideki,K. and Senshu,U.
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  TITLE     Method for analyzing DNA fragment
  JOURNAL   Patent: JP 1999196874-A 9 27-JUL-1999;
            HITACHI LTD
COMMENT     OS   Unidentified
            PN   JP 1999196874-A/9
            PD   27-JUL-1999
            PF   14-JAN-1998 JP 1998005399
            PR
            PI   HIDEKI KAMIBARA,SENSHU UEMATSU
            PC   C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 6.5e+02;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
Db         19 BAAAAAAAAAAAAAAAAAA 1


RESULT 999
AR084981
LOCUS       AR084981                 23 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 15 from patent US 5981251.
ACCESSION   AR084981
VERSION     AR084981.1  GI:10011752
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Ullrich,A. and Vogel,W.
  TITLE     PTP 1D: a novel protein tyrosine phosphatase
  JOURNAL   Patent: US 5981251-A 15 09-NOV-1999;
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTT 2184
              |||   ||||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTTT 23


RESULT 1000
AR100207
LOCUS       AR100207                 23 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 6 from patent US 6080576.
ACCESSION   AR100207
VERSION     AR100207.1  GI:12810655
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Zambrowicz,B., Friedrich,G. and Sands,A.T.
  TITLE     Vectors for gene trapping and gene activation
  JOURNAL   Patent: US 6080576-A 6 27-JUN-2000;
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1999 CTAGCTTCTTCAGAGATCAAGTC 2021
              | ||  ||||||||||||||||||
Db          1 CCAGAGTCTTCAGAGATCAAGTC 23


RESULT 1001
AR123791/c
LOCUS       AR123791                 23 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 7 from patent US 6171803.
ACCESSION   AR123791
VERSION     AR123791.1  GI:14109152
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kinet,J.Pierre.
  TITLE     Isolation, characterization, and use of the human .beta. subunit of
            the high affinity receptor for immunoglobulin E
  JOURNAL   Patent: US 6171803-A 7 09-JAN-2001;
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              | ||||||||||||| |||| ||
Db         23 CATTTTTTTTTTTTGTTTTATT 1


RESULT 1002
BD263052
LOCUS       BD263052                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Vectors for gene mutagenesis and gene discovery by gene trapping.
ACCESSION   BD263052
VERSION     BD263052.1  GI:33072820
KEYWORDS    JP 2002539764-A/17.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Zambrowicz,B., Friedrich,G.A., Lilleberg,S. and Sands,A.T.
  TITLE     Vectors for gene mutagenesis and gene discovery by gene trapping
  JOURNAL   Patent: JP 2002539764-A 17 26-NOV-2002;
            LEXICON GENETICS INC
COMMENT     OS   Mus musculus (mouse)
            PN   JP 2002539764-A/17
            PD   26-NOV-2002
            PF   19-NOV-1999 JP 2000584047
            PR   20-NOV-1998 US    60/109302,25-MAR-1999 US    09/276533 PI
            BRIAN ZAMBROWICZ,GLENN A FRIEDRICH,STAN LILLEBERG,ARTHUR T  PI
            SANDS
            PC   C12N15/09,A01K67/027,C12N5/10,C12N7/00//(C12N7/00,C12R1:93),
            PC   C12N15/00,
            PC   C12N5/00
            CC   Vectors for gene mutagenesis and gene discovery by gene  CC
               trapping
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Mus musculus (mouse)'.
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FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"

  Query Match              0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1999 CTAGCTTCTTCAGAGATCAAGTC 2021
              | ||  ||||||||||||||||||
Db          1 CCAGAGTCTTCAGAGATCAAGTC 23


RESULT 1003
I32906
LOCUS       I32906                   23 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 15 from patent US 5589375.
ACCESSION   I32906
VERSION     I32906.1  GI:1823697
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Ullrich,A. and Vogel,W.
  TITLE     PTP 1D: a novel protein tyrosine phosphatase
  JOURNAL   Patent: US 5589375-A 15 31-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTT 2184
              |||   ||||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTTT 23


RESULT 1004
AR306617
LOCUS       AR306617                 23 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 15 from patent US 6548641.
ACCESSION   AR306617
VERSION     AR306617.1  GI:31696809
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Ullrich,A. and Vogel,W.
  TITLE     PTP 1D: a novel protein tyrosine phosphatase
  JOURNAL   Patent: US 6548641-A 15 15-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTT 2184
              |||   ||||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTTT 23


RESULT 1005
BD105197
LOCUS       BD105197                 23 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel glucosyltransferase gene.
ACCESSION   BD105197
VERSION     BD105197.1  GI:22650771
KEYWORDS    WO 0192509-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Mizutani,M., Sakakibara,K., Tanaka,Y., Kusumi,T. and Ono,E.
  TITLE     Novel glucosyltransferase gene
  JOURNAL   Patent: WO 0192509-A 3 06-DEC-2001;
            INTERNATIONAL FLOWER DEVELOPMENTS PROPRIETARY LTD,MASAKO MIZUTANI,
            KEIKO SAKAKIBARA,YOSHIKAZU TANAKA,TAKAAKI KUSUMI,EIICHIRO ONO
COMMENT     OS   Artificial Sequence
            PN   WO 0192509-A/3
            PD   06-DEC-2001
            PF   01-JUN-2001 WO 2001JP004675
            PR   02-JUN-2000 JP 00P   170436
            PI   MASAKO MIZUTANI,KEIKO SAKAKIBARA,YOSHIKAZU TANAKA,TAKAAKI  PI
             KUSUMI,
            PI   EIICHIRO ONO
            PC   C12N15/09,C12N15/29,C12N15/54,C12N1/15,C12N1/19,C12N1/21 PC
            ,C12N5/10,C12N9/10,
            PC   A01H5/00
            CC   Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 18.2;  DB 1;  Length 23;
  Best Local Similarity   87.0%;  Pred. No. 9.6e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTT 2184
              |||   ||||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTTT 23


RESULT 1006
AX454028/c
LOCUS       AX454028                 25 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 4 from Patent WO0198539.
ACCESSION   AX454028
VERSION     AX454028.1  GI:21713668
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mitsuhashi,M., Kambara,H., Matsunaga,H. and Kawamura,M.
  TITLE     Gene markers for lung cancer
  JOURNAL   Patent: WO 0198539-A 4 27-DEC-2001;
            Hitachi Chemical Co., Ltd. (JP) ; HITACHI CHEMICAL RESEARCH CENTER,
            INC. (US) ; Hitachi, Ltd. (JP)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="anchor primer P4."

  Query Match              0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   94.7%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              :||||||||||||||||||
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Db         24 BAAAAAAAAAAAAAAAAA 6


RESULT 1007
AX042942/c
LOCUS       AX042942                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 508 from Patent WO0065088.
ACCESSION   AX042942
VERSION     AX042942.1  GI:11341550
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 508 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAA 2798
              |||| || | ||||||||||||||
Db         23 GTTAAAACTCAAAAAAAAAAAAA 1


RESULT 1008
I20186
LOCUS       I20186                    25 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5514546.
ACCESSION   I20186
VERSION     I20186.1  GI:1600541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kool,E.T.
  TITLE     Stem-loop oligonucleotides containing parallel and antiparallel
            binding domains
  JOURNAL   Patent: US 5514546-A 1 07-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||| | | ||||||||
Db          1 CCTTTTTTTTCTCTCTTTTTTT 23


RESULT 1009
AX042923
LOCUS       AX042923                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 489 from Patent WO0065088.
ACCESSION   AX042923
VERSION     AX042923.1  GI:11341531
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 489 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||||| |||  ||
Db          1 TTTTTTTTTTTTTTTAAACGCTG 23


RESULT 1010
AX043281
LOCUS       AX043281                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 847 from Patent WO0065088.
ACCESSION   AX043281
VERSION     AX043281.1  GI:11341889
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 847 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTAACTTTGA 2194
              |||||||||||| |||  |||||
Db          1 TTTTTTTTTTTTCTTAGATTTGA 23


RESULT 1011
AX115988
LOCUS       AX115988                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 1111 from Patent WO0129262.
ACCESSION   AX115988
VERSION     AX115988.1  GI:14032930
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 1111 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
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  Query Match             0.6%;  Score 18.2;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 1.2e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
              |||  |||||||||||| ||||||
Db          2 CCTAGTTTTTTTTTTGTTTTTT 24


RESULT 1012
AR172578
LOCUS       AR172578                 26 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 10 from patent US 6303328.
ACCESSION   AR172578
VERSION     AR172578.1  GI:17912069
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Re,R. and Cook,J.
  TITLE     Inhibition of cellular proliferation in vitro by oligonucleotide
            binding to a chromosomal binding site for p53 protein
  JOURNAL   Patent: US 6303328-A 10 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 26;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||  |||||||| |||||
Db          2 CCTTTTTTCCTTTTTTTCTTTTT 24


RESULT 1013
AR430169
LOCUS       AR430169                 26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 10 from patent US 6645944.
ACCESSION   AR430169
VERSION     AR430169.1  GI:40190841
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Re,R. and Cook,J.
  TITLE     Inhibition of cellular proliferation by oligonucleotide binding to
            a chromosomal binding site for p53 protein
  JOURNAL   Patent: US 6645944-A 10 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 26;
  Best Local Similarity   87.0%;  Pred. No. 1.3e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||  |||||||| |||||
Db          2 CCTTTTTTCCTTTTTTTCTTTTT 24


RESULT 1014
AX391845/c
LOCUS       AX391845                 28 bp    RNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 10 from Patent WO0216574.
ACCESSION   AX391845
VERSION     AX391845.1  GI:19700427
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Reimholz,R. and Ploeger,F.
  TITLE     Method for identifying peptides that can be specifically cleaved
            and the use of peptide sequences of this type
  JOURNAL   Patent: WO 0216574-A 10 28-FEB-2002;
            Xzillion GmbH & CO.KG (DE)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Puromycin-Linker-RNA-Teil"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   87.0%;  Pred. No. 1.6e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||| | |
Db         28 TTTTTTTTTTTTTTTTTTGCATC 6


RESULT 1015
AR055117/c
LOCUS       AR055117                 28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 22 from patent US 5837468.
ACCESSION   AR055117
VERSION     AR055117.1  GI:5980694
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA substractive cloning method
  JOURNAL   Patent: US 5837468-A 22 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   87.0%;  Pred. No. 1.6e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||   ||
Db         28 CTTTTTTTTTTTTTTTTGCCTA 6


RESULT 1016
AR068458/c
LOCUS       AR068458                 28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 22 from patent US 5853991.
ACCESSION   AR068458
VERSION     AR068458.1  GI:6000665
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA subtractive cloning method
  JOURNAL   Patent: US 5853991-A 22 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   87.0%;  Pred. No. 1.6e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||   ||
Db         28 CTTTTTTTTTTTTTTTTTGCCTA 6


RESULT 1017
AJ600024/c
LOCUS       AJ600024                 28 bp    DNA     linear   PLN 23-OCT-2003
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            498E01.
ACCESSION   AJ600024
VERSION     AJ600024.1  GI:37949652
KEYWORDS    right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
    PUBMED  12446565
REFERENCE   2  (bases 1 to 28)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="498E01"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .28
                     /note="T-DNA flanking sequence
                     right border"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 28;
  Best Local Similarity   87.0%;  Pred. No. 1.6e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||  | |||  ||||||||
Db         23 CCTTTTTTGTGTTTGTTTTTTT 1


RESULT 1018
BD274324/c
LOCUS       BD274324                 29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION   BD274324
VERSION     BD274324.1  GI:33084092
KEYWORDS    JP 2002526030-A/291.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
  TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
  JOURNAL   Patent: JP 2002526030-A 291 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526030-A/291
            PD   20-AUG-2002
            PF   12-MAY-1999 JP 2000548510
            PR   12-MAY-1998 US    60/085092,12-MAY-1998 US    09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC   Description
            of Artificial Sequence: Novel Sequence CC   N is any nucleotide
            FH   Key             Location/Qualifiers
            FT   misc_feature    (28). .(29).
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 29;
  Best Local Similarity   87.0%;  Pred. No. 1.7e+03;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||||  | |
Db         27 TTTTTTTTTTTTTTTTTAGGTCT 5


RESULT 1019
BD274342/c
LOCUS       BD274342                 29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION   BD274342
VERSION     BD274342.1  GI:33084110
KEYWORDS    JP 2002526030-A/309.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
  TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
  JOURNAL   Patent: JP 2002526030-A 309 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526030-A/309
            PD   20-AUG-2002
            PF   12-MAY-1999 JP 2000548510
            PR   12-MAY-1998 US    60/085092,12-MAY-1998 US    09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC   Description
            of Artificial Sequence: Novel Sequence CC   N is any nucleotide
            FH   Key             Location/Qualifiers
            FT   misc_feature    (28). .(29).
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18.2;  DB 1;  Length 29;
  Best Local Similarity   87.0%;  Pred. No. 1.7e+03;
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  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||||||| | |
Db         27 TTTTTTTTTTTTTTTTTAGGTCT 5


RESULT 1020
AR034896
LOCUS       AR034896                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5869643.
ACCESSION   AR034896
VERSION     AR034896.1  GI:5950501
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 12 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1021
AR034896/c
LOCUS       AR034896                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5869643.
ACCESSION   AR034896
VERSION     AR034896.1  GI:5950501
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 12 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 1022
AR034899
LOCUS       AR034899                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 18 from patent US 5869643.
ACCESSION   AR034899
VERSION     AR034899.1  GI:5950504
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 18 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 18


RESULT 1023
AR034899/c
LOCUS       AR034899                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 18 from patent US 5869643.
ACCESSION   AR034899
VERSION     AR034899.1  GI:5950504
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Chatelain,F. and Kumarev,V.
  TITLE     Process for preparing polynucleotides on a solid support in a
            tightly packed bed
  JOURNAL   Patent: US 5869643-A 18 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTT 1


RESULT 1024
AR058305
LOCUS       AR058305                 18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5837820.
ACCESSION   AR058305
VERSION     AR058305.1  GI:5983882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
  TITLE     Seed specific biotinylated protein, SBP65, from leguminous plants
  JOURNAL   Patent: US 5837820-A 3 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 18


RESULT 1025
AR058305/c
LOCUS       AR058305                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5837820.
ACCESSION   AR058305
VERSION     AR058305.1  GI:5983882
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   De Rose,R., Douce,R., Duval,M., Job,C. and Job,D.
  TITLE     Seed specific biotinylated protein, SBP65, from leguminous plants
  JOURNAL   Patent: US 5837820-A 3 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTT 1


RESULT 1026
AR097579
LOCUS       AR097579                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6071745.
ACCESSION   AR097579
VERSION     AR097579.1  GI:12806309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6071745-A 9 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1027
AR097579/c
LOCUS       AR097579                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 9 from patent US 6071745.
ACCESSION   AR097579
VERSION     AR097579.1  GI:12806309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.Patsy., Wallace,R.Bruce., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6071745-A 9 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 1028
AR106506
LOCUS       AR106506                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 30 from patent US 6107060.
ACCESSION   AR106506
VERSION     AR106506.1  GI:12821036
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Keeling,P. and Guan,H.
  TITLE     Starch encapsulation
  JOURNAL   Patent: US 6107060-A 30 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 18


RESULT 1029
AR106506/c
LOCUS       AR106506                  18 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 30 from patent US 6107060.
ACCESSION   AR106506
VERSION     AR106506.1  GI:12821036
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Keeling,P. and Guan,H.
  TITLE     Starch encapsulation
  JOURNAL   Patent: US 6107060-A 30 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
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Db          18 TTTTTTTTTTTTTTTTT 1


RESULT 1030
E28535
LOCUS       E28535                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28535
VERSION     E28535.1  GI:13025387
KEYWORDS    JP 1999075880-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 2 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/2
            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1031
E28535/c
LOCUS       E28535                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28535
VERSION     E28535.1  GI:13025387
KEYWORDS    JP 1999075880-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 2 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/2
            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          18 TTTTTTTTTTTTTTTTT 1


RESULT 1032
E28536
LOCUS       E28536                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28536
VERSION     E28536.1  GI:13025388
KEYWORDS    JP 1999075880-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 3 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/3
            PD   23-MAR-1999
            PF   10-JUL-1998 JP 1998195719
            PR
            PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
            C12N15/09,C12Q1/68,G01N33/58,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1033
E28536/c
LOCUS       E28536                    18 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Method for labeling oligonucleotide and utilization thereof.
ACCESSION   E28536
VERSION     E28536.1  GI:13025388
KEYWORDS    JP 1999075880-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
  TITLE     Method for labeling oligonucleotide and utilization thereof
  JOURNAL   Patent: JP 1999075880-A 3 23-MAR-1999;
            CHEMO SERO THERAPEUT RES INST
COMMENT     OS   Unidentified
            PN   JP 1999075880-A/3
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          PD   23-MAR-1999
          PF   10-JUL-1998 JP 1998195719
          PR
          PI   KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
          C12N15/09,C12Q1/68,G01N33/58,C12N15/00
          CC   Strandedness: Single;
          CC   Topology: Linear;
          FH   Key             Location/Qualifiers
          FT   source          1. .18
          FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1034
I79509
LOCUS       I79509                   18 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 16 from patent US 5707807.
ACCESSION   I79509
VERSION     I79509.1  GI:3207799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 16 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1035
I79509/c
LOCUS       I79509                   18 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 16 from patent US 5707807.
ACCESSION   I79509
VERSION     I79509.1  GI:3207799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 16 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1036
AR208427/c
LOCUS       AR208427                 18 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 7 from patent US 6383754.
ACCESSION   AR208427
VERSION     AR208427.1  GI:21509578
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: US 6383754-A 7 07-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              ||||||||||||||||||
Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 1037
AR215435
LOCUS       AR215435                 18 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 9 from patent US 6410321.
ACCESSION   AR215435
VERSION     AR215435.1  GI:23313691
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6410321-A 9 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1038
AR215435/c
LOCUS       AR215435                 18 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 9 from patent US 6410321.
ACCESSION   AR215435
VERSION     AR215435.1  GI:23313691
KEYWORDS    .
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
  TITLE     Method and formulation for lyophilizing cultured human cells to
            preserve RNA and DNA contained in cells for use in molecular
            biology experiments
  JOURNAL   Patent: US 6410321-A 9 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1039
AR222464
LOCUS       AR222464                  18 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 24 from patent US 6429300.
ACCESSION   AR222464
VERSION     AR222464.1  GI:23329995
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 24 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1040
AR222464/c
LOCUS       AR222464                  18 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 24 from patent US 6429300.
ACCESSION   AR222464
VERSION     AR222464.1  GI:23329995
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 24 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1041
AR412363
LOCUS       AR412363                  18 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 14 from patent US 6639062.
ACCESSION   AR412363
VERSION     AR412363.1  GI:40167473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleosidic compounds and oligomeric compounds
            prepared therefrom
  JOURNAL   Patent: US 6639062-A 14 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1042
AR412363/c
LOCUS       AR412363                  18 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 14 from patent US 6639062.
ACCESSION   AR412363
VERSION     AR412363.1  GI:40167473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleosidic compounds and oligomeric compounds
            prepared therefrom
  JOURNAL   Patent: US 6639062-A 14 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1043
AX004875
LOCUS       AX004875                  18 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 4 from Patent WO9910527.
ACCESSION   AX004875
VERSION     AX004875.1  GI:9928275
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
```

```
            artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 4 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3' palmityl oligonucleotide"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1044
AX004875/c
LOCUS       AX004875                 18 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 4 from Patent WO9910527.
ACCESSION   AX004875
VERSION     AX004875.1  GI:9928275
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 4 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="3' palmityl oligonucleotide"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1045
AX004879
LOCUS       AX004879                 18 bp    RNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 8 from Patent WO9910527.
ACCESSION   AX004879
VERSION     AX004879.1  GI:9928279
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 8 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="2' methyl-modified oligonucleotide"
     modified_base   1. .18
                     /mod_base=um

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1046
AX004879/c
LOCUS       AX004879                 18 bp    RNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 8 from Patent WO9910527.
ACCESSION   AX004879
VERSION     AX004879.1  GI:9928279
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 8 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="2' methyl-modified oligonucleotide"
     modified_base   1. .18
                     /mod_base=um

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1047
AX008117
LOCUS       AX008117                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 2 from Patent WO9967378.
ACCESSION   AX008117
VERSION     AX008117.1  GI:9995742
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 2 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 1048
AX008117/c
LOCUS AX008117 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9967378.
ACCESSION AX008117
VERSION AX008117.1 GI:9995742
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 2 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 18 TTTTTTTTTTTTTTTTTT 1

RESULT 1049
AX008118
LOCUS AX008118 18 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 3 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 1050
AX008118/c
LOCUS AX008118 18 bp RNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 3 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803
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Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 1051
AX008122
LOCUS AX008122 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO9967378.
ACCESSION AX008122
VERSION AX008122.1 GI:9995747
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and Borkow,G.
TITLE Antisense oligonucleotide constructs based on beta -arabinofuranose and its analogues
JOURNAL Patent: WO 9967378-A 7 29-DEC-1999;
DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA); BORKOW GADI (IL)
FEATURES Location/Qualifiers
source 1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match 0.6%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1052
AX008122/c
LOCUS       AX008122                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 7 from Patent WO9967378.
ACCESSION   AX008122
VERSION     AX008122.1  GI:9995747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 7 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1053
AX008123
LOCUS       AX008123                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 8 from Patent WO9967378.
ACCESSION   AX008123
VERSION     AX008123.1  GI:9995748
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 8 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1054
AX008123/c
LOCUS       AX008123                 18 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 8 from Patent WO9967378.
ACCESSION   AX008123
VERSION     AX008123.1  GI:9995748
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
  TITLE     Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
  JOURNAL   Patent: WO 9967378-A 8 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Use as an oligomer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTT 1


RESULT 1055
AX028843
LOCUS       AX028843                 18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 27 from Patent WO9732023.
ACCESSION   AX028843
VERSION     AX028843.1  GI:10189946
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 27 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTA 18


RESULT 1056
AX028844/c
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LOCUS       AX028844                 18 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 28 from Patent WO9732023.
ACCESSION   AX028844
VERSION     AX028844.1  GI:10189947
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brugliera,F., Holton,T.A. and Michael,M.Z.
  TITLE     Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
  JOURNAL   Patent: WO 9732023-A 28 04-SEP-1997;
            FLORIGENE LIMITED (AU) ; BRUGLIERA FILIPPA (AU) ; HOLTON TIMOTHY
            ALBERT (AU) ; MICHAEL MICHAEL ZENON (AU)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         18 GAAAAAAAAAAAAAAAAA 1


RESULT 1057
AX047271
LOCUS       AX047271                 18 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 21 from Patent WO0068422.
ACCESSION   AX047271
VERSION     AX047271.1  GI:11876551
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
            Gumbiowski,K. and Zulauf,M.
  TITLE     High density labeling of dna with modified or chromophore carrying
            nucleotides and dna polymerases used
  JOURNAL   Patent: WO 0068422-A 21 16-NOV-2000;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="second fragment of SEQ ID NO: 6"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1058
AX047271/c
LOCUS       AX047271                 18 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 21 from Patent WO0068422.
ACCESSION   AX047271
VERSION     AX047271.1  GI:11876551
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
            Gumbiowski,K. and Zulauf,M.
  TITLE     High density labeling of dna with modified or chromophore carrying
            nucleotides and dna polymerases used
  JOURNAL   Patent: WO 0068422-A 21 16-NOV-2000;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="second fragment of SEQ ID NO: 6"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1059
AX047273
LOCUS       AX047273                 18 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 23 from Patent WO0068422.
ACCESSION   AX047273
VERSION     AX047273.1  GI:11876553
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
            Gumbiowski,K. and Zulauf,M.
  TITLE     High density labeling of dna with modified or chromophore carrying
            nucleotides and dna polymerases used
  JOURNAL   Patent: WO 0068422-A 23 16-NOV-2000;
            Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="second fragment of SEQ ID NO: 6"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1060
AX047273/c
LOCUS       AX047273                 18 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 23 from Patent WO0068422.
ACCESSION   AX047273
VERSION     AX047273.1  GI:11876553
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
            Gumbiowski,K. and Zulauf,M.
  TITLE     High density labeling of dna with modified or chromophore carrying
            nucleotides and dna polymerases used
  JOURNAL   Patent: WO 0068422-A 23 16-NOV-2000;
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           Roche Diagnostics GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="second fragment of SEQ ID NO: 6"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1061
AX085253/c
LOCUS       AX085253                 18 bp    DNA     linear   PAT 09-MAR-2001
DEFINITION  Sequence 7 from Patent WO0112855.
ACCESSION   AX085253
VERSION     AX085253.1  GI:13275311
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
  TITLE     Binary encoded sequence tags
  JOURNAL   Patent: WO 0112855-A 7 22-FEB-2001;
            YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAA 2801
              ||||||||||||||||||
Db         18 TGAAAAAAAAAAAAAAAA 1


RESULT 1062
AX104721
LOCUS       AX104721                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 913 from Patent WO0122972.
ACCESSION   AX104721
VERSION     AX104721.1  GI:13920918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 913 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1063
AX104721/c
LOCUS       AX104721                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 913 from Patent WO0122972.
ACCESSION   AX104721
VERSION     AX104721.1  GI:13920918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 913 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1064
AX104747
LOCUS       AX104747                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 939 from Patent WO0122972.
ACCESSION   AX104747
VERSION     AX104747.1  GI:13920944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 939 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1065
AX104747/c
LOCUS       AX104747                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 939 from Patent WO0122972.
ACCESSION   AX104747
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VERSION     AX104747.1  GI:13920944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 939 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1066
AX105651
LOCUS       AX105651                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 10 from Patent WO0123564.
ACCESSION   AX105651
VERSION     AX105651.1  GI:13921674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and Kapoun,A.M.
  TITLE     Secreted factors
  JOURNAL   Patent: WO 0123564-A 10 05-APR-2001;
            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1067
AX105651/c
LOCUS       AX105651                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 10 from Patent WO0123564.
ACCESSION   AX105651
VERSION     AX105651.1  GI:13921674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and Kapoun,A.M.
  TITLE     Secreted factors
  JOURNAL   Patent: WO 0123564-A 10 05-APR-2001;
            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1068
AX108642
LOCUS       AX108642                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 10 from Patent WO0123419.
ACCESSION   AX108642
VERSION     AX108642.1  GI:13923875
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and Kapoun,A.M.
  TITLE     Differentially expressed genes
  JOURNAL   Patent: WO 0123419-A 10 05-APR-2001;
            SCIOS INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1069
AX108642/c
LOCUS       AX108642                 18 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 10 from Patent WO0123419.
ACCESSION   AX108642
VERSION     AX108642.1  GI:13923875
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and Kapoun,A.M.
  TITLE     Differentially expressed genes
  JOURNAL   Patent: WO 0123419-A 10 05-APR-2001;
            SCIOS INC. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
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                    ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1070
AX268883
LOCUS       AX268883                 18 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 84 from Patent WO0174901.
ACCESSION   AX268883
VERSION     AX268883.1  GI:16541910
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and White,R.T.
  TITLE     Secreted factors
  JOURNAL   Patent: WO 0174901-A 84 11-OCT-2001;
            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligos corresponding to polylinker sequence."

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
                ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1071
AX268883/c
LOCUS       AX268883                 18 bp    DNA     linear   PAT 29-OCT-2001
DEFINITION  Sequence 84 from Patent WO0174901.
ACCESSION   AX268883
VERSION     AX268883.1  GI:16541910
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stanton,L.W. and White,R.T.
  TITLE     Secreted factors
  JOURNAL   Patent: WO 0174901-A 84 11-OCT-2001;
            Scios Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligos corresponding to polylinker sequence."

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
                ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1072
AX355809
LOCUS       AX355809                 18 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 837 from Patent WO0197843.
ACCESSION   AX355809
VERSION     AX355809.1  GI:18620477
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 837 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
                ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1073
AX355809/c
LOCUS       AX355809                 18 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 837 from Patent WO0197843.
ACCESSION   AX355809
VERSION     AX355809.1  GI:18620477
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 837 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
                ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1074
AX547774
LOCUS       AX547774                 18 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 913 from Patent WO02053141.
ACCESSION   AX547774
VERSION     AX547774.1  GI:25812918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 913 11-JUL-2002;
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            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1075
AX547774/c
LOCUS       AX547774                  18 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 913 from Patent WO02053141.
ACCESSION   AX547774
VERSION     AX547774.1  GI:25812918
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 913 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1076
AX547800
LOCUS       AX547800                  18 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 939 from Patent WO02053141.
ACCESSION   AX547800
VERSION     AX547800.1  GI:25812944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 939 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1077
AX547800/c
LOCUS       AX547800                  18 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 939 from Patent WO02053141.
ACCESSION   AX547800
VERSION     AX547800.1  GI:25812944
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 939 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1078
AX814716
LOCUS       AX814716                  18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 1 from Patent WO03064441.
ACCESSION   AX814716
VERSION     AX814716.1  GI:39103916
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 1 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1079
AX814716/c
LOCUS       AX814716                  18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 1 from Patent WO03064441.
ACCESSION   AX814716
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VERSION     AX814716.1  GI:39103916
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 1 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1080
AX814723
LOCUS       AX814723                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 8 from Patent WO03064441.
ACCESSION   AX814723
VERSION     AX814723.1  GI:39103922
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 8 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .17
                     /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                     2'-O-methyl-D-uridi ne"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1081
AX814723/c
LOCUS       AX814723                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 8 from Patent WO03064441.
ACCESSION   AX814723
VERSION     AX814723.1  GI:39103922
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 8 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .17
                     /note="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are
                     2'-O-methyl-D-uridi ne"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1082
AX814724
LOCUS       AX814724                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 9 from Patent WO03064441.
ACCESSION   AX814724
VERSION     AX814724.1  GI:39103923
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 9 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .15
                     /note="Residues 1-3, 7-9, and 13-15 are
                     2'-O-methyl-D-uridine"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1083
AX814724/c
LOCUS       AX814724                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 9 from Patent WO03064441.
ACCESSION   AX814724
VERSION     AX814724.1  GI:39103923
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 9 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .15
                     /note="Residues 1-3, 7-9, and 13-15 are
                     2'-O-methyl-D-uridine"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1084
AX814725
LOCUS       AX814725                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 10 from Patent WO03064441.
ACCESSION   AX814725
VERSION     AX814725.1  GI:39103924
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 10 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .18
                     /note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1085
AX814725/c
LOCUS       AX814725                 18 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 10 from Patent WO03064441.
ACCESSION   AX814725
VERSION     AX814725.1  GI:39103924
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 10 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
     misc_feature    1. .18
                     /note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1086
AX814736
LOCUS       AX814736                 18 bp    RNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 21 from Patent WO03064441.
ACCESSION   AX814736
VERSION     AX814736.1  GI:39103935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 21 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Target RNA oligonucleotide"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1087
AX814736/c
LOCUS       AX814736                 18 bp    RNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 21 from Patent WO03064441.
ACCESSION   AX814736
VERSION     AX814736.1  GI:39103935
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Damha,M.J. and Parniak,M.A.
  TITLE     Oligonucleotides comprising alternating segments and uses thereof
  JOURNAL   Patent: WO 03064441-A 21 07-AUG-2003;
            McGILL UNIVERSITY (CA)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Target RNA oligonucleotide"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1088
BD085545
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LOCUS       BD085545                 18 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Method of comparison and detection of RNA amount and DNA amount.
ACCESSION   BD085545
VERSION     BD085545.1  GI:22631155
KEYWORDS    JP 2001333800-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Shimada,K.
  TITLE     Method of comparison and detection of RNA amount and DNA amount
  JOURNAL   Patent: JP 2001333800-A 2 04-DEC-2001;
            UNITECH CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001333800-A/2
            PD   04-DEC-2001
            PF   30-MAY-2000 JP 2000160324
            PI   KAORI SHIMADA
            PC   C12Q1/68,C12N15/09,G01N33/50,C12N15/00
            CC   Method of comparison and detection of RNA amount and DNA  CC
                 amount
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1089
BD085545/c
LOCUS       BD085545                 18 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Method of comparison and detection of RNA amount and DNA amount.
ACCESSION   BD085545
VERSION     BD085545.1  GI:22631155
KEYWORDS    JP 2001333800-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Shimada,K.
  TITLE     Method of comparison and detection of RNA amount and DNA amount
  JOURNAL   Patent: JP 2001333800-A 2 04-DEC-2001;
            UNITECH CO LTD
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001333800-A/2
            PD   04-DEC-2001
            PF   30-MAY-2000 JP 2000160324
            PI   KAORI SHIMADA
            PC   C12Q1/68,C12N15/09,G01N33/50,C12N15/00
            CC   Method of comparison and detection of RNA amount and DNA  CC
                 amount
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Homo sapiens"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          18 AAAAAAAAAAAAAAAAAA 1


RESULT 1090
BD190553
LOCUS       BD190553                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Secretory proteins and polynucleotides encoding the same.
ACCESSION   BD190553
VERSION     BD190553.1  GI:33000292
KEYWORDS    JP 2002515753-A/12.
SOURCE      Rattus
  ORGANISM  Rattus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,
            Treacy,M., Spaulding,V. and Agostino,M.J.
  TITLE     Secretory proteins and polynucleotides encoding the same
  JOURNAL   Patent: JP 2002515753-A 12 28-MAY-2002;
            GENETICS INSTITUTE INC
COMMENT     PN   JP 2002515753-A/12
            PD   28-MAY-2002
            PF   31-OCT-1997 JP 1998521609
            PR   01-NOV-1996 US     08/724973
            PI   KENNETH JACOBS,JOHN M MCCOY,EDWARD R LAVALLIE,LISA A RACIE, PI
              DAVID MERBERG,
            PI   MAURICE TREACY,VIKKI SPAULDING,MICHAEL J AGOSTINO PC
            C12N15/12,C12N5/10,C07K14/47,C12Q1/68,A61K38/17 CC   Strandedness:
            Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Rattus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10114"

  Query Match             0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db          1 GAAAAAAAAAAAAAAAAA 18


RESULT 1091
BD222596
LOCUS       BD222596                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom.
ACCESSION   BD222596
VERSION     BD222596.1  GI:33032366
KEYWORDS    JP 2002522447-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom
  JOURNAL   Patent: JP 2002522447-A 14 23-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002522447-A/14
            PD   23-JUL-2002
            PF   09-AUG-1999 JP 2000563675
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            PR   07-AUG-1998 US    09/130973
            PI   MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
            PI   KAWASAKI
            PC   C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence: antisense sequence FH
            Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1092
BD222596/c
LOCUS       BD222596                 18 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom.
ACCESSION   BD222596
VERSION     BD222596.1  GI:33032366
KEYWORDS    JP 2002522447-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified nucleoside compound and oligomer compound
            produced therefrom
  JOURNAL   Patent: JP 2002522447-A 14 23-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002522447-A/14
            PD   23-JUL-2002
            PF   09-AUG-1999 JP 2000563675
            PR   07-AUG-1998 US    09/130973
            PI   MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
            PI   KAWASAKI
            PC   C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence: antisense sequence FH
            Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.6%;  Score 18;  DB 1;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 5.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1093
AR432617
LOCUS       AR432617                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6653458.
ACCESSION   AR432617
VERSION     AR432617.1  GI:40195150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D. and Guinosso,C.J.
  TITLE     Modified oligonucleotides
  JOURNAL   Patent: US 6653458-A 7 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1094
AR432617/c
LOCUS       AR432617                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6653458.
ACCESSION   AR432617
VERSION     AR432617.1  GI:40195150
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D. and Guinosso,C.J.
  TITLE     Modified oligonucleotides
  JOURNAL   Patent: US 6653458-A 7 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.6%;  Score 18;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1095
AR139961/c
LOCUS       AR139961                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 33 from patent US 6207417.
ACCESSION   AR139961
VERSION     AR139961.1  GI:14482457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     DNA encoding stem cell factor
  JOURNAL   Patent: US 6207417-A 33 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1096
AR139962
LOCUS       AR139962                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 34 from patent US 6207417.
ACCESSION   AR139962
VERSION     AR139962.1  GI:14482458
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     DNA encoding stem cell factor
  JOURNAL   Patent: US 6207417-A 34 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1097
AR140280/c
LOCUS       AR140280                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 33 from patent US 6207454.
ACCESSION   AR140280
VERSION     AR140280.1  GI:14482776
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method for enhancing the effciency of gene transfer with stem cell
            factor (SCF) polypeptide
  JOURNAL   Patent: US 6207454-A 33 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1098
AR140281
LOCUS       AR140281                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 34 from patent US 6207454.
ACCESSION   AR140281
VERSION     AR140281.1  GI:14482777
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method for enhancing the effciency of gene transfer with stem cell
            factor (SCF) polypeptide
  JOURNAL   Patent: US 6207454-A 34 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1099
AR140558/c
LOCUS       AR140558                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 33 from patent US 6207802.
ACCESSION   AR140558
VERSION     AR140558.1  GI:14483054
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Stem cell factor and compositions
  JOURNAL   Patent: US 6207802-A 33 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1100
AR140559
LOCUS       AR140559                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 34 from patent US 6207802.
ACCESSION   AR140559
VERSION     AR140559.1  GI:14483055
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Stem cell factor and compositions
  JOURNAL   Patent: US 6207802-A 34 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
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Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1101
AR139960
LOCUS       AR139960                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207417.
ACCESSION   AR139960
VERSION     AR139960.1  GI:14482456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     DNA encoding stem cell factor
  JOURNAL   Patent: US 6207417-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1102
AR139960/c
LOCUS       AR139960                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207417.
ACCESSION   AR139960
VERSION     AR139960.1  GI:14482456
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     DNA encoding stem cell factor
  JOURNAL   Patent: US 6207417-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 1103
AR140279
LOCUS       AR140279                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207454.
ACCESSION   AR140279
VERSION     AR140279.1  GI:14482775
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method for enhancing the effciency of gene transfer with stem cell
            factor (SCF) polypeptide
  JOURNAL   Patent: US 6207454-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1104
AR140279/c
LOCUS       AR140279                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207454.
ACCESSION   AR140279
VERSION     AR140279.1  GI:14482775
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method for enhancing the effciency of gene transfer with stem cell
            factor (SCF) polypeptide
  JOURNAL   Patent: US 6207454-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 1105
AR140557
LOCUS       AR140557                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207802.
ACCESSION   AR140557
VERSION     AR140557.1  GI:14483053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Stem cell factor and compositions
  JOURNAL   Patent: US 6207802-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1106
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AR140557/c
LOCUS       AR140557                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 32 from patent US 6207802.
ACCESSION   AR140557
VERSION     AR140557.1  GI:14483053
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Stem cell factor and compositions
  JOURNAL   Patent: US 6207802-A 32 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1107
BD234126
LOCUS       BD234126                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION   BD234126
VERSION     BD234126.1  GI:33043896
KEYWORDS    JP 2002532072-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipovsek,D.
  TITLE     Protein skeleton of antibody mimetics and other binding proteins
  JOURNAL   Patent: JP 2002532072-A 14 02-OCT-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002532072-A/14
            PD   02-OCT-2002
            PF   09-DEC-1999 JP 2000587187
            PR   10-DEC-1998 US    60/111737
            PI   DASA LIPOVSEK
            PC   C12N15/09,C07K1/04,C07K14/78,C07K16/46,C07K17/00,C07K19/00, PC
              C12P21/02,
            PC   C12N15/00
            CC   Puromycin linker oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1108
BD234126/c
LOCUS       BD234126                 20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION   BD234126
VERSION     BD234126.1  GI:33043896
KEYWORDS    JP 2002532072-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lipovsek,D.
  TITLE     Protein skeleton of antibody mimetics and other binding proteins
  JOURNAL   Patent: JP 2002532072-A 14 02-OCT-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002532072-A/14
            PD   02-OCT-2002
            PF   09-DEC-1999 JP 2000587187
            PR   10-DEC-1998 US    60/111737
            PI   DASA LIPOVSEK
            PC   C12N15/09,C07K1/04,C07K14/78,C07K16/46,C07K17/00,C07K19/00, PC
              C12P21/02,
            PC   C12N15/00
            CC   Puromycin linker oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1109
AX825109/c
LOCUS       AX825109                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 7 from Patent WO03072818.
ACCESSION   AX825109
VERSION     AX825109.1  GI:39750838
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 7 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1110
AX825115/c
LOCUS       AX825115                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 13 from Patent WO03072818.
ACCESSION   AX825115
VERSION     AX825115.1  GI:39750844
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 13 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1111
AX825118/c
LOCUS       AX825118                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 16 from Patent WO03072818.
ACCESSION   AX825118
VERSION     AX825118.1  GI:39750847
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 16 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1112
AX825127
LOCUS       AX825127                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 25 from Patent WO03072818.
ACCESSION   AX825127
VERSION     AX825127.1  GI:39750856
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 25 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
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                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
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     modified_base   12
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1113
AX825131/c
LOCUS       AX825131                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 29 from Patent WO03072818.
ACCESSION   AX825131
VERSION     AX825131.1  GI:39750860
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 29 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1114
AX825134/c
LOCUS       AX825134                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 32 from Patent WO03072818.
ACCESSION   AX825134
VERSION     AX825134.1  GI:39750863
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 32 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1115
AX825139
LOCUS       AX825139                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 37 from Patent WO03072818.
ACCESSION   AX825139
VERSION     AX825139.1  GI:39750868
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
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  JOURNAL    Patent: WO 03072818-A 37 04-SEP-2003;
             Degussa Bioactives GmbH (DE)
FEATURES               Location/Qualifiers
     source            1. .21
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"
                       /note="Beschreibung der kuenstlichen
                       Sequenz:Capture-Oligonukleotid"
     misc_binding      1
                       /bound_moiety="Biotin"
     modified_base     3
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     6
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     9
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     12
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     15
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     18
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1116
AX825143
LOCUS       AX825143                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 41 from Patent WO03072818.
ACCESSION   AX825143
VERSION     AX825143.1  GI:39750872
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 41 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES               Location/Qualifiers
     source            1. .21
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"
                       /note="Beschreibung der kuenstlichen
                       Sequenz:Capture-Oligonukleotid"
     misc_binding      1
                       /bound_moiety="Biotin"
     modified_base     3
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     6
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     9
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     12
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     15
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     18
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1117
AX825107/c
LOCUS       AX825107                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 5 from Patent WO03072818.
ACCESSION   AX825107
VERSION     AX825107.1  GI:39750836
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 5 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES               Location/Qualifiers
     source            1. .21
                       /organism="synthetic construct"
                       /mol_type="unassigned DNA"
                       /db_xref="taxon:32630"
                       /note="Beschreibung der kuenstlichen
                       Sequenz:Capture-Oligonukleotid"
     misc_binding      1
                       /bound_moiety="Biotin"
     modified_base     3
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     6
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     9
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     12
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     15
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER
     modified_base     18
                       /note="LNA-T (Locked Nucleic Acid)"
                       /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1118
AX825108/c
LOCUS       AX825108                 21 bp    DNA     linear   PAT 11-DEC-2003
```

```
DEFINITION  Sequence 6 from Patent WO03072818.
ACCESSION   AX825108
VERSION     AX825108.1  GI:39750837
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 6 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1119
AX825110/c
LOCUS       AX825110                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 8 from Patent WO03072818.
ACCESSION   AX825110
VERSION     AX825110.1  GI:39750839
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 8 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1120
AX825116/c
LOCUS       AX825116                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 14 from Patent WO03072818.
ACCESSION   AX825116
VERSION     AX825116.1  GI:39750845
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 14 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
```

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  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1121
AX825140
LOCUS       AX825140                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 38 from Patent WO03072818.
ACCESSION   AX825140
VERSION     AX825140.1  GI:39750869
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 38 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1122
AX825141
LOCUS       AX825141                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 39 from Patent WO03072818.
ACCESSION   AX825141
VERSION     AX825141.1  GI:39750870
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 39 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1123
AX825142
LOCUS       AX825142                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 40 from Patent WO03072818.
ACCESSION   AX825142
VERSION     AX825142.1  GI:39750871
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 40 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1124
AX825144
LOCUS       AX825144                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 42 from Patent WO03072818.
ACCESSION   AX825144
VERSION     AX825144.1  GI:39750873
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 42 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1125
AX825145
LOCUS       AX825145                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 43 from Patent WO03072818.
ACCESSION   AX825145
VERSION     AX825145.1  GI:39750874
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 43 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1126
AX825146
LOCUS       AX825146                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 44 from Patent WO03072818.
ACCESSION   AX825146
VERSION     AX825146.1  GI:39750875
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 44 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
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                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1127
AX825128
LOCUS       AX825128                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 26 from Patent WO03072818.
ACCESSION   AX825128
VERSION     AX825128.1  GI:39750857
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 26 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1128
AX825129
LOCUS       AX825129                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 27 from Patent WO03072818.
ACCESSION   AX825129
VERSION     AX825129.1  GI:39750858
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 27 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1129
AX825130
LOCUS       AX825130                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 28 from Patent WO03072818.
ACCESSION   AX825130
VERSION     AX825130.1  GI:39750859
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 28 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
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FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1130
AX825132/c
LOCUS       AX825132                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 30 from Patent WO03072818.
ACCESSION   AX825132
VERSION     AX825132.1  GI:39750861
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 30 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1131
AX825123
LOCUS       AX825123                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 21 from Patent WO03072818.
ACCESSION   AX825123
VERSION     AX825123.1  GI:39750852
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 21 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1132
AX825123/c
LOCUS       AX825123                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 21 from Patent WO03072818.
ACCESSION   AX825123
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VERSION     AX825123.1  GI:39750852
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 21 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1133
AX825124
LOCUS       AX825124                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 22 from Patent WO03072818.
ACCESSION   AX825124
VERSION     AX825124.1  GI:39750853
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 22 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1134
AX825124/c
LOCUS       AX825124                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 22 from Patent WO03072818.
ACCESSION   AX825124
VERSION     AX825124.1  GI:39750853
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 22 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 1135
AX825125
LOCUS       AX825125                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 23 from Patent WO03072818.
ACCESSION   AX825125
VERSION     AX825125.1  GI:39750854
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 23 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTT 18


RESULT 1136
AX825125/c
LOCUS       AX825125                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 23 from Patent WO03072818.
ACCESSION   AX825125
VERSION     AX825125.1  GI:39750854
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 23 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAA 1


RESULT 1137
AX825126
LOCUS       AX825126                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 24 from Patent WO03072818.
ACCESSION   AX825126
VERSION     AX825126.1  GI:39750855
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 24 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
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                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 18


RESULT 1138
AX825126/c
LOCUS       AX825126                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 24 from Patent WO03072818.
ACCESSION   AX825126
VERSION     AX825126.1  GI:39750855
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 24 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.6%;  Score 18;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         18 AAAAAAAAAAAAAAAAAA 1


RESULT 1139
AR164318
LOCUS       AR164318                 22 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6271369.
ACCESSION   AR164318
VERSION     AR164318.1  GI:16235432
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
  TITLE     Chimeric molecules targeted to viral RNAs
  JOURNAL   Patent: US 6271369-A 1 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTT 22


RESULT 1140
AR164318/c
LOCUS       AR164318                 22 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6271369.
ACCESSION   AR164318
VERSION     AR164318.1  GI:16235432
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
  TITLE     Chimeric molecules targeted to viral RNAs
  JOURNAL   Patent: US 6271369-A 1 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         22 AAAAAAAAAAAAAAAAAA 5


RESULT 1141
AR164319
LOCUS       AR164319                 22 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 2 from patent US 6271369.
ACCESSION   AR164319
VERSION     AR164319.1  GI:16235434
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
  TITLE     Chimeric molecules targeted to viral RNAs
  JOURNAL   Patent: US 6271369-A 2 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTT 22


RESULT 1142
AR164319/c
LOCUS       AR164319                 22 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 2 from patent US 6271369.
ACCESSION   AR164319
VERSION     AR164319.1  GI:16235434
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
  TITLE     Chimeric molecules targeted to viral RNAs
  JOURNAL   Patent: US 6271369-A 2 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         22 AAAAAAAAAAAAAAAAAA 5


RESULT 1143
I31810
LOCUS       I31810                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5583032.
ACCESSION   I31810
VERSION     I31810.1  GI:1822601
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA
  JOURNAL   Patent: US 5583032-A 1 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTT 22


RESULT 1144
I31810/c
LOCUS       I31810                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 1 from patent US 5583032.
ACCESSION   I31810
VERSION     I31810.1  GI:1822601
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA
  JOURNAL   Patent: US 5583032-A 1 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         22 AAAAAAAAAAAAAAAAAA 5


RESULT 1145
I31811
LOCUS       I31811                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 2 from patent US 5583032.
ACCESSION   I31811
VERSION     I31811.1  GI:1822602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA
  JOURNAL   Patent: US 5583032-A 2 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTT 22


RESULT 1146
I31811/c
LOCUS       I31811                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 2 from patent US 5583032.
ACCESSION   I31811
VERSION     I31811.1  GI:1822602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA
  JOURNAL   Patent: US 5583032-A 2 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         22 AAAAAAAAAAAAAAAAAA 5


RESULT 1147
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I69407
LOCUS       I69407                  22 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 1 from patent US 5677289.
ACCESSION   I69407
VERSION     I69407.1  GI:2831529
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA and medical treatments
            thereby
  JOURNAL   Patent: US 5677289-A 1 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTT 22


RESULT 1148
I69407/c
LOCUS       I69407                  22 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 1 from patent US 5677289.
ACCESSION   I69407
VERSION     I69407.1  GI:2831529
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA and medical treatments
            thereby
  JOURNAL   Patent: US 5677289-A 1 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         22 AAAAAAAAAAAAAAAAAA 5


RESULT 1149
I69408
LOCUS       I69408                  22 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 2 from patent US 5677289.
ACCESSION   I69408
VERSION     I69408.1  GI:2831530
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA and medical treatments
            thereby
  JOURNAL   Patent: US 5677289-A 2 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTT 22


RESULT 1150
I69408/c
LOCUS       I69408                  22 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 2 from patent US 5677289.
ACCESSION   I69408
VERSION     I69408.1  GI:2831530
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA and medical treatments
            thereby
  JOURNAL   Patent: US 5677289-A 2 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         22 AAAAAAAAAAAAAAAAAA 5


RESULT 1151
BD245230
LOCUS       BD245230                23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of electrochemically detecting nucleic acid.
ACCESSION   BD245230
VERSION     BD245230.1  GI:33055000
KEYWORDS    JP 2002532386-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hartwich,G. and Heller,A.
  TITLE     Method of electrochemically detecting nucleic acid
  JOURNAL   Patent: JP 2002532386-A 16 02-OCT-2002;
            FRIZ BIOCHEM GMBH
COMMENT     OS   Artificial Sequence
            PN   JP 2002532386-A/16
            PD   02-OCT-2002
            PF   19-NOV-1999 JP 2000583928
            PR   23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
            GERHARD HARTWICH,ADAM HELLER
            PC   C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
              G01N27/30,
            PC
            G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
             G01N27/46
            CC   Method of electrochemically detecting nucleic acid FH   Key
                 Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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    source          1. .23
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match              0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          6 AAAAAAAAAAAAAAAAAA 23


RESULT 1152
E12391
LOCUS       E12391                    23 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide primer.
ACCESSION   E12391
VERSION     E12391.1  GI:3251224
KEYWORDS    JP 1996322598-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Katou,K.
  TITLE     INDEXING METHOD OF DNA MOLECULE
  JOURNAL   Patent: JP 1996322598-A 1 10-DEC-1996;
            RES DEV CORP OF JAPAN
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996322598-A/1
            PD   10-DEC-1996
            PF   12-SEP-1995 JP 1995234122
            PR   28-MAR-1995 JP 95P    69695
            PI   KATOU KIKUYA
            PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .23
            FT                   /organism='Artificial sequences'.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match              0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||
Db          5 CCTTTTTTTTTTTTTTTT 22


RESULT 1153
AX394607
LOCUS       AX394607                  23 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 5 from Patent EP1186673.
ACCESSION   AX394607
VERSION     AX394607.1  GI:21065720
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 5 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="probes to target sequences"

  Query Match              0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1154
AX394607/c
LOCUS       AX394607                  23 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 5 from Patent EP1186673.
ACCESSION   AX394607
VERSION     AX394607.1  GI:21065720
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 5 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="probes to target sequences"

  Query Match              0.6%;  Score 18;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1155
AR168453/c
LOCUS       AR168453                  24 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 82 from patent US 6287854.
ACCESSION   AR168453
VERSION     AR168453.1  GI:17904379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Spurr,N.K., Gray,I.C. and Stewart,L.M.
  TITLE     Diagnosis of susceptibility to cancer and treatment thereof
  JOURNAL   Patent: US 6287854-A 82 11-SEP-2001;
FEATURES              Location/Qualifiers
     source           1. .24
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAA 7
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RESULT 1156
AX394609
LOCUS       AX394609                 24 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 7 from Patent EP1186673.
ACCESSION   AX394609
VERSION     AX394609.1  GI:21065722
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 7 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1157
AX394609/c
LOCUS       AX394609                 24 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 7 from Patent EP1186673.
ACCESSION   AX394609
VERSION     AX394609.1  GI:21065722
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 7 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1158
BD097127
LOCUS       BD097127                 24 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Support for immobilizing nucleotide and process for producing the
            same.
ACCESSION   BD097127
VERSION     BD097127.1  GI:22642701
KEYWORDS    WO 0155365-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
  TITLE     Support for immobilizing nucleotide and process for producing the
  JOURNAL   Patent: WO 0155365-A 1 02-AUG-2001;
            TOYO KOHAN CO LTD,MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,
            KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0155365-A/1
            PD   02-AUG-2001
            PF   24-JAN-2001 WO 2001JP000443
            PR   27-JAN-2000 JP 00P   019301
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,KOJIRO  PI
            TAKAHASHI
            PC   C12N15/10,C07H21/04//G01N33/50,C12Q1/68
            CC   Support for immobilizing nucleotide and process for producing
            CC          the same
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          6 TTTTTTTTTTTTTTTTTT 23


RESULT 1159
BD097127/c
LOCUS       BD097127                 24 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Support for immobilizing nucleotide and process for producing the
            same.
ACCESSION   BD097127
VERSION     BD097127.1  GI:22642701
KEYWORDS    WO 0155365-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
  TITLE     Support for immobilizing nucleotide and process for producing the
  JOURNAL   Patent: WO 0155365-A 1 02-AUG-2001;
            TOYO KOHAN CO LTD,MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,
            KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0155365-A/1
            PD   02-AUG-2001
            PF   24-JAN-2001 WO 2001JP000443
            PR   27-JAN-2000 JP 00P   019301
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,KOJIRO  PI
            TAKAHASHI
            PC   C12N15/10,C07H21/04//G01N33/50,C12Q1/68
            CC   Support for immobilizing nucleotide and process for producing
            CC          the same
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
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 Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
 Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAA 6


RESULT 1160
BD161931
LOCUS       BD161931                 24 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate.
ACCESSION   BD161931
VERSION     BD161931.1  GI:27867689
KEYWORDS    JP 2002191369-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
  TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate
  JOURNAL   Patent: JP 2002191369-A 8 09-JUL-2002;
            TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   JP 2002191369-A/8
            PD   09-JUL-2002
            PF   27-DEC-2000 JP 2000399573
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
            C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC   Method for
            carrying out thermal cycle of PCR using DNA- CC
            immobilized
            CC   substrate
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db          6 TTTTTTTTTTTTTTTTTT 23


RESULT 1161
BD161931/c
LOCUS       BD161931                 24 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate.
ACCESSION   BD161931
VERSION     BD161931.1  GI:27867689
KEYWORDS    JP 2002191369-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
  TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate
  JOURNAL   Patent: JP 2002191369-A 8 09-JUL-2002;
            TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   JP 2002191369-A/8
            PD   09-JUL-2002
            PF   27-DEC-2000 JP 2000399573
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
            C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC   Method for
            carrying out thermal cycle of PCR using DNA- CC
            immobilized
            CC   substrate
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         23 AAAAAAAAAAAAAAAAAA 6


RESULT 1162
AX394611
LOCUS       AX394611                 25 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 9 from Patent EP1186673.
ACCESSION   AX394611
VERSION     AX394611.1  GI:21065724
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 9 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1163
AX394611/c
LOCUS       AX394611                 25 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 9 from Patent EP1186673.
ACCESSION   AX394611
VERSION     AX394611.1  GI:21065724
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 9 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1164
AR144828/c
LOCUS       AR144828                  26 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 59 from patent US 6210942.
ACCESSION   AR144828
VERSION     AR144828.1  GI:15106695
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Sarkanen,S. and Ford,J.D.
  TITLE     Recombinant pinoresinol/lariciresinol reductase, recombinant
            dirigent protein, and methods of use
  JOURNAL   Patent: US 6210942-A 59 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAA 9


RESULT 1165
AR410280/c
LOCUS       AR410280                  26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 59 from patent US 6635459.
ACCESSION   AR410280
VERSION     AR410280.1  GI:40161559
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Sarkanen,S. and Ford,J.D.
  TITLE     Nucleotide sequences encoding pinoresinol/lariciresinol reductase
            proteins and their methods of use
  JOURNAL   Patent: US 6635459-A 59 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAA 9


RESULT 1166
AX191907/c
LOCUS       AX191907                  26 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 59 from Patent WO0149833.
ACCESSION   AX191907
VERSION     AX191907.1  GI:15210057
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Ford,J.D. and Sarkanen,S.
  TITLE     Recombinant pinoresinol/lariciresinol reductase, recombinant
            dirigent protein, and methods of use
  JOURNAL   Patent: WO 0149833-A 59 12-JUL-2001;
            Washington State University Research Foundation (US) ; REGENTS OF
            THE UNIVERSITY OF MINNESOTA (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
     misc_feature    1. .26
                     /note="cDNA synthesis linker primer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAA 9


RESULT 1167
BD064385/c
LOCUS       BD064385                  26 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Recombinant pinoresinol/lariciresinol reductases,recombinant
            dirigent proteins and methods of use.
ACCESSION   BD064385
VERSION     BD064385.1  GI:22609988
KEYWORDS    JP 2001507931-A/26.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lewis,N.G., Davin,L.B., Kostova,A.T.D., Fujita,M., Gang,D.R. and
            Sarkanen,S.
  TITLE     Recombinant pinoresinol/lariciresinol reductases,recombinant
            dirigent proteins and methods of use
  JOURNAL   Patent: JP 2001507931-A 26 19-JUN-2001;
            WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
COMMENT     PN   JP 2001507931-A/26
            PD   19-JUN-2001
            PF   07-NOV-1997 JP 1998521816
            PR   08-NOV-1996 US    60/030522,31-JUL-1997 US    60/054380 PI
            NORMAN G LEWIS,LAURENCE B DAVIN,ALBENA T DINKOVA KOSTOVA, PI
            MASAYUKI FUJITA,
            PI   DAVID R GANG,SIMO SARKANEN
            PC   C12N9/02,C12N15/53,C12N15/29
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   'cDNA synthesis linker primer'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
```

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 Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAA 9


RESULT 1168
AR013918/c
LOCUS       AR013918                  26 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5773223.
ACCESSION   AR013918
VERSION     AR013918.1  GI:3971372
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Shyamala,V. and Olson,P.Tekamp.
  TITLE     Endothelin B.sub.1, (ETB.sub.1) receptor polypeptide and its
            encoding nucleic acid methods, and uses thereof
  JOURNAL   Patent: US 5773223-A 3 30-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAA 9


RESULT 1169
AR136778/c
LOCUS       AR136778                  26 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6162437.
ACCESSION   AR136778
VERSION     AR136778.1  GI:14478028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Pyun,K.-H., Choi,I., Kang,H.-S., Lee,J.-J. and Kim,Y.-H.
  TITLE     Method for inhibiting interleukin-6 production by administering
            extracts from root of Stephania tetrandra
  JOURNAL   Patent: US 6162437-A 1 19-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAA 9


RESULT 1170
AR050239
LOCUS       AR050239                  26 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5827518.
ACCESSION   AR050239
VERSION     AR050239.1  GI:5972964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Webb,B.Allen. and Cui,L.
  TITLE     Viral and insect genes that inhibit the immune system and methods
            of use thereof
  JOURNAL   Patent: US 5827518-A 8 27-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2182
              ||||||||||||||||||
Db          9 CTTTTTTTTTTTTTTTTT 26


RESULT 1171
AR090583
LOCUS       AR090583                  26 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 703 from patent US 5994076.
ACCESSION   AR090583
VERSION     AR090583.1  GI:10017338
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 703 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   80.8%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1093 AGCTGTTCATTTGGCTAGGGACTTTG 1118
              ||||||  ||  | ||  ||||||||||
Db          1 AGCTGTCCACCTAGCCAGGGACTTTG 26


RESULT 1172
AR106358/c
LOCUS       AR106358                  26 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 20 from patent US 6107028.
ACCESSION   AR106358
VERSION     AR106358.1  GI:12820888
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kay,M.A. and Lieber,A.
  TITLE     Ribozymes for treating hepatitis C
  JOURNAL   Patent: US 6107028-A 20 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   80.8%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        437 CACCAGCCGGCGCCCACAGGCAGCCA 462
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                  ||||| ||| |||||||||| | ||
Db          26 CACCAACCGTCGCCCACAGGACGTCA 1


RESULT 1173
AR164510
LOCUS       AR164510                 26 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 1 from patent US 6274147.
ACCESSION   AR164510
VERSION     AR164510.1  GI:16237563
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Vakharia,V.N. and Yao,K.
  TITLE     Method for generating nonpathogenic infectious pancreatic necrosis
            virus (IPNV) from synthetic RNA transcripts
  JOURNAL   Patent: US 6274147-A 1 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTT 2181
              ||||||||||||||||||
Db          9 CCTTTTTTTTTTTTTTTT 26


RESULT 1174
AR197618
LOCUS       AR197618                 26 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 703 from patent US 6352829.
ACCESSION   AR197618
VERSION     AR197618.1  GI:20247467
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6352829-A 703 05-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   80.8%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1093 AGCTGTTCATTTGGCTAGGGACTTTG 1118
              ||||||  ||  | || ||||||||||
Db          1 AGCTGTCCACCTAGCCAGGGACTTTG 26


RESULT 1175
AR259772
LOCUS       AR259772                 26 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 703 from patent US 6489455.
ACCESSION   AR259772
VERSION     AR259772.1  GI:27310283
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 6489455-A 703 03-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   80.8%;  Pred. No. 1.4e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1093 AGCTGTTCATTTGGCTAGGGACTTTG 1118
              ||||||  ||  | || ||||||||||
Db          1 AGCTGTCCACCTAGCCAGGGACTTTG 26


RESULT 1176
AX394613
LOCUS       AX394613                 26 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 11 from Patent EP1186673.
ACCESSION   AX394613
VERSION     AX394613.1  GI:21065726
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 11 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1177
AX394613/c
LOCUS       AX394613                 26 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 11 from Patent EP1186673.
ACCESSION   AX394613
VERSION     AX394613.1  GI:21065726
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 11 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTT 1


RESULT 1178
AX827015
LOCUS       AX827015                  26 bp    RNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 12 from Patent EP1344835.
ACCESSION   AX827015
VERSION     AX827015.1  GI:39837222
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
            Liu,D.
  TITLE     Real-time nucleic acid detection processes and compositions
  JOURNAL   Patent: EP 1344835-A 12 17-SEP-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 18


RESULT 1179
AX827015/c
LOCUS       AX827015                  26 bp    RNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 12 from Patent EP1344835.
ACCESSION   AX827015
VERSION     AX827015.1  GI:39837222
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
            Liu,D.
  TITLE     Real-time nucleic acid detection processes and compositions
  JOURNAL   Patent: EP 1344835-A 12 17-SEP-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTT 1


RESULT 1180
AX839907
LOCUS       AX839907                  26 bp    RNA     linear   PAT 16-DEC-2003
DEFINITION  Sequence 12 from Patent EP1348713.
ACCESSION   AX839907
VERSION     AX839907.1  GI:39978438
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stavrianopoulos,J.G. and Rabbani,E.
  TITLE     Labeling reagents and labeled tabeled targets, target labeling
            processes and other processes for using same in nucleic acid
            determinations and analyses
  JOURNAL   Patent: EP 1348713-A 12 01-OCT-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAA 18


RESULT 1181
AX839907/c
LOCUS       AX839907                  26 bp    RNA     linear   PAT 16-DEC-2003
DEFINITION  Sequence 12 from Patent EP1348713.
ACCESSION   AX839907
VERSION     AX839907.1  GI:39978438
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Stavrianopoulos,J.G. and Rabbani,E.
  TITLE     Labeling reagents and labeled tabeled targets, target labeling
            processes and other processes for using same in nucleic acid
            determinations and analyses
  JOURNAL   Patent: EP 1348713-A 12 01-OCT-2003;
            Enzo Life Sciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"

  Query Match             0.6%;  Score 18;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTT 1


RESULT 1182
AR142409/c
LOCUS       AR142409                  27 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 16 from patent US 6174992.
ACCESSION   AR142409
VERSION     AR142409.1  GI:15102709
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
```

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  AUTHORS   Ni,J., Yu,G.-L. and Gentz,R.
  TITLE     Human endometrial specific steroid-binding factor I, II and III
  JOURNAL   Patent: US 6174992-A 16 16-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAA 10


RESULT 1183
AR182555/c
LOCUS       AR182555                  27 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 16 from patent US 6338948.
ACCESSION   AR182555
VERSION     AR182555.1  GI:20225762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Ni,J., Yu,G.-L. and Gentz,R.
  TITLE     Human endometrial specific steroid-binding factor I, II and III
  JOURNAL   Patent: US 6338948-A 16 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAA 10


RESULT 1184
AR027002/c
LOCUS       AR027002                  27 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5856138.
ACCESSION   AR027002
VERSION     AR027002.1  GI:5937842
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Fukuda,T.
  TITLE     Human parathyroid hormone muteins and production thereof
  JOURNAL   Patent: US 5856138-A 14 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   80.8%;  Pred. No. 1.6e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1498 AATGGAGAAACACAGGAAATAAAATT 1523
              ||||| | | |||||| || ||||||
Db         26 AATGGGGCACCACAGGCAACAAAATT 1


RESULT 1185
AX394614
LOCUS       AX394614                  27 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 12 from Patent EP1186673.
ACCESSION   AX394614
VERSION     AX394614.1  GI:21065727
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 12 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1186
AX394614/c
LOCUS       AX394614                  27 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 12 from Patent EP1186673.
ACCESSION   AX394614
VERSION     AX394614.1  GI:21065727
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 12 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||
Db         18 TTTTTTTTTTTTTTTTTT 1


RESULT 1187
AR055110/c
LOCUS       AR055110                  28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5837468.
ACCESSION   AR055110
VERSION     AR055110.1  GI:5980687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
```

```
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA substractive cloning method
  JOURNAL   Patent: US 5837468-A 15 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         28 GAAAAAAAAAAAAAAAAA 11


RESULT 1188
AR068451/c
LOCUS       AR068451                28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5853991.
ACCESSION   AR068451
VERSION     AR068451.1  GI:6000658
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA subtractive cloning method
  JOURNAL   Patent: US 5853991-A 15 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||
Db         28 GAAAAAAAAAAAAAAAAA 11


RESULT 1189
AR371171/c
LOCUS       AR371171                28 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 10 from patent US 6395306.
ACCESSION   AR371171
VERSION     AR371171.1  GI:34608085
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Cui,X. and Lu,Y.
  TITLE     Bee venom protein and gene encoding same
  JOURNAL   Patent: US 6395306-A 10 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAA 11


RESULT 1190
BD015304/c
LOCUS       BD015304                28 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Primer single-stranded DNA, process for preparing double-stranded
            cDNA by using the same and process for amplifying one side
            single-stranded DNA.
ACCESSION   BD015304
VERSION     BD015304.1  GI:22556442
KEYWORDS    JP 2001204472-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Nakamura,T.
  TITLE     Primer single-stranded DNA, process for preparing double-stranded
            cDNA by using the same and process for amplifying one side
  JOURNAL   Patent: JP 2001204472-A 5 31-JUL-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001204472-A/5
            PD   31-JUL-2001
            PF   21-JAN-2000 JP 2000012535
            PI   TAKESHI NAKAMURA
            PC   C12N15/09,C12P19/34,G01N33/50//C12Q1/68,C12N15/00 CC   PCR
            primer
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAA 11


RESULT 1191
AX394616
LOCUS       AX394616                28 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 14 from Patent EP1186673.
ACCESSION   AX394616
VERSION     AX394616.1  GI:21065729
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 14 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1192
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```
AX394617
LOCUS       AX394617                28 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 15 from Patent EP1186673.
ACCESSION   AX394617
VERSION     AX394617.1  GI:21065730
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 15 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1193
AX394619
LOCUS       AX394619                29 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 17 from Patent EP1186673.
ACCESSION   AX394619
VERSION     AX394619.1  GI:21065732
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 17 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1194
AX394621
LOCUS       AX394621                30 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 19 from Patent EP1186673.
ACCESSION   AX394621
VERSION     AX394621.1  GI:21065734
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 19 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1195
AR242448/c
LOCUS       AR242448                30 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 23 from patent US 6472509.
ACCESSION   AR242448
VERSION     AR242448.1  GI:27288865
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 23 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAA 13


RESULT 1196
AR280216/c
LOCUS       AR280216                30 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 23 from patent US 6518045.
ACCESSION   AR280216
VERSION     AR280216.1  GI:29715606
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 23 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAA 13
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RESULT 1197
AR322431/c
LOCUS       AR322431                  30 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 23 from patent US 6566097.
ACCESSION   AR322431
VERSION     AR322431.1  GI:33708184
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 23 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAA 13


RESULT 1198
AX394623
LOCUS       AX394623                  31 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 21 from Patent EP1186673.
ACCESSION   AX394623
VERSION     AX394623.1  GI:21065736
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 21 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1199
AR051291/c
LOCUS       AR051291                  32 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5830662.
ACCESSION   AR051291
VERSION     AR051291.1  GI:5974655
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Soares,M.B. and Efstratiadis,A.
  TITLE     Method for construction of normalized cDNA libraries
  JOURNAL   Patent: US 5830662-A 8 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1200
I16939/c
LOCUS       I16939                    32 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 8 from patent US 5482845.
ACCESSION   I16939
VERSION     I16939.1  GI:1251847
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Soares,M.B. and Efstratiadis,A.
  TITLE     Method for construction of normalized cDNA libraries
  JOURNAL   Patent: US 5482845-A 8 09-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1201
I45733/c
LOCUS       I45733                    32 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 8 from patent US 5637685.
ACCESSION   I45733
VERSION     I45733.1  GI:2469835
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Soares,M.B. and Efstratiadis,A.
  TITLE     Normalized cDNA libraries
  JOURNAL   Patent: US 5637685-A 8 10-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1202
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AX394625
LOCUS       AX394625                  32 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 23 from Patent EP1186673.
ACCESSION   AX394625
VERSION     AX394625.1  GI:21065738
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 23 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAA 18


RESULT 1203
AR014684/c
LOCUS       AR014684                  32 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 7 from patent US 5773696.
ACCESSION   AR014684
VERSION     AR014684.1  GI:3972138
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
  TITLE     Antifungal polypeptide and methods for controlling plant pathogenic
            fungi
  JOURNAL   Patent: US 5773696-A 7 30-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1204
AR341692/c
LOCUS       AR341692                  32 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 16 from patent US 6573361.
ACCESSION   AR341692
VERSION     AR341692.1  GI:33734520
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Bunkers,G.J., Liang,J., Mittanck,C.A., Seale,J.W. and Wu,Y.S.
  TITLE     Antifungal proteins and methods for their use
  JOURNAL   Patent: US 6573361-A 16 03-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1205
AR366811/c
LOCUS       AR366811                  32 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 8 from patent US 6329504.
ACCESSION   AR366811
VERSION     AR366811.1  GI:34599783
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Liang,J., Shah,D.M., Wu,Y.S., Rosenberger,C.A. and Hakimi,S.
  TITLE     Antifungal polypeptide and methods for controlling plant pathogenic
            fungi
  JOURNAL   Patent: US 6329504-A 8 11-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1206
AR432384/c
LOCUS       AR432384                  32 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6653280.
ACCESSION   AR432384
VERSION     AR432384.1  GI:40194661
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
  TITLE     Antifungal polypeptide AlyAFP from Alyssum and methods for
            controlling plant pathogenic fungi
  JOURNAL   Patent: US 6653280-A 7 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+03;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAA 15


RESULT 1207
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AR409897/c
LOCUS       AR409897                 32 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 10 from patent US 6635422.
ACCESSION   AR409897
VERSION     AR409897.1  GI:40161032
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 10 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.6%;  Score 18;  DB 1;  Length 32;
  Best Local Similarity   80.8%;  Pred. No. 2.2e+03;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||    |||||||||| ||||||||
Db         28 AGACCAAAAAAAAAAAAGAAAAAAAA 3


RESULT 1208
A79657
LOCUS       A79657                   19 bp    DNA     linear   PAT 20-OCT-1999
DEFINITION  Sequence 6 from Patent WO9720069.
ACCESSION   A79657
VERSION     A79657.1  GI:6092611
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Emrich,T. and Leying,H.
  TITLE     METHOD OF DETECTING TELOMERASE ACTIVITY
  JOURNAL   Patent: WO 9720069-A 6 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE); EMRICH THOMAS (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||::
Db          1 TTTTTTTTTTTTTTTTMH 19


RESULT 1209
A79657/c
LOCUS       A79657                   19 bp    DNA     linear   PAT 20-OCT-1999
DEFINITION  Sequence 6 from Patent WO9720069.
ACCESSION   A79657
VERSION     A79657.1  GI:6092611
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Emrich,T. and Leying,H.
  TITLE     METHOD OF DETECTING TELOMERASE ACTIVITY
  JOURNAL   Patent: WO 9720069-A 6 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE); EMRICH THOMAS (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ::|||||||||||||||||
Db         19 DKAAAAAAAAAAAAAAAAA 1


RESULT 1210
AR147331
LOCUS       AR147331                 19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6221584.
ACCESSION   AR147331
VERSION     AR147331.1  GI:15111134
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Emrich,T., Leying,H., Hinzpeter,M. and Karl,G.
  TITLE     Method of detecting telomerase activity
  JOURNAL   Patent: US 6221584-A 6 24-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||::
Db          1 TTTTTTTTTTTTTTTTMH 19


RESULT 1211
AR147331/c
LOCUS       AR147331                 19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6221584.
ACCESSION   AR147331
VERSION     AR147331.1  GI:15111134
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Emrich,T., Leying,H., Hinzpeter,M. and Karl,G.
  TITLE     Method of detecting telomerase activity
  JOURNAL   Patent: US 6221584-A 6 24-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 19;
  Best Local Similarity   89.5%;  Pred. No. 6.6e+02;
  Matches   17;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAA 2802
              ::|||||||||||||||||
Db         19 DKAAAAAAAAAAAAAAAAA 1


RESULT 1212
AX103869
```

```
LOCUS       AX103869                 22 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 61 from Patent WO0122972.
ACCESSION   AX103869
VERSION     AX103869.1  GI:13920066
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 61 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 1e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||| ||||||| ||||
Db          1 TTTTTTTTGTTTTTTGTTTT 21


RESULT 1213
AX457060
LOCUS       AX457060                 22 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 21 from Patent WO0231186.
ACCESSION   AX457060
VERSION     AX457060.1  GI:21715842
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K.
  TITLE     Method for the detection of cytosine methylations
  JOURNAL   Patent: WO 0231186-A 21 18-APR-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 1e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||| ||||||| |||
Db          1 TTTTTTTTATTTTTTTATTA 21


RESULT 1214
AX546922
LOCUS       AX546922                 22 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 61 from Patent WO02053141.
ACCESSION   AX546922
VERSION     AX546922.1  GI:25812066
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 61 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 22;
  Best Local Similarity   90.5%;  Pred. No. 1e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||| ||||||| ||||
Db          1 TTTTTTTGTTTTTTTGTTTT 21


RESULT 1215
AX457061
LOCUS       AX457061                 23 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 22 from Patent WO0231186.
ACCESSION   AX457061
VERSION     AX457061.1  GI:21715843
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Berlin,K.
  TITLE     Method for the detection of cytosine methylations
  JOURNAL   Patent: WO 0231186-A 22 18-APR-2002;
            Epigenomics AG (DE)
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 23;
  Best Local Similarity   90.5%;  Pred. No. 1.1e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAA 2188
              |||||||| || ||||||||
Db          2 TTTTTTTTTATTATTTTTAA 22


RESULT 1216
AR431313
LOCUS       AR431313                 24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6651008.
ACCESSION   AR431313
VERSION     AR431313.1  GI:40193281
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 7 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 24;
  Best Local Similarity   90.5%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||| |||||||||| ||
Db          2 TTTTTTGTTTTTTTTTTTCTA 22


RESULT 1217
AX103868
LOCUS       AX103868                 24 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 60 from Patent WO0122972.
ACCESSION   AX103868
VERSION     AX103868.1  GI:13920065
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 60 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 24;
  Best Local Similarity   90.5%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||| ||||||| |||||
Db          4 TTTTTTTGTTTTTTTGTTTTT 24


RESULT 1218
AX546921
LOCUS       AX546921                 24 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 60 from Patent WO02053141.
ACCESSION   AX546921
VERSION     AX546921.1  GI:25812065
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 60 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 24;
  Best Local Similarity   90.5%;  Pred. No. 1.3e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||| ||||||| |||||
Db          4 TTTTTTTGTTTTTTTGTTTTT 24


RESULT 1219
E36888/c
LOCUS       E36888                   25 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Human telomerase catalytic subunit promoter.
ACCESSION   E36888
VERSION     E36888.1  GI:13022851
KEYWORDS    JP 1999253177-A/96.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
            Calvin,B.H. and William,H.A.
  TITLE     Human telomerase catalytic subunit promoter
  JOURNAL   Patent: JP 1999253177-A 96 21-SEP-1999;
            JERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT     OS   Unidentified
            PN   JP 1999253177-A/96
            PD   21-SEP-1999
            PF   15-OCT-1998 JP 1998320169
            PR   01-OCT-1996 US   08/724.643,18-APR-1997 US   08/844.419, PR
            25-APR-1997 US   08/846.017,06-MAY-1997 US   08/851.843, PR
            09-MAY-1997 US   08/854.050,14-AUG-1997 US   08/911.312, PR
            14-AUG-1997 US   08/912.951,14-AUG-1997 US   08/915.503 PI   THOMAS
            R SECHI,JOCHIMU RINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI   GREG B
            MORIN,
            PI   CALVIN B HAREI,WILLIAM H ANDREWS
            PC   C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
            PC   C12Q1/02,
            PC   C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
              C07K16/40,
            PC   C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,(C12N1/19, PC
            C12R1:84),
            PC   (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
            PC   (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTGG 809
              |||| | ||||||||||||||||
Db         21 CCTGCCTGAAGGAGCTGGTGG 1


RESULT 1220
AR207710
LOCUS       AR207710                 25 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 50 from patent US 6379897.
ACCESSION   AR207710
VERSION     AR207710.1  GI:21507535
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Weidenhammer,E.M., Wang,L., Xu,X., Heller,M.J. and Kahl,B.F.
  TITLE     Methods for gene expression monitoring on electronic microarrays
  JOURNAL   Patent: US 6379897-A 50 30-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGGCT 507
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                  ||||||||| ||||||| |||||
Db          1 GAGCCAGGGGGGAGCAGGGCT 21


RESULT 1221
AR243409/c
LOCUS       AR243409                 25 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 202 from patent US 6475789.
ACCESSION   AR243409
VERSION     AR243409.1  GI:27290620
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
            Harley,C.B. and Andrews,W.H.
  TITLE     Human telomerase catalytic subunit: diagnostic and therapeutic
            methods
  JOURNAL   Patent: US 6475789-A 202 05-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTGG 809
              |||| | |||||||||||||||
Db         21 CCTGCCTGAAGGAGCTGGTGG 1


RESULT 1222
AR265036
LOCUS       AR265036                 25 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 50 from patent US 6492122.
ACCESSION   AR265036
VERSION     AR265036.1  GI:29693423
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Weidenhammer,E.M., Wang,L., Xu,X., Heller,M.J. and Kahl,B.F.
  TITLE     Quantitative analysis methods on active electronic microarrays
  JOURNAL   Patent: US 6492122-A 50 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        487 GAGCCAGGAGGGAGCGGGGCT 507
              |||||||| ||||||| |||||
Db          1 GAGCCAGGGGGGAGCAGGGCT 21


RESULT 1223
AR390565/c
LOCUS       AR390565                 25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 435 from patent US 6610839.
ACCESSION   AR390565
VERSION     AR390565.1  GI:40112491
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Morin,G.B. and Andrews,W.H.
  TITLE     Promoter for telomerase reverse transcriptase
  JOURNAL   Patent: US 6610839-A 435 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTGG 809
              |||| | |||||||||||||||
Db         21 CCTGCCTGAAGGAGCTGGTGG 1


RESULT 1224
AR393179/c
LOCUS       AR393179                 25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 435 from patent US 6617110.
ACCESSION   AR393179
VERSION     AR393179.1  GI:40118470
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
            Harley,C.B. and Andrews,W.H.
  TITLE     Cells immortalized with telomerase reverse transcriptase for use in
            drug screening
  JOURNAL   Patent: US 6617110-A 435 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTGG 809
              |||| | |||||||||||||||
Db         21 CCTGCCTGAAGGAGCTGGTGG 1


RESULT 1225
AR435375
LOCUS       AR435375                 25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1798 from patent US 6656700.
ACCESSION   AR435375
VERSION     AR435375.1  GI:40198218
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1798 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTGT 2330
              |||| | |||||||||||||||
Db          5 AAGCCAGTTGTTGCTGCTTGT 25
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RESULT 1226
AR435376
LOCUS       AR435376                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1799 from patent US 6656700.
ACCESSION   AR435376
VERSION     AR435376.1  GI:40198219
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1799 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTGT 2330
             |||| | ||||||||||||||||
Db          4 AAGCCAGTTGTTGCTGCTTGT 24


RESULT 1227
AR435377
LOCUS       AR435377                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1800 from patent US 6656700.
ACCESSION   AR435377
VERSION     AR435377.1  GI:40198220
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1800 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTGT 2330
             |||| | ||||||||||||||||
Db          3 AAGCCAGTTGTTGCTGCTTGT 23


RESULT 1228
AR435378
LOCUS       AR435378                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1801 from patent US 6656700.
ACCESSION   AR435378
VERSION     AR435378.1  GI:40198221
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1801 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTGT 2330
             |||| | ||||||||||||||||
Db          2 AAGCCAGTTGTTGCTGCTTGT 22


RESULT 1229
AR435379
LOCUS       AR435379                  25 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1802 from patent US 6656700.
ACCESSION   AR435379
VERSION     AR435379.1  GI:40198222
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Gu,Y. and Shannon,M.E.
  TITLE     Isoforms of human pregnancy-associated protein-E
  JOURNAL   Patent: US 6656700-A 1802 02-DEC-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match           0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2310 AAGCAATTTGTTGCTGCTTGT 2330
             |||| | ||||||||||||||||
Db          1 AAGCCAGTTGTTGCTGCTTGT 21


RESULT 1230
AX042571/c
LOCUS       AX042571                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 137 from Patent WO0065088.
ACCESSION   AX042571
VERSION     AX042571.1  GI:11341179
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 137 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match           0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAA 2799
             ||| ||| ||||||||||||||
Db         21 AGACTTGGAAAAAAAAAAAAA 1


RESULT 1231
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AX042981
LOCUS       AX042981                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 547 from Patent WO0065088.
ACCESSION   AX042981
VERSION     AX042981.1  GI:11341589
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 547 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
                ||||||||||||||||  ||||
Db          1 TTTTTTTTTTTTTTTGGAACT 21


RESULT 1232
AX115872
LOCUS       AX115872                 25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 995 from Patent WO0129262.
ACCESSION   AX115872
VERSION     AX115872.1  GI:14032814
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 995 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
                ||||||  |||||  ||||||||
Db          5 TTTTTTCTTTTTCTTTTTTT 25


RESULT 1233
AX692823
LOCUS       AX692823                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5555 from Patent EP1281758.
ACCESSION   AX692823
VERSION     AX692823.1  GI:29415786
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5555 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
                || |||||||||||||||| |
Db          5 TTCTTTTTTTTTTTTTTTGA 25


RESULT 1234
AX692823/c
LOCUS       AX692823                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5555 from Patent EP1281758.
ACCESSION   AX692823
VERSION     AX692823.1  GI:29415786
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5555 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
                | ||||||||||||||||| ||
Db         25 TCAAAAAAAAAAAAAAAAGAA 5


RESULT 1235
AX692824
LOCUS       AX692824                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5556 from Patent EP1281758.
ACCESSION   AX692824
VERSION     AX692824.1  GI:29415787
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5556 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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                /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || ||||||||||||||||| |
Db          4 TTCTTTTTTTTTTTTTTTGA 24


RESULT 1236
AX692824/c
LOCUS       AX692824                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5556 from Patent EP1281758.
ACCESSION   AX692824
VERSION     AX692824.1  GI:29415787
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5556 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | |||||||||||||||| ||
Db         24 TCAAAAAAAAAAAAAAAAGAA 4


RESULT 1237
AX692825
LOCUS       AX692825                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5557 from Patent EP1281758.
ACCESSION   AX692825
VERSION     AX692825.1  GI:29415788
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5557 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || ||||||||||||||||| |
Db          3 TTCTTTTTTTTTTTTTTTGA 23


RESULT 1238
AX692825/c
LOCUS       AX692825                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5557 from Patent EP1281758.
ACCESSION   AX692825
VERSION     AX692825.1  GI:29415788
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5557 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | |||||||||||||||| ||
Db         23 TCAAAAAAAAAAAAAAAAGAA 3


RESULT 1239
AX692826
LOCUS       AX692826                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5558 from Patent EP1281758.
ACCESSION   AX692826
VERSION     AX692826.1  GI:29415789
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5558 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || ||||||||||||||||| |
Db          2 TTCTTTTTTTTTTTTTTTGA 22


RESULT 1240
AX692826/c
LOCUS       AX692826                 25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5558 from Patent EP1281758.
ACCESSION   AX692826
VERSION     AX692826.1  GI:29415789
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5558 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||| ||
Db         22 TCAAAAAAAAAAAAAAAAAGAA 2

RESULT 1241
AX692827
LOCUS       AX692827                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5559 from Patent EP1281758.
ACCESSION   AX692827
VERSION     AX692827.1  GI:29415790
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5559 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              || |||||||||||||||| |
Db          1 TTCTTTTTTTTTTTTTTTGA 21

RESULT 1242
AX692827/c
LOCUS       AX692827                  25 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 5559 from Patent EP1281758.
ACCESSION   AX692827
VERSION     AX692827.1  GI:29415790
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 5559 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||| ||
Db         21 TCAAAAAAAAAAAAAAAAAGAA 1

RESULT 1243
AX744662
LOCUS       AX744662                  25 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 627 from Patent WO03031621.
ACCESSION   AX744662
VERSION     AX744662.1  GI:30723329
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 627 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          5 GGGGACCTTCTGGTCTTAGGA 25

RESULT 1244
AX744663
LOCUS       AX744663                  25 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 628 from Patent WO03031621.
ACCESSION   AX744663
VERSION     AX744663.1  GI:30723330
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 628 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          4 GGGGACCTTCTGGTCTTAGGA 24


RESULT 1245
AX744664
LOCUS       AX744664                  25 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 629 from Patent WO03031621.
ACCESSION   AX744664
VERSION     AX744664.1  GI:30723331
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 629 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          3 GGGGACCTTCTGGTCTTAGGA 23


RESULT 1246
AX744665
LOCUS       AX744665                  25 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 630 from Patent WO03031621.
ACCESSION   AX744665
VERSION     AX744665.1  GI:30723332
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 630 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          2 GGGGACCTTCTGGTCTTAGGA 22


RESULT 1247
AX744666
LOCUS       AX744666                  25 bp    DNA     linear   PAT 14-MAY-2003
DEFINITION  Sequence 631 from Patent WO03031621.
ACCESSION   AX744666
VERSION     AX744666.1  GI:30723333
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zhang,J.
  TITLE     A human G protein coupled receptor
  JOURNAL   Patent: WO 03031621-A 631 17-APR-2003;
            Amersham Biosciences (SV) Corp. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2105 GGGGGCCTTCTGGTTTTAGGA 2125
              |||| ||||||||| ||||||
Db          1 GGGGACCTTCTGGTCTTAGGA 21


RESULT 1248
AX810470/c
LOCUS       AX810470                  25 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 435 from Patent EP1333094.
ACCESSION   AX810470
VERSION     AX810470.1  GI:38523962
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
            Harley,C.B. and Andrews,W.H.
  TITLE     Human telomerase catalytic subunit
  JOURNAL   Patent: EP 1333094-A 435 06-AUG-2003;
            Geron Corporation (US) ; University Technology Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTGG 809
              |||| | ||||||||||||||
Db         21 CCTGCCTGAAGGAGCTGGTGG 1


RESULT 1249
BD011139/c
LOCUS       BD011139                  25 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Human telomerase catalytic subunit.
ACCESSION   BD011139
VERSION     BD011139.1  GI:18639512
KEYWORDS    JP 2001081042-A/96.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
            Harley,C.B. and Andrews,W.H.
  TITLE     Human telomerase catalytic subunit
  JOURNAL   Patent: JP 2001081042-A 96 27-MAR-2001;
            GERON CORP,UNIVERSITY TECHNOLOGY CORP
COMMENT     OS   Unidentified
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            PN   JP 2001081042-A/96
            PD   27-MAR-2001
            PF   27-JUL-2000 JP 2000227474
            PR   01-OCT-1996 US    08/724643,18-APR-1997 US    08/844419 PR
            25-APR-1997 US    08/846017,06-MAY-1997 US    08/851843 PR
            09-MAY-1997 US    08/854050,14-AUG-1997 US    08/911312 PR
            14-AUG-1997 US    08/912951,14-AUG-1997 US    08/915503 PI   THOMAS
            R SECHI,JOACHIM LINGNER,TORU NAKAMURA,KAREN B CHAPMAN, PI   GREG B
            MORIN,
            PI   CALVIN B HARLEY,WILLIAM H ANDREWS
            PC   A61K38/00,A61K31/7088,A61K39/00,A61K48/00,A61P35/00,A61P43/00,
            PC   C07K5/10,
            PC   C07K5/107,C07K5/117,C07K7/06,C07K7/08,C07K16/40,C12N9/12, PC
            C12N15/09,
            PC   C12Q1/02,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53, PC
            G01N33/53,
            PC   G01N33/566,G01N33/573//C12P21/08,A61K37/02,C12N15/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT   /organism='Unidentified'.
FEATURES                Location/Qualifiers
     source             1. .25
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"

  Query Match              0.6%;  Score 17.8;  DB 1;  Length 25;
  Best Local Similarity   90.5%;  Pred. No. 1.4e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTGG 809
              |||| | ||||||||||||||||
Db         21 CCTGCCTGAAGGAGCTGGTGG 1


RESULT 1250
E33560/c
LOCUS       E33560                    26 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Stress-responsive gene promoter.
ACCESSION   E33560
VERSION     E33560.1  GI:18624133
KEYWORDS    JP 2000078977-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Tsujimoto,Y., Izawa,S., Inoue,Y., Kimura,H. and Sato,N.
  TITLE     Stress-responsive gene promoter
  JOURNAL   Patent: JP 2000078977-A 5 21-MAR-2000;
            MARUHA CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2000078977-A/5
            PD   21-MAR-2000
            PF   04-SEP-1998 JP 1998251390
            PR
            PI   YOSHIYUKI TSUJIMOTO,SHINGO IZAWA,YOSHIHARU INOUE,HIKARU
            KIMURA,
            PI   NOBUYUKI SATO
            PC   C12N15/09,C12N1/19,C12P21/02//(C12N15/09,C12R1:865),(C12N1/19,
            PC   C12R1:865),
            PC   (C12P21/02,C12R1:865),C12N15/00,(C12N15/00,C12R1:865) CC
            FH   Key             Location/Qualifiers
            FT   source          1. .36
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
     source             1. .26
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match              0.6%;  Score 17.8;  DB 1;  Length 26;
  Best Local Similarity   90.5%;  Pred. No. 1.5e+03;
  Matches   19;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||| ||||||||||||
Db         24 TCAAAAAAATAAAAAAAAAAA 4


RESULT 1251
AR159556/c
LOCUS       AR159556                  24 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 16 from patent US 6251589.
ACCESSION   AR159556
VERSION     AR159556.1  GI:16222248
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Tsuji,S. and Sanpei,K.
  TITLE     Method for diagnosing spinocerebellar ataxia type 2 and primers
            therefor
  JOURNAL   Patent: US 6251589-A 16 26-JUN-2001;
FEATURES                Location/Qualifiers
     source             1. .24
                        /organism="unknown"
                        /mol_type="unassigned DNA"

  Query Match              0.6%;  Score 17.6;  DB 1;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.4e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy         46 CGCGCGCGGCGGGGGCGGCGGCAG 69
              |||| |||||||  |||||||| |
Db         24 CGCGGGCGGCGGCTGCGGCGGCTG 1


RESULT 1252
AX443659
LOCUS       AX443659                  24 bp    DNA     linear   PAT 03-JUL-2002
DEFINITION  Sequence 114 from Patent WO0216649.
ACCESSION   AX443659
VERSION     AX443659.1  GI:21690937
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Gunderson,K.
  TITLE     Probes and decoder oligonucleotides
  JOURNAL   Patent: WO 0216649-A 114 28-FEB-2002;
            Illumina, Inc. (US)
FEATURES                Location/Qualifiers
     source             1. .24
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="Computer Generated Probe Sequence."

  Query Match              0.6%;  Score 17.6;  DB 1;  Length 24;
  Best Local Similarity   83.3%;  Pred. No. 1.4e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1086 AAGGTGAAGCTGTTCATTTGGCTA 1109
              ||||||  ||  ||||||||||||
Db          1 AAGGTGGTGCCATTCATTTGGCTA 24


RESULT 1253
A71580
LOCUS       A71580                    25 bp    DNA     linear   PAT 07-MAY-1999
DEFINITION  Sequence 13 from Patent WO9813478.
ACCESSION   A71580
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VERSION     A71580.1  GI:4775190
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Sela-Buurlage,M.B., Melchers,L.S., Stuiver,M.H., Lageweg,W.,
            Custers,J.H., Ponstein,A.S. and Van,D.J.
  TITLE     ANTIFUNGAL PROTEINS, DNA CODING THEREFORE, AND HOSTS INCORPORATING
            SAM
  JOURNAL   Patent: WO 9813478-A 13 02-APR-1998;
            SELA BUURLAGE MARIANNE BEATRIX (IL)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1004 GAGAAGTTGGACAAGATCGGGTTG 1027
              | ||||||| | ||||| ||||||
Db          2 GGGAAGTTGCAGAAGATTGGGTTG 25


RESULT 1254
BD245989
LOCUS       BD245989                  25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Development of novel antibiotics based on bacteriophage genomics.
ACCESSION   BD245989
VERSION     BD245989.1  GI:33055759
KEYWORDS    JP 2002531107-A/724.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Pelletier,J., Gros,P. and Dubow,M.
  TITLE     Development of novel antibiotics based on bacteriophage genomics
  JOURNAL   Patent: JP 2002531107-A 724 24-SEP-2002;
            PHAGETECH INC
COMMENT     OS   Staphylococcus aureus bacteriophage 96
            PN   JP 2002531107-A/724
            PD   24-SEP-2002
            PF   03-DEC-1999 JP 2000585456
            PR   03-DEC-1998 US    60/110992,03-JUN-1999 US    09/326144 PR
            28-SEP-1999 US    09/407804,30-SEP-1999 US    60/157218 PR
            01-DEC-1999 US    60/168777,02-DEC-1999 US    09/454252 PI   JERRY
            PELLETIER,PHILLIPPE GROS,MICHAEL DUBOW
            PC   C12N15/09,A01N63/00,A61K38/00,A61K45/00,A61P31/04,C07K14/005,
            PC   C12M1/00,
            PC   C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
             C12N15/00,
            PC   A61K37/02
            CC   Ribosome binding sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Staphylococcus
            aureus bacteriophage
            FT                   96'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2760 TAATAAAAGTATTCTTGTTAGAAT 2783
              | ||||||||||||||  ||| ||
Db          2 TCATAAAAGTATTCTTTGTAGTAT 25


RESULT 1255
AR237790
LOCUS       AR237790                  25 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 10 from patent US 6465636.
ACCESSION   AR237790
VERSION     AR237790.1  GI:27282610
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Stuiver,M.H., Custers,J.H.H.V. and Simons,L.H.
  TITLE     Pathogen-inducible promoter
  JOURNAL   Patent: US 6465636-A 10 15-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1004 GAGAAGTTGGACAAGATCGGGTTG 1027
              | ||||||| | ||||| ||||||
Db          2 GGGAAGTTGCAGAAGATTGGGTTG 25


RESULT 1256
AX015674
LOCUS       AX015674                  25 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 10 from Patent WO9950428.
ACCESSION   AX015674
VERSION     AX015674.1  GI:10041503
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Simons,L.H., Stuiver,M.H. and Custers,J.H.
  TITLE     Pathogen-inducible promoter
  JOURNAL   Patent: WO 9950428-A 10 07-OCT-1999;
            SIMONS LAMBERTUS HENRICUS (NL); STUIVER MAARTEN HENDRIK (NL); MOGEN
            INT (NL); CUSTERS JEROME HUBERTINA HENRI (NL)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="primer"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1004 GAGAAGTTGGACAAGATCGGGTTG 1027
              | ||||||| | ||||| ||||||
Db          2 GGGAAGTTGCAGAAGATTGGGTTG 25


RESULT 1257
AX042589/c
LOCUS       AX042589                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 155 from Patent WO0065088.
ACCESSION   AX042589
VERSION     AX042589.1  GI:11341197
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
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REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 155 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Homozygote primer sequence"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
             ||||  ||  ||||||||||||||||
Db         24 AGAAGGGAGGAAAAAAAAAAAAAA 1


RESULT 1258
AX042901/c
LOCUS       AX042901                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 467 from Patent WO0065088.
ACCESSION   AX042901
VERSION     AX042901.1  GI:11341509
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 467 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
             ||||   ||  ||||||||||||||||
Db         24 AATTCCGAATAAAAAAAAAAAAAA 1


RESULT 1259
AX043100/c
LOCUS       AX043100                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 666 from Patent WO0065088.
ACCESSION   AX043100
VERSION     AX043100.1  GI:11341708
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 666 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="16S rRNA Homozygote Primer Sequence"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAA 2799
             |||  | |||  ||||||||||||||
Db         24 GTTCTACTTGCAAAAAAAAAAAAA 1


RESULT 1260
AX043152/c
LOCUS       AX043152                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 718 from Patent WO0065088.
ACCESSION   AX043152
VERSION     AX043152.1  GI:11341760
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 718 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DPB1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAA 2798
             || ||  | ||  ||||||||||||
Db         24 TGGTACACTTAAAAAAAAAAAAAA 1


RESULT 1261
AX043290/c
LOCUS       AX043290                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 856 from Patent WO0065088.
ACCESSION   AX043290
VERSION     AX043290.1  GI:11341898
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 856 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAA 2802
             ||||  ||  ||||||||||||||||
Db         24 AGAAGGGAGGAAAAAAAAAAAAAA 1


RESULT 1262
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AX043309/c
LOCUS       AX043309                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 875 from Patent WO0065088.
ACCESSION   AX043309
VERSION     AX043309.1  GI:11341917
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 875 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAA 2801
             |||| ||| |  ||||||||||||
Db         24 TAGAGTTGTAGCAAAAAAAAAAAA 1


RESULT 1263
AX043412
LOCUS       AX043412                 25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 978 from Patent WO0065088.
ACCESSION   AX043412
VERSION     AX043412.1  GI:11342020
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 978 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DRB345 Heterozygote Primer Sequence"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACT 2190
             |||||||||||||||| ||  | ||
Db          1 TTTTTTTTTTTTTTCTTGGAGCT 24


RESULT 1264
AX115700/c
LOCUS       AX115700                 25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 823 from Patent WO0129262.
ACCESSION   AX115700
VERSION     AX115700.1  GI:14032642
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 823 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTAA 2188
              ||  | ||||||||||||||| ||||
Db         25 CTGATCTTTTTTTTTTTTTCTTAA 2


RESULT 1265
BD008572
LOCUS       BD008572                 25 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Antifungal proteins, DNA coding therefor, and hosts incorporating
            same.
ACCESSION   BD008572
VERSION     BD008572.1  GI:18636945
KEYWORDS    JP 2001502525-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Stuiver,M.H., Custers,J.H.H.V., Buurlage,M.B.S., Melchers,L.S.,
            Deventer,J.P.E.V., Lageweg,W. and Ponstein,A.S.
  TITLE     Antifungal proteins, DNA coding therefor, and hosts incorporating
  JOURNAL   Patent: JP 2001502525-A 10 27-FEB-2001;
            MOGEN INTERNATIONAL NV
COMMENT     OS   Unidentified
            PN   JP 2001502525-A/10
            PD   27-FEB-2001
            PF   04-SEP-1997 JP 1998515200
            PR
            PI   MAARTEN HENDRIK STUIVER,
            PI   JEROME HUBERTUS HENRICUS VICTOR CUSTERS,
            PI   MARIANNE BEATRIX SELA BUURLAGE,LEO SJOERD MELCHERS, PI
            JOHANNA PIETERNELLA ELS VAN DEVENTER TROOST,WESSEL LAGEWEG, PI
            ANNE SILENE PONSTEIN
            PC   C12N15/82,C12N9/02,C12Q1/68,C07K16/40,C12N15/62,A01H5/00 CC
            Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1004 GAGAAGTTGGACAAGATCGGGTTG 1027
              | |||||||  | |||||  ||||||
Db          2 GGGAAGTTGCAGAAGATTGGGTTG 25


RESULT 1266
BD222040
LOCUS       BD222040                 25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Pathogen-inducible promoter.
ACCESSION   BD222040
VERSION     BD222040.1  GI:33031810
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KEYWORDS    JP 2002509728-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Stuiver,M.H., Custers,J.H.H.V. and Simons,L.H.
  TITLE     Pathogen-inducible promoter
  JOURNAL   Patent: JP 2002509728-A 10 02-APR-2002;
            ZENECA MOGEN BV
COMMENT     OS   Artificial Sequence
            PN   JP 2002509728-A/10
            PD   02-APR-2002
            PF   25-MAR-1999 JP 2000541316
            PR   01-APR-1998 EP   98201024.1
            PI   MAARTEN HENDRIK STUIVER,JEROME HUBERTINA HENRICUS VICTOR  PI
            CUSTERS,
            PI   LAMBERTUS HENRICUS SIMONS
            PC   C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/
            PC   10,C12N15/00,
            PC   C12N5/00,C12N5/00
            CC   Description of Artificial Sequence:primer
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 25;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1004 GAGAAGTTGGACAAGATCGGGTTG 1027
              | ||||||| | ||||| ||||||
Db          2 GGGAAGTTGCAGAAGATTGGGTTG 25


RESULT 1267
AR098647
LOCUS       AR098647                 26 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 5 from patent US 6077668.
ACCESSION   AR098647
VERSION     AR098647.1  GI:12808413
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kool,E.T.
  TITLE     Highly sensitive multimeric nucleic acid probes
  JOURNAL   Patent: US 6077668-A 5 20-JUN-2000;
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||| ||||||||||
Db          2 AAAAAAAAAAAACAAAAAAAAAA 25


RESULT 1268
AR204721
LOCUS       AR204721                 26 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6368802.
ACCESSION   AR204721
VERSION     AR204721.1  GI:21502120
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kool,E.T.
  TITLE     Circular DNA vectors for synthesis of RNA and DNA
  JOURNAL   Patent: US 6368802-A 5 09-APR-2002;
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 26;
  Best Local Similarity   83.3%;  Pred. No. 1.7e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||| ||||||||||
Db          2 AAAAAAAAAAAACAAAAAAAAAA 25


RESULT 1269
AX589115/c
LOCUS       AX589115                 27 bp    DNA     linear   PAT 24-JAN-2003
DEFINITION  Sequence 33 from Patent WO02083179.
ACCESSION   AX589115
VERSION     AX589115.1  GI:27900764
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mckerracher,L.
  TITLE     Fusion proteins
  JOURNAL   Patent: WO 02083179-A 33 24-OCT-2002;
            Bioaxone Therapeutique Inc. (CA)
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Oligonucleotide used in the cloning of a reverse
                      HIV Tat sequence in C3Basic3"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 27;
  Best Local Similarity   83.3%;  Pred. No. 1.8e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1492 GGAGAAAATGGAGAAACACAGGAA 1515
              | |||||| | ||||||| |||||
Db         26 GAAGAAAAAGAAGAAACAAAGGAA 3


RESULT 1270
AR098648/c
LOCUS       AR098648                 29 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 6 from patent US 6077668.
ACCESSION   AR098648
VERSION     AR098648.1  GI:12808414
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kool,E.T.
  TITLE     Highly sensitive multimeric nucleic acid probes
  JOURNAL   Patent: US 6077668-A 6 20-JUN-2000;
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="unknown"
                      /mol_type="unassigned DNA"
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  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.1e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||| ||||||||||
Db         29 AAAAAAAAAAAACAAAAAAAAAAA 6


RESULT 1271
AR204722/c
LOCUS       AR204722                  29 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6368802.
ACCESSION   AR204722
VERSION     AR204722.1  GI:21502121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kool,E.T.
  TITLE     Circular DNA vectors for synthesis of RNA and DNA
  JOURNAL   Patent: US 6368802-A 6 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.6;  DB 1;  Length 29;
  Best Local Similarity   83.3%;  Pred. No. 2.1e+03;
  Matches   20;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||| ||||||||||
Db         29 AAAAAAAAAAAACAAAAAAAAAAA 6


RESULT 1272
AX078001
LOCUS       AX078001                  20 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 15 from Patent WO0105435.
ACCESSION   AX078001
VERSION     AX078001.1  GI:13157746
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.
  TITLE     Antisense therapy for hormone-regulated tumors
  JOURNAL   Patent: WO 0105435-A 15 25-JAN-2001;
            THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTCAA 19


RESULT 1273
AR211367/c
LOCUS       AR211367                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6399305.
ACCESSION   AR211367
VERSION     AR211367.1  GI:21514670
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Makino,Y., Abe,Y., Takagi,M., Takenaka,S., Yamashita,K. and
            Ogawa,M.
  TITLE     Protection of partial complementary nucleic acid fragment using a
            electroconductive chip and intercalator
  JOURNAL   Patent: US 6399305-A 5 04-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||| |||||||||
Db         20 AAAAAAAAATAAAAAAAAA 2


RESULT 1274
AR371268
LOCUS       AR371268                  20 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 4 from patent US 6395474.
ACCESSION   AR371268
VERSION     AR371268.1  GI:34608200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
  TITLE     Peptide nucleic acids
  JOURNAL   Patent: US 6395474-A 4 28-MAY-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||
Db          1 AAAAAGAAAAAAAAAAAAA 19


RESULT 1275
AX136903/c
LOCUS       AX136903                  20 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 5 from Patent EP1065278.
ACCESSION   AX136903
VERSION     AX136903.1  GI:14273252
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Makino,Y., Abe,Y., Ogawa,M., Takagi,M., Takenaka,S. and
            Yamashita,K.
  TITLE     Detection of partly complementary nucleic acid fragment
  JOURNAL   Patent: EP 1065278-A 5 03-JAN-2001;
            FUJI PHOTO FILM CO., LTD. (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:32630"
                     /note="sample nucleic acid fragment"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||  |||||||||
Db         20 AAAAAAAAATAAAAAAAA 2

RESULT 1276
E59328/c
LOCUS       E59328                    20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method for purifying oligonucleotide.
ACCESSION   E59328
VERSION     E59328.1  GI:18622505
KEYWORDS    JP 2000342265-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hirose,K. and Yoshida,T.
  TITLE     Method for purifying oligonucleotide
  JOURNAL   Patent: JP 2000342265-A 9 12-DEC-2000;
            TOAGOSEI CHEM IND CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000342265-A/9
            PD   12-DEC-2000
            PF   02-JUN-1999 JP 1999154974
            PR
            PI   KUNIHIKO HIROSE,TADAO YOSHIDA
            PC   C12N15/09,B01D15/08,C12N15/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 20;
  Best Local Similarity   94.7%;  Pred. No. 9e+02;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTA 2187
              ||||||||  ||||||||||
Db         19 TTTTTTTTCTTTTTTTTA 1

RESULT 1277
AR241831/c
LOCUS       AR241831                  21 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 119 from patent US 6472154.
ACCESSION   AR241831
VERSION     AR241831.1  GI:27287643
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 119 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||||||  |||||||||
Db         21 AAAAAAAAATAAAAAAAA 3

RESULT 1278
AX838821
LOCUS       AX838821                  21 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 26 from Patent WO03076667.
ACCESSION   AX838821
VERSION     AX838821.1  GI:39922376
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Jeney,C. and Takacs,T.
  TITLE     Amplification-hybridisation method for detecting and typing
            humanpapillomavirus
  JOURNAL   Patent: WO 03076667-A 26 18-SEP-2003;
            Jeney, Csaba (HU) ; Takacs, Tibor (HU)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PCR primer (L1CR52)"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 21;
  Best Local Similarity   94.7%;  Pred. No. 1e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2533 ATACAGGGTATTAAGAATT 2551
              |||||||||||| ||||||
Db          3 ATACAGGGTATTTAGAATT 21

RESULT 1279
E12392
LOCUS       E12392                    23 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide primer.
ACCESSION   E12392
VERSION     E12392.1  GI:3251225
KEYWORDS    JP 1996322598-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Katou,K.
  TITLE     INDEXING METHOD OF DNA MOLECULE
  JOURNAL   Patent: JP 1996322598-A 2 10-DEC-1996;
            RES DEV CORP OF JAPAN
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996322598-A/2
            PD   10-DEC-1996
            PF   12-SEP-1995 JP 1995234122
            PR   28-MAR-1995 JP 95P    69695
            PI   KATOU KIKUYA
            PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .23
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /mol_type="genomic DNA"
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                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              || |||||||||||||||||
Db          4 CTGTTTTTTTTTTTTTTTT 22


RESULT 1280
E12392/c
LOCUS       E12392                     23 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Oligonucleotide primer.
ACCESSION   E12392
VERSION     E12392.1  GI:3251225
KEYWORDS    JP 1996322598-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Katou,K.
  TITLE     INDEXING METHOD OF DNA MOLECULE
  JOURNAL   Patent: JP 1996322598-A 2 10-DEC-1996;
            RES DEV CORP OF JAPAN
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996322598-A/2
            PD   10-DEC-1996
            PF   12-SEP-1995 JP 1995234122
            PR   28-MAR-1995 JP 95P    69695
            PI   KATOU KIKUYA
            PC   C12Q1/68,C07H21/02,C07H21/04,C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .23
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||  |
Db         23 GAAAAAAAAAAAAAAAACA 5


RESULT 1281
I79498
LOCUS       I79498                     23 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 5 from patent US 5707807.
ACCESSION   I79498
VERSION     I79498.1  GI:3207788
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 5 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTT 2183
              || |||||||||||||||||
Db          4 CTGTTTTTTTTTTTTTTTT 22


RESULT 1282
I79498/c
LOCUS       I79498                     23 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 5 from patent US 5707807.
ACCESSION   I79498
VERSION     I79498.1  GI:3207788
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 5 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 23;
  Best Local Similarity   94.7%;  Pred. No. 1.3e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||  |
Db         23 GAAAAAAAAAAAAAAAACA 5


RESULT 1283
AR431312/c
LOCUS       AR431312                   24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6651008.
ACCESSION   AR431312
VERSION     AR431312.1  GI:40193280
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 6 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.6%;  Score 17.4;  DB 1;  Length 24;
  Best Local Similarity   94.7%;  Pred. No. 1.5e+03;
  Matches   18;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAA 2804
              |||||  ||||||||||||
Db         24 AAAAACAAAAAAAAAAAA 6


RESULT 1284
AR431308/c
LOCUS       AR431308                   24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from patent US 6651008.
ACCESSION   AR431308
VERSION     AR431308.1  GI:40193276
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     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 873
AX825164/c
LOCUS       AX825164                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 62 from Patent WO03072818.
ACCESSION   AX825164
VERSION     AX825164.1  GI:39750893
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 62 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 874
BD087491
LOCUS       BD087491                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis.
ACCESSION   BD087491
VERSION     BD087491.1  GI:22633101
KEYWORDS    JP 2001525193-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
            Edman,C.F.
  TITLE     Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis
  JOURNAL   Patent: JP 2001525193-A 2 11-DEC-2001;
            NANOGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001525193-A/2
            PD   11-DEC-2001
            PF   01-DEC-1998 JP 2000524303
            PR   05-DEC-1997 US    08/986065
            PI   RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I  PI
            NERENBERG,
            PI   MICHAEL J HELLER,CARL F EDMAN
            PC   C12Q1/68,C12N15/09,C12N15/00
            CC   Description of Artificial Sequence: Synthesized with u at 3'
            CC           terminus to
            CC   provide ribonucleic acid base for reactivity; Poly A sequence
            CC           for reduced
            CC   secondary structure
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 875
AX825111
LOCUS       AX825111                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 9 from Patent WO03072818.
ACCESSION   AX825111
VERSION     AX825111.1  GI:39750840
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 9 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
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Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 870
AX825154/c
LOCUS       AX825154                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 52 from Patent WO03072818.
ACCESSION   AX825154
VERSION     AX825154.1  GI:39750883
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 52 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 871
AX825160
LOCUS       AX825160                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 58 from Patent WO03072818.
ACCESSION   AX825160
VERSION     AX825160.1  GI:39750889
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 58 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 872
AX825161
LOCUS       AX825161                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 59 from Patent WO03072818.
ACCESSION   AX825161
VERSION     AX825161.1  GI:39750890
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 59 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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          diagnostics
  JOURNAL   Patent: US 6238624-A 2 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 867
I36166
LOCUS       I36166                  21 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 2 from patent US 5605662.
ACCESSION   I36166
VERSION     I36166.1  GI:2086679
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Heller,M.J. and Tu,E.
  TITLE     Active programmable electronic devices for molecular biological
            analysis and diagnostics
  JOURNAL   Patent: US 5605662-A 2 25-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 868
AX825152/c
LOCUS       AX825152                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 50 from Patent WO03072818.
ACCESSION   AX825152
VERSION     AX825152.1  GI:39750881
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 50 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 869
AX825153/c
LOCUS       AX825153                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 51 from Patent WO03072818.
ACCESSION   AX825153
VERSION     AX825153.1  GI:39750882
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 51 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 64 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 864
BD080832/c
LOCUS       BD080832                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Mammaglobin, a secreted mammary specific breast cancer protein.
ACCESSION   BD080832
VERSION     BD080832.1  GI:22626435
KEYWORDS    JP 2001516569-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Mammaglobin, a secreted mammary specific breast cancer protein
  JOURNAL   Patent: JP 2001516569-A 10 02-OCT-2001;
            WASHINGTON UNIVERSITY
COMMENT     OS   Unidentified
            PN   JP 2001516569-A/10
            PD   02-OCT-2001
            PF   18-SEP-1998 JP 2000511779
            PR   18-SEP-1997 US    08/933149
            PI   MARK A WATSON,TIMOTHY P FLEMING
            PC   C12N15/09,A61K35/26,A61K39/00,A61K39/00,A61K39/395,A61K39/395,
            PC   A61P35/00,
            PC   C07K14/47,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Mammaglobin, a secreted mammary specific breast cancer protein
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 865
BD224108/c
LOCUS       BD224108                 21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Mammaglobin, breast cancer secretory protein specific to mamma.
ACCESSION   BD224108
VERSION     BD224108.1  GI:33033878
KEYWORDS    JP 2002525098-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Mammaglobin, breast cancer secretory protein specific to mamma
  JOURNAL   Patent: JP 2002525098-A 10 13-AUG-2002;
            WASHINGTON UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002525098-A/10
            PD   13-AUG-2002
            PF   29-SEP-1999 JP 2000572241
            PR   29-SEP-1998 US    09/162622
            PI   MARK A WATSON,TIMOTHY P FLEMING
            PC
            C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/577//G01N33/574, PC
             C12N15/00
            CC   Description of Artificial Sequence:Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 866
AR153849
LOCUS       AR153849                 21 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6238624.
ACCESSION   AR153849
VERSION     AR153849.1  GI:15121902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
  TITLE     Methods for transport in molecular biological analysis and
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            cancer protein
  JOURNAL   Patent: US 5668267-A 13 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 859
AR322245/c
LOCUS       AR322245                21 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 13 from patent US 6566072.
ACCESSION   AR322245
VERSION     AR322245.1  GI:33707814
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Mammaglobin, a secreted mammary-specific breast cancer protein
  JOURNAL   Patent: US 6566072-A 13 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 860
AX104720/c
LOCUS       AX104720                21 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 912 from Patent WO0122972.
ACCESSION   AX104720
VERSION     AX104720.1  GI:13920917
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 912 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 861
AX355812/c
LOCUS       AX355812                21 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 840 from Patent WO0197843.
ACCESSION   AX355812
VERSION     AX355812.1  GI:18620480
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 840 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 862
AX547773/c
LOCUS       AX547773                21 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 912 from Patent WO02053141.
ACCESSION   AX547773
VERSION     AX547773.1  GI:25812917
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 912 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 863
AX825166/c
LOCUS       AX825166                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 64 from Patent WO03072818.
ACCESSION   AX825166
VERSION     AX825166.1  GI:39750895
KEYWORDS    .
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            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Mammaglobin, a mammary-specific breast cancer protein
  JOURNAL   Patent: US 5968754-A 13 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 854
AR084521
LOCUS       AR084521                 21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 10 from patent US 5981185.
ACCESSION   AR084521
VERSION     AR084521.1  GI:10011292
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 10 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 855
AR084524/c
LOCUS       AR084524                 21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 13 from patent US 5981185.
ACCESSION   AR084524
VERSION     AR084524.1  GI:10011295
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 13 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 856
AR093143/c
LOCUS       AR093143                 21 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 12 from patent US 5998596.
ACCESSION   AR093143
VERSION     AR093143.1  GI:10019895
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bergan,R. and Neckers,L.
  TITLE     Inhibition of protein kinase activity by aptameric action of
            oligonucleotides
  JOURNAL   Patent: US 5998596-A 12 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 857
AR095412/c
LOCUS       AR095412                 21 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 13 from patent US 6004756.
ACCESSION   AR095412
VERSION     AR095412.1  GI:10023262
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Method for detecting the presence of breast cancer by detecting an
            increase in mammaglobin mRNA expression
  JOURNAL   Patent: US 6004756-A 13 21-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         21 AAAAAAAAAAAAAAAAAAA 3


RESULT 858
I65744/c
LOCUS       I65744                   21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 13 from patent US 5668267.
ACCESSION   I65744
VERSION     I65744.1  GI:2482314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Polynucleotides encoding mammaglobin, a mammary-specific breast
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method for enhancing the effciency of gene transfer with stem cell
            factor (SCF) polypeptide
  JOURNAL   Patent: US 6207454-A 33 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 849
AR140281/c
LOCUS       AR140281                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 34 from patent US 6207454.
ACCESSION   AR140281
VERSION     AR140281.1  GI:14482777
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Method for enhancing the effciency of gene transfer with stem cell
            factor (SCF) polypeptide
  JOURNAL   Patent: US 6207454-A 34 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 850
AR140558
LOCUS       AR140558                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 33 from patent US 6207802.
ACCESSION   AR140558
VERSION     AR140558.1  GI:14483054
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Stem cell factor and compositions
  JOURNAL   Patent: US 6207802-A 33 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 851
AR140559/c
LOCUS       AR140559                 20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 34 from patent US 6207802.
ACCESSION   AR140559
VERSION     AR140559.1  GI:14483055
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     Stem cell factor and compositions
  JOURNAL   Patent: US 6207802-A 34 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 852
AX078001/c
LOCUS       AX078001                 20 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 15 from Patent WO0105435.
ACCESSION   AX078001
VERSION     AX078001.1  GI:13157746
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gleave,M.
  TITLE     Antisense therapy for hormone-regulated tumors
  JOURNAL   Patent: WO 0105435-A 15 25-JAN-2001;
            THE UNIVERSITY OF BRITISH COLUMBIA (CA) ; Miyake, Hideaki (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAA 2801
              ||||||||||||||||||
Db         19 TTGAAAAAAAAAAAAAAAA 1


RESULT 853
AR080294/c
LOCUS       AR080294                 21 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 13 from patent US 5968754.
ACCESSION   AR080294
VERSION     AR080294.1  GI:10007029
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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REFERENCE   1  (bases 1 to 20)
  AUTHORS   Segawa,M., Takarada,H., Aono,T. and Yoshiga,S.
  TITLE     Method of detecting single base polymorphism
  JOURNAL   Patent: JP 2002034599-A 9 05-FEB-2002;
            TOYOBO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002034599-A/9
            PD   05-FEB-2002
            PF   26-JUL-2000 JP 2000225354
            PI   MASAYA SEGAWA,HIROSHI TAKARADA,TOSHIYA AONO,SATOKO YOSHIGA PC
             C12Q1/68,C12N15/09,C12N15/00
            CC   Description of Artificial Sequence:primer
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 845
BD218101
LOCUS       BD218101                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Compositions derived from mycobacterium vaccae and methods for
            their use.
ACCESSION   BD218101
VERSION     BD218101.1  GI:33027871
KEYWORDS    JP 2002514385-A/26.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tan,P., Watson,J., Visser,E.S., Skinner,M.A. and Prestid,R.L.
  TITLE     Compositions derived from mycobacterium vaccae and methods for
            their
  JOURNAL   Patent: JP 2002514385-A 26 21-MAY-2002;
            GENESIS RESEARCH AND DEVELOPMENT CORP LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002514385-A/26
            PD   21-MAY-2002
            PF   23-DEC-1998 JP 2000525553
            PR   23-DEC-1997 US    08/997362,23-DEC-1997 US    08/997080 PR
            23-DEC-1997 US    08/996624,11-JUN-1998 US    09/095855 PR
            17-SEP-1998 US    09/156181,04-DEC-1998 US    09/205426 PI   PAUL
            TAN,JAMES WATSON,ELIZABETH S VISSER,MARGOT A SKINNER,ROSS
            PI   L PRESTIDGE
            PC   C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
            PC   A61P17/00,
            PC   A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
            PC   C07K19/00,
            PC   C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
            G01N33/68//
            PC   (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
            CC   Made in a lab
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 846
AR139961
LOCUS       AR139961                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 33 from patent US 6207417.
ACCESSION   AR139961
VERSION     AR139961.1  GI:14482457
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     DNA encoding stem cell factor
  JOURNAL   Patent: US 6207417-A 33 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTA 2187
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTA 19


RESULT 847
AR139962/c
LOCUS       AR139962                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 34 from patent US 6207417.
ACCESSION   AR139962
VERSION     AR139962.1  GI:14482458
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
  TITLE     DNA encoding stem cell factor
  JOURNAL   Patent: US 6207417-A 34 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAA 2803
             |||||||||||||||||||
Db         19 GAAAAAAAAAAAAAAAAAA 1


RESULT 848
AR140280
LOCUS       AR140280                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 33 from patent US 6207454.
ACCESSION   AR140280
VERSION     AR140280.1  GI:14482776
KEYWORDS    .
SOURCE      Unknown.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic Oligomer Sequence~Synthetic Probe Sequence"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 841
AX741052
LOCUS AX741052 20 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 26 from Patent WO03027328.
ACCESSION AX741052
VERSION AX741052.1 GI:30523913
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE Methods, kits and compositions pertaining to the suppression of detectable probe binding to randomly distributed repeat sequences in genomic nucleic acid
JOURNAL Patent: WO 03027328-A 26 03-APR-2003;
Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic Oligomer Sequence~Synthetic Probe Sequence"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 842
BD008523
LOCUS BD008523 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Compounds and methods for treatment and diagnosis of Mycobacterial infections.
ACCESSION BD008523
VERSION BD008523.1 GI:18636896
KEYWORDS JP 2001503969-A/26.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Hiyama,J., Visser,E.S., Skinner,M.A., Scott,L.M. and Prestidge,R.L.
TITLE Compounds and methods for treatment and diagnosis of Mycobacterial infections
JOURNAL Patent: JP 2001503969-A 26 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT OS Unidentified
PN JP 2001503969-A/26
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR
PI PAUL TAN,JUN HIYAMA,ELIZABETH S VISSER,MARGOT A SKINNER, PI LINDA M SCOTT,
PI ROSS L PRESTIDGE
PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1. .20
FT /organism='Unidentified'.
FEATURES Location/Qualifiers
source 1. .20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 843
BD080522/c
LOCUS BD080522 20 bp RNA linear PAT 27-AUG-2002
DEFINITION Ribonucleoside-derivative and method for preparing the same.
ACCESSION BD080522
VERSION BD080522.1 GI:22626125
KEYWORDS JP 2001515087-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pitsch,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: JP 2001515087-A 1 18-SEP-2001;
STEFAN PITSCH,PATRICK A WEISS,LUZI JENNY
COMMENT OS Artificial Sequence
PN JP 2001515087-A/1
PD 18-SEP-2001
PF 17-AUG-1998 JP 2000509723
PR 18-AUG-1997 CH 1931/97
PI STEFAN PITSCH,PATRICK A WEISS,LUZI JENNY
PC C07H19/06,C07F7/18,C07H19/16,C07H21/02,C07H23/00 CC
Description of Artificial Sequence:synthetic polynucleotide FH
Key Location/Qualifiers
FT source 1. .20
FT /organism='Artificial Sequence'.
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
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Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 844
BD107450/c
LOCUS BD107450 20 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of detecting single base polymorphism.
ACCESSION BD107450
VERSION BD107450.1 GI:23202268
KEYWORDS JP 2002034599-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

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ACCESSION   AX556124
VERSION     AX556124.1  GI:25899506
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 55 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
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                     /db_xref="taxon:32630"
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 837
AX556139
LOCUS       AX556139                 20 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 70 from Patent WO0246472.
ACCESSION   AX556139
VERSION     AX556139.1  GI:25899521
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 70 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 838
AX664307
LOCUS       AX664307                 20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 5 from Patent WO0246398.
ACCESSION   AX664307
VERSION     AX664307.1  GI:29164237
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Willson,R.C. and Murphy,J.C.
  TITLE     Nucleic acid separation using immobilized metal affinity
            chromatography
  JOURNAL   Patent: WO 0246398-A 5 13-JUN-2002;
            The University of Houston System (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Sequence"

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 839
AX664308/c
LOCUS       AX664308                 20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 6 from Patent WO0246398.
ACCESSION   AX664308
VERSION     AX664308.1  GI:29164238
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Willson,R.C. and Murphy,J.C.
  TITLE     Nucleic acid separation using immobilized metal affinity
            chromatography
  JOURNAL   Patent: WO 0246398-A 6 13-JUN-2002;
            The University of Houston System (US)
FEATURES             Location/Qualifiers
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                     /note="Synthetic Oligonucleotide Sequence"

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 840
AX741040/c
LOCUS       AX741040                 20 bp    DNA     linear   PAT 10-MAY-2003
DEFINITION  Sequence 14 from Patent WO03027328.
ACCESSION   AX741040
VERSION     AX741040.1  GI:30523901
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
  TITLE     Methods, kits and compositions pertaining to the suppression of
            detectable probe binding to randomly distributed repeat sequences
            in genomic nucleic acid
  JOURNAL   Patent: WO 03027328-A 14 03-APR-2003;
            Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
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FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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                     /note="random synthetic sequence"

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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 832
AX465326
LOCUS       AX465326                 20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 70 from Patent WO0218643.
ACCESSION   AX465326
VERSION     AX465326.1  GI:21899689
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0218643-A 70 07-MAR-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 833
AX547087/c
LOCUS       AX547087                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 226 from Patent WO02053141.
ACCESSION   AX547087
VERSION     AX547087.1  GI:25812231
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 226 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 834
AX547417/c
LOCUS       AX547417                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 556 from Patent WO02053141.
ACCESSION   AX547417
VERSION     AX547417.1  GI:25812561
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 556 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
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                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

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  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 835
AX547421
LOCUS       AX547421                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 560 from Patent WO02053141.
ACCESSION   AX547421
VERSION     AX547421.1  GI:25812565
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 560 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 836
AX556124
LOCUS       AX556124                 20 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 55 from Patent WO0246472.
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LOCUS       AX355810                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 838 from Patent WO0197843.
ACCESSION   AX355810
VERSION     AX355810.1  GI:18620478
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 838 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 828
AX355811/c
LOCUS       AX355811                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 839 from Patent WO0197843.
ACCESSION   AX355811
VERSION     AX355811.1  GI:18620479
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 839 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphodiester backbone"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 829
AX440125
LOCUS       AX440125                  20 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 55 from Patent WO0173123.
ACCESSION   AX440125
VERSION     AX440125.1  GI:21664936
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0173123-A 55 04-OCT-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 830
AX440140
LOCUS       AX440140                  20 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 70 from Patent WO0173123.
ACCESSION   AX440140
VERSION     AX440140.1  GI:21664951
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0173123-A 70 04-OCT-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
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  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 831
AX465311
LOCUS       AX465311                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 55 from Patent WO0218643.
ACCESSION   AX465311
VERSION     AX465311.1  GI:21899674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0218643-A 55 07-MAR-2002;
            Nanosphere, Inc. (US)
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FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 823
AX104368
LOCUS       AX104368                 20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 560 from Patent WO0122972.
ACCESSION   AX104368
VERSION     AX104368.1  GI:13920565
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 560 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
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  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db          1 AAAAAAAAAAAAAAAAAAA 19

RESULT 824
AX196224
LOCUS       AX196224                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 55 from Patent WO0151665.
ACCESSION   AX196224
VERSION     AX196224.1  GI:15386427
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0151665-A 55 19-JUL-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
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  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db          1 AAAAAAAAAAAAAAAAAAA 19

RESULT 825
AX196239
LOCUS       AX196239                 20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 70 from Patent WO0151665.
ACCESSION   AX196239
VERSION     AX196239.1  GI:15386442
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0151665-A 70 19-JUL-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19

RESULT 826
AX354974
LOCUS       AX354974                 20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 2 from Patent WO0197843.
ACCESSION   AX354974
VERSION     AX354974.1  GI:18619641
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 2 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphodiester backbone"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db          1 AAAAAAAAAAAAAAAAAAA 19

RESULT 827
AX355810/c
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DEFINITION  Sequence 9 from Patent WO0067023.
ACCESSION   AX045779
VERSION     AX045779.1  GI:11344146
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Noll,B.O., Schetter,C. and Krieg,A.M.
  TITLE     Screening for immunostimulatory dna functional modifyers
  JCURNAL   Patent: WO 0067023-A 9 09-NOV-2000;
            CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
            FOUNDATION (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"
     misc_feature    1
                     /note="modified with digoxigenin"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 819
AX045787/c
LOCUS       AX045787                  20 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 17 from Patent WO0067023.
ACCESSION   AX045787
VERSION     AX045787.1  GI:11344154
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Noll,B.O., Schetter,C. and Krieg,A.M.
  TITLE     Screening for immunostimulatory dna functional modifyers
  JOURNAL   Patent: WO 0067023-A 17 09-NOV-2000;
            CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
            FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"
     misc_feature    1. .20
                     /note="phosphorothioate backbone"
     misc_feature    1
                     /note="modified with digoxigenin"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 820
AX045790/c
LOCUS       AX045790                  20 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 20 from Patent WO0067023.
ACCESSION   AX045790
VERSION     AX045790.1  GI:11344157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Noll,B.O., Schetter,C. and Krieg,A.M.
  TITLE     Screening for immunostimulatory dna functional modifyers
  JOURNAL   Patent: WO 0067023-A 20 09-NOV-2000;
            CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
            FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 821
AX104034/c
LOCUS       AX104034                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 226 from Patent WO0122972.
ACCESSION   AX104034
VERSION     AX104034.1  GI:13920231
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 226 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 822
AX104364/c
LOCUS       AX104364                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 556 from Patent WO0122972.
ACCESSION   AX104364
VERSION     AX104364.1  GI:13920561
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 556 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            thereof
  JOURNAL   Patent: US 6582921-A 55 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 814
AR365970
LOCUS       AR365970                 20 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 83 from patent US 6328978.
ACCESSION   AR365970
VERSION     AR365970.1  GI:34598223
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watson,J.D., Tan,P.L.J. and Prestidge,R.
  TITLE     Methods for the treatment of immunologically-mediated skin
            disorders
  JOURNAL   Patent: US 6328978-A 83 11-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 815
AR382312
LOCUS       AR382312                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 55 from patent US 6610491.
ACCESSION   AR382312
VERSION     AR382312.1  GI:40090724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6610491-A 55 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 816
AR429653
LOCUS       AR429653                 20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 55 from patent US 6645721.
ACCESSION   AR429653
VERSION     AR429653.1  GI:40189949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6645721-A 55 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 817
AX004876/c
LOCUS       AX004876                 20 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 5 from Patent WO9910527.
ACCESSION   AX004876
VERSION     AX004876.1  GI:9928276
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 5 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="phosphorthioate oligonucleotide"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2

RESULT 818
AX045779/c
LOCUS       AX045779                 20 bp    DNA     linear   PAT 24-NOV-2000
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tan,P., Visser,E., Prestidge,R. and Watson,J.D.
  TITLE     Compounds and methods for treatment and diagnosis of mycobacterial
            infections
  JOURNAL   Patent: US 6406704-A 83 18-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 809
AR222466
LOCUS       AR222466                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 26 from patent US 6429300.
ACCESSION   AR222466
VERSION     AR222466.1  GI:23329997
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 26 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 810
AR236083/c
LOCUS       AR236083                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6462184.
ACCESSION   AR236083
VERSION     AR236083.1  GI:27279782
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6462184-A 1 08-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 811
AR274394
LOCUS       AR274394                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 55 from patent US 6506564.
ACCESSION   AR274394
VERSION     AR274394.1  GI:29706840
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6506564-A 55 14-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 812
AR343047/c
LOCUS       AR343047                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6576752.
ACCESSION   AR343047
VERSION     AR343047.1  GI:33738375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
  TITLE     Aminooxy functionalized oligomers
  JOURNAL   Patent: US 6576752-A 10 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 813
AR344936
LOCUS       AR344936                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 55 from patent US 6582921.
ACCESSION   AR344936
VERSION     AR344936.1  GI:33741017
KEYWORDS    .
SOURCE      Unknown.
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Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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Db         20 AAAAAAAAAAAAAAAAAAA 2
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RESULT 804
AR154115/c
LOCUS       AR154115                 20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 14 from patent US 6238865.
ACCESSION   AR154115
VERSION     AR154115.1  GI:15122168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Huang,Z. and Szostak,J.W.
  TITLE     Simple and efficient method to label and modify 3'-termini of RNA
            using DNA polymerase and a synthetic template with defined overhang
            nucleotides
  JOURNAL   Patent: US 6238865-A 14 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2
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RESULT 805
AR164658
LOCUS       AR164658                 20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 13 from patent US 6274321.
ACCESSION   AR164658
VERSION     AR164658.1  GI:16237754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Blumberg,B.
  TITLE     High throughput functional screening of cDNAs
  JOURNAL   Patent: US 6274321-A 13 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19
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RESULT 806
E12676/c
LOCUS       E12676                   20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Anti-HTLV-1 antisense oligonucleotide.
ACCESSION   E12676
VERSION     E12676.1  GI:3251508
KEYWORDS    JP 1997052898-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mizuguchi,M., Kurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.
  TITLE     ANTI-HTLV-I ANTI-SENSE OLIGONUCLEOTIDE
  JOURNAL   Patent: JP 1997052898-A 10 25-FEB-1997;
            SOYAKU GIJUTSU KENKYUSHO:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997052898-A/10
            PD   25-FEB-1997
            PF   09-AUG-1995 JP 1995224606
            PI   MIZUGUCHI MASATSUGU, KUROSAKI NAOKO, MAKINO KEISUKE, PI
            KOYANAGI YOSHIO,
            PI   YAMAMOTO NAOKI
            PC   C07H21/04//A61K31/70;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2
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RESULT 807
I36180/c
LOCUS       I36180                   20 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 16 from patent US 5605662.
ACCESSION   I36180
VERSION     I36180.1  GI:2086693
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heller,M.J. and Tu,E.
  TITLE     Active programmable electronic devices for molecular biological
            analysis and diagnostics
  JOURNAL   Patent: US 5605662-A 16 25-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2
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RESULT 808
AR213738
LOCUS       AR213738                 20 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 83 from patent US 6406704.
ACCESSION   AR213738
VERSION     AR213738.1  GI:23311025
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Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 799
AR093312
LOCUS AR093312 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 83 from patent US 6001361.
ACCESSION AR093312
VERSION AR093312.1 GI:10020062
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Hiyama,J., Visser,E., Skinner,M., Scott,L. and Prestidge,R.
TITLE Mycobacterium vaccae antigens
JOURNAL Patent: US 6001361-A 83 14-DEC-1999;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 800
AR118970/c
LOCUS AR118970 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 96 from patent US 6150092.
ACCESSION AR118970
VERSION AR118970.1 GI:14100880
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 96 21-NOV-2000;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 20 AAAAAAAAAAAAAAAAAAA 2

RESULT 801
AR121692
LOCUS AR121692 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 83 from patent US 6160093.
ACCESSION AR121692
VERSION AR121692.1 GI:14105268
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Visser,E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial infections
JOURNAL Patent: US 6160093-A 83 12-DEC-2000;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 802
AR123335
LOCUS AR123335 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6169176.
ACCESSION AR123335
VERSION AR123335.1 GI:14108301
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bruice,T.C. and Dev,A.P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 1 02-JAN-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAA 2804
||||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAA 19

RESULT 803
AR141070/c
LOCUS AR141070 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6207819.
ACCESSION AR141070
VERSION AR141070.1 GI:14483566
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 1 27-MAR-2001;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION  Prostatic cancer gene.
ACCESSION   BD196900
VERSION     BD196900.1  GI:33006670
KEYWORDS    JP 2002516657-A/489.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
  TITLE     Prostatic cancer gene
  JOURNAL   Patent: JP 2002516657-A 489 11-JUN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516657-A/489
            PD   11-JUN-2002
            PF   22-DEC-1998 JP 2000525562
            PR   22-DEC-1997 US    08/996306,09-SEP-1998 US    60/099658 PI
            DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
            C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
            ,C12N15/00,C12N5/00,
            PC   C12N5/00,C12N15/00
            CC   potential microsequencing oligo for 4-4-187.mis2 FH   Key
                   Location/Qualifiers
            FT   primer_bind     1. .19.
FEATURES                Location/Qualifiers
     source             1. .19
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 795
AR064875/c
LOCUS       AR064875                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5849480.
ACCESSION   AR064875
VERSION     AR064875.1  GI:5995091
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cros,P., Kurfurst,R., Battail,N. and Piga,N.
  TITLE     Process and device for assaying a hapten
  JOURNAL   Patent: US 5849480-A 5 15-DEC-1998;
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="unknown"
                        /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         20 AAAAAAAAAAAAAAAAAAA 2


RESULT 796
AR080000
LOCUS       AR080000                  20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 83 from patent US 5968524.
ACCESSION   AR080000
VERSION     AR080000.1  GI:10006735
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watson,J.D. and Tan,P.L.J.
  TITLE     Methods and compounds for the treatment of immunologically-mediated
            psoriasis
  JOURNAL   Patent: US 5968524-A 83 19-OCT-1999;
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="unknown"
                        /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 797
AR085926
LOCUS       AR085926                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 83 from patent US 5985287.
ACCESSION   AR085926
VERSION     AR085926.1  GI:10012692
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tan,P., Skinner,M. and Prestidge,R.
  TITLE     Compounds and methods for treatment and diagnosis of mycobacterial
            infections
  JOURNAL   Patent: US 5985287-A 83 16-NOV-1999;
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="unknown"
                        /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 798
AR087520/c
LOCUS       AR087520                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5986084.
ACCESSION   AR087520
VERSION     AR087520.1  GI:10014283
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Pitsch,S., Weiss,P.A. and Jenny,L.
  TITLE     Ribonucleoside-derivative and method for preparing the same
  JOURNAL   Patent: US 5986084-A 1 16-NOV-1999;
FEATURES                Location/Qualifiers
     source             1. .20
                        /organism="unknown"
                        /mol_type="unassigned DNA"
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          designating self address, compartment device, mechanism, method and
          operation for molecular biological analysis and diagnosis.
ACCESSION BD087505
VERSION   BD087505.1  GI:22633115
KEYWORDS  JP 2001525193-A/16.
SOURCE    synthetic construct
  ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1  (bases 1 to 19)
  AUTHORS Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
          Edman,C.F.
  TITLE   Self-assembling microelectronic integration system capable of
          designating self address, compartment device, mechanism, method and
          operation for molecular biological analysis and diagnosis
  JOURNAL Patent: JP 2001525193-A 16 11-DEC-2001;
          NANOGEN INC
COMMENT   OS   Artificial Sequence
          PN   JP 2001525193-A/16
          PD   11-DEC-2001
          PF   01-DEC-1998 JP 2000524303
          PR   05-DEC-1997 US    08/986065
          PI   RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I  PI
          NERENBERG,
          PI   MICHAEL J HELLER,CARL F EDMAN
          PC   C12Q1/68,C12N15/09,C12N15/00
          CC   Description of Artificial Sequence: Amine
          conjugate to provide
          CC            reactivity
          CC   with dyes
          FH   Key             Location/Qualifiers
          FT   source          1. .19
          FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 792
BD087505/c
LOCUS       BD087505                 19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis.
ACCESSION   BD087505
VERSION     BD087505.1  GI:22633115
KEYWORDS    JP 2001525193-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
            Edman,C.F.
  TITLE     Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis
  JOURNAL   Patent: JP 2001525193-A 16 11-DEC-2001;
            NANOGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001525193-A/16
            PD   11-DEC-2001
            PF   01-DEC-1998 JP 2000524303
            PR   05-DEC-1997 US    08/986065
            PI   RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I  PI
            NERENBERG,
            PI   MICHAEL J HELLER,CARL F EDMAN
            PC   C12Q1/68,C12N15/09,C12N15/00
            CC   Description of Artificial Sequence: Amine
            conjugate to provide
            CC            reactivity
            CC   with dyes
            FH   Key             Location/Qualifiers
            FT   source          1. .19
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 793
BD196900
LOCUS       BD196900                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Prostatic cancer gene.
ACCESSION   BD196900
VERSION     BD196900.1  GI:33006670
KEYWORDS    JP 2002516657-A/489.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
  TITLE     Prostatic cancer gene
  JOURNAL   Patent: JP 2002516657-A 489 11-JUN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516657-A/489
            PD   11-JUN-2002
            PF   22-DEC-1998 JP 2000525562
            PR   22-DEC-1997 US    08/996306,09-SEP-1998 US    60/099658 PI
            DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
            C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
            ,C12N15/00,C12N5/00,
            PC   C12N5/00,C12N15/00
            CC   potential microsequencing oligo for 4-4-187.mis2 FH   Key
                   Location/Qualifiers
            FT   primer_bind     1. .19.
FEATURES              Location/Qualifiers
     source           1. .19
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                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"

  Query Match              0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 794
BD196900/c
LOCUS       BD196900                 19 bp    DNA     linear   PAT 17-JUL-2003
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.D., Manoharan,M., Maier,M. and An,H.
  TITLE     C3'-methylene hydrogen phosphonate oligomers and related compounds
  JOURNAL   Patent: US 6639061-A 1 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 787
AR432616
LOCUS       AR432616                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6653458.
ACCESSION   AR432616
VERSION     AR432616.1  GI:40195149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D. and Guinosso,C.J.
  TITLE     Modified oligonucleotides
  JOURNAL   Patent: US 6653458-A 6 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 788
AR432616/c
LOCUS       AR432616                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6653458.
ACCESSION   AR432616
VERSION     AR432616.1  GI:40195149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D. and Guinosso,C.J.
  TITLE     Modified oligonucleotides
  JOURNAL   Patent: US 6653458-A 6 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 789
AX349249
LOCUS       AX349249                 19 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 33 from Patent WO0202810.
ACCESSION   AX349249
VERSION     AX349249.1  GI:18615281
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bickel,R., Ehricht,R., Ellinger,T., Ermantraut,E., Kaiser,T.,
            Schulz,T. and Wagner,G.
  TITLE     Method for qualitative and/or quantitative detecting of molecular
            interactions on probe arrays
  JOURNAL   Patent: WO 0202810-A 33 10-JAN-2002;
            Clondiag Chip Technologies GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotidsonde"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 790
AX349249/c
LOCUS       AX349249                 19 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 33 from Patent WO0202810.
ACCESSION   AX349249
VERSION     AX349249.1  GI:18615281
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bickel,R., Ehricht,R., Ellinger,T., Ermantraut,E., Kaiser,T.,
            Schulz,T. and Wagner,G.
  TITLE     Method for qualitative and/or quantitative detecting of molecular
            interactions on probe arrays
  JOURNAL   Patent: WO 0202810-A 33 10-JAN-2002;
            Clondiag Chip Technologies GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotidsonde"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 791
BD087505
LOCUS       BD087505                 19 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Self-assembling microelectronic integration system capable of
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```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 15 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 782
AR403614/c
LOCUS       AR403614                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 15 from patent US 6624294.
ACCESSION   AR403614
VERSION     AR403614.1  GI:40151200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 15 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 783
AR403623
LOCUS       AR403623                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 25 from patent US 6624294.
ACCESSION   AR403623
VERSION     AR403623.1  GI:40151209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 25 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
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                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 784
AR403623/c
LOCUS       AR403623                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 25 from patent US 6624294.
ACCESSION   AR403623
VERSION     AR403623.1  GI:40151209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 25 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 785
AR412338
LOCUS       AR412338                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6639061.
ACCESSION   AR412338
VERSION     AR412338.1  GI:40167448
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.D., Manoharan,M., Maier,M. and An,H.
  TITLE     C3'-methylene hydrogen phosphonate oligomers and related compounds
  JOURNAL   Patent: US 6639061-A 1 28-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 786
AR412338/c
LOCUS       AR412338                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6639061.
ACCESSION   AR412338
VERSION     AR412338.1  GI:40167448
KEYWORDS    .
SOURCE      Unknown.
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VERSION     AR403608.1  GI:40151194
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 8 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 777
AR403612
LOCUS       AR403612                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 12 from patent US 6624294.
ACCESSION   AR403612
VERSION     AR403612.1  GI:40151198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 12 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 778
AR403612/c
LOCUS       AR403612                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 12 from patent US 6624294.
ACCESSION   AR403612
VERSION     AR403612.1  GI:40151198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 12 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 779
AR403613
LOCUS       AR403613                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 14 from patent US 6624294.
ACCESSION   AR403613
VERSION     AR403613.1  GI:40151199
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 14 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 780
AR403613/c
LOCUS       AR403613                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 14 from patent US 6624294.
ACCESSION   AR403613
VERSION     AR403613.1  GI:40151199
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 14 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 781
AR403614
LOCUS       AR403614                19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 15 from patent US 6624294.
ACCESSION   AR403614
VERSION     AR403614.1  GI:40151200
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```
ACCESSION   AR403606
VERSION     AR403606.1  GI:40151192
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 6 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1  .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 772
AR403606/c
LOCUS       AR403606                  19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6624294.
ACCESSION   AR403606
VERSION     AR403606.1  GI:40151192
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 6 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 773
AR403607
LOCUS       AR403607                  19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6624294.
ACCESSION   AR403607
VERSION     AR403607.1  GI:40151193
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 7 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 774
AR403607/c
LOCUS       AR403607                  19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6624294.
ACCESSION   AR403607
VERSION     AR403607.1  GI:40151193
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 7 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 775
AR403608
LOCUS       AR403608                  19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 8 from patent US 6624294.
ACCESSION   AR403608
VERSION     AR403608.1  GI:40151194
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 8 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 776
AR403608/c
LOCUS       AR403608                  19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 8 from patent US 6624294.
ACCESSION   AR403608
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DEFINITION  Sequence 3 from patent US 6624294.
ACCESSION   AR403603
VERSION     AR403603.1  GI:40151189
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 3 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             ||||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 767
AR403604
LOCUS       AR403604                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6624294.
ACCESSION   AR403604
VERSION     AR403604.1  GI:40151190
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 4 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 768
AR403604/c
LOCUS       AR403604                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6624294.
ACCESSION   AR403604
VERSION     AR403604.1  GI:40151190
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 4 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             ||||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 769
AR403605
LOCUS       AR403605                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6624294.
ACCESSION   AR403605
VERSION     AR403605.1  GI:40151191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 5 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 770
AR403605/c
LOCUS       AR403605                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 5 from patent US 6624294.
ACCESSION   AR403605
VERSION     AR403605.1  GI:40151191
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 5 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             ||||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 771
AR403606
LOCUS       AR403606                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6624294.
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LOCUS       AR403601                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6624294.
ACCESSION   AR403601
VERSION     AR403601.1  GI:40151187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 1 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 762
AR403601/c
LOCUS       AR403601                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6624294.
ACCESSION   AR403601
VERSION     AR403601.1  GI:40151187
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 1 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 763
AR403602
LOCUS       AR403602                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from patent US 6624294.
ACCESSION   AR403602
VERSION     AR403602.1  GI:40151188
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 2 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 764
AR403602/c
LOCUS       AR403602                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from patent US 6624294.
ACCESSION   AR403602
VERSION     AR403602.1  GI:40151188
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 2 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 765
AR403603
LOCUS       AR403603                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 3 from patent US 6624294.
ACCESSION   AR403603
VERSION     AR403603.1  GI:40151189
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6624294-A 3 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 766
AR403603/c
LOCUS       AR403603                 19 bp    DNA     linear   PAT 18-DEC-2003
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                  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 19


RESULT 756
AR367447/c
LOCUS       AR367447                 19 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 4 from patent US 6329519.
ACCESSION   AR367447
VERSION     AR367447.1  GI:34600659
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Collingwood,S.P., Moser,H.E., Altmann,K.-H. and Douglas,M.E.
  TITLE     Intermediates for oligonucleotide synthesis
  JOURNAL   Patent: US 6329519-A 4 11-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                  ||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 757
AR399177
LOCUS       AR399177                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17 from patent US 6617442.
ACCESSION   AR399177
VERSION     AR399177.1  GI:40137667
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
  TITLE     Human Rnase H1 and oligonucleotide compositions thereof
  JOURNAL   Patent: US 6617442-A 17 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
                  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 758
AR399177/c
LOCUS       AR399177                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 17 from patent US 6617442.
ACCESSION   AR399177
VERSION     AR399177.1  GI:40137667
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
  TITLE     Human Rnase H1 and oligonucleotide compositions thereof
  JOURNAL   Patent: US 6617442-A 17 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                  ||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 759
AR399178
LOCUS       AR399178                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 18 from patent US 6617442.
ACCESSION   AR399178
VERSION     AR399178.1  GI:40137669
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
  TITLE     Human Rnase H1 and oligonucleotide compositions thereof
  JOURNAL   Patent: US 6617442-A 18 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
                  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 760
AR399178/c
LOCUS       AR399178                 19 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 18 from patent US 6617442.
ACCESSION   AR399178
VERSION     AR399178.1  GI:40137669
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
  TITLE     Human Rnase H1 and oligonucleotide compositions thereof
  JOURNAL   Patent: US 6617442-A 18 09-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
                  ||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 761
AR403601
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  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 751
AR359805
LOCUS       AR359805                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 4 from patent US 6593466.
ACCESSION   AR359805
VERSION     AR359805.1  GI:33766603
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
  TITLE     Guanidinium functionalized nucleotides and precursors thereof
  JOURNAL   Patent: US 6593466-A 4 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 752
AR359805/c
LOCUS       AR359805                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 4 from patent US 6593466.
ACCESSION   AR359805
VERSION     AR359805.1  GI:33766603
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
  TITLE     Guanidinium functionalized nucleotides and precursors thereof
  JOURNAL   Patent: US 6593466-A 4 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 753
AR359806
LOCUS       AR359806                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6593466.
ACCESSION   AR359806
VERSION     AR359806.1  GI:33766604
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
  TITLE     Guanidinium functionalized nucleotides and precursors thereof
  JOURNAL   Patent: US 6593466-A 5 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 754
AR359806/c
LOCUS       AR359806                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5 from patent US 6593466.
ACCESSION   AR359806
VERSION     AR359806.1  GI:33766604
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
  TITLE     Guanidinium functionalized nucleotides and precursors thereof
  JOURNAL   Patent: US 6593466-A 5 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 755
AR367447
LOCUS       AR367447                  19 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 4 from patent US 6329519.
ACCESSION   AR367447
VERSION     AR367447.1  GI:34600659
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Collingwood,S.P., Moser,H.E., Altmann,K.-H. and Douglas,M.E.
  TITLE     Intermediates for oligonucleotide synthesis
  JOURNAL   Patent: US 6329519-A 4 11-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
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  JOURNAL   Patent: US 6465628-A 1 15-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 746
AR237463/c
LOCUS       AR237463                  19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6465628.
ACCESSION   AR237463
VERSION     AR237463.1  GI:27282213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
            Guzaev,A.
  TITLE     Process for the synthesis of oligomeric compounds
  JOURNAL   Patent: US 6465628-A 1 15-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 747
AR321589
LOCUS       AR321589                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6562960.
ACCESSION   AR321589
VERSION     AR321589.1  GI:33706818
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Baxter,A.D., Collingwood,S.P., Douglas,M.E. and Taylor,R.J.
  TITLE     Oligonucleotide analogues
  JOURNAL   Patent: US 6562960-A 10 13-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 748
AR321589/c
LOCUS       AR321589                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6562960.
ACCESSION   AR321589
VERSION     AR321589.1  GI:33706818
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Baxter,A.D., Collingwood,S.P., Douglas,M.E. and Taylor,R.J.
  TITLE     Oligonucleotide analogues
  JOURNAL   Patent: US 6562960-A 10 13-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 749
AR359804
LOCUS       AR359804                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3 from patent US 6593466.
ACCESSION   AR359804
VERSION     AR359804.1  GI:33766602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
  TITLE     Guanidinium functionalized nucleotides and precursors thereof
  JOURNAL   Patent: US 6593466-A 3 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 750
AR359804/c
LOCUS       AR359804                  19 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 3 from patent US 6593466.
ACCESSION   AR359804
VERSION     AR359804.1  GI:33766602
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
  TITLE     Guanidinium functionalized nucleotides and precursors thereof
  JOURNAL   Patent: US 6593466-A 3 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"
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  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 15 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 741
AR213512
LOCUS       AR213512                 19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 25 from patent US 6403779.
ACCESSION   AR213512
VERSION     AR213512.1  GI:23310743
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 25 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 742
AR213512/c
LOCUS       AR213512                 19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 25 from patent US 6403779.
ACCESSION   AR213512
VERSION     AR213512.1  GI:23310743
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 25 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 743
AR222465
LOCUS       AR222465                 19 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 25 from patent US 6429300.
ACCESSION   AR222465
VERSION     AR222465.1  GI:23329996
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 25 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAA 19


RESULT 744
AR222465/c
LOCUS       AR222465                 19 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 25 from patent US 6429300.
ACCESSION   AR222465
VERSION     AR222465.1  GI:23329996
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 25 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db         19 TTTTTTTTTTTTTTTTTTT 1


RESULT 745
AR237463
LOCUS       AR237463                 19 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6465628.
ACCESSION   AR237463
VERSION     AR237463.1  GI:27282213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and
            Guzaev,A.
  TITLE     Process for the synthesis of oligomeric compounds
```

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REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 12 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 736
AR213501/c
LOCUS       AR213501                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 12 from patent US 6403779.
ACCESSION   AR213501
VERSION     AR213501.1  GI:23310732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 12 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 737
AR213502
LOCUS       AR213502                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 14 from patent US 6403779.
ACCESSION   AR213502
VERSION     AR213502.1  GI:23310733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 14 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 738
AR213502/c
LOCUS       AR213502                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 14 from patent US 6403779.
ACCESSION   AR213502
VERSION     AR213502.1  GI:23310733
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 14 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 739
AR213503
LOCUS       AR213503                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 15 from patent US 6403779.
ACCESSION   AR213503
VERSION     AR213503.1  GI:23310734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 15 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 740
AR213503/c
LOCUS       AR213503                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 15 from patent US 6403779.
ACCESSION   AR213503
VERSION     AR213503.1  GI:23310734
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
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           Unclassified.
REFERENCE  1  (bases 1 to 19)
  AUTHORS  Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
           Prakash,T.P.
  TITLE    Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL  Patent: US 6403779-A 6 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 731
AR213496
LOCUS       AR213496                 19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 7 from patent US 6403779.
ACCESSION   AR213496
VERSION     AR213496.1  GI:23310727
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 7 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 732
AR213496/c
LOCUS       AR213496                 19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 7 from patent US 6403779.
ACCESSION   AR213496
VERSION     AR213496.1  GI:23310727
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 7 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 733
AR213497
LOCUS       AR213497                 19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 8 from patent US 6403779.
ACCESSION   AR213497
VERSION     AR213497.1  GI:23310728
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 8 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 734
AR213497/c
LOCUS       AR213497                 19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 8 from patent US 6403779.
ACCESSION   AR213497
VERSION     AR213497.1  GI:23310728
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 8 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 735
AR213501
LOCUS       AR213501                 19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 12 from patent US 6403779.
ACCESSION   AR213501
VERSION     AR213501.1  GI:23310732
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 4 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 726
AR213493/c
LOCUS       AR213493                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 4 from patent US 6403779.
ACCESSION   AR213493
VERSION     AR213493.1  GI:23310724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 4 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 727
AR213494
LOCUS       AR213494                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 5 from patent US 6403779.
ACCESSION   AR213494
VERSION     AR213494.1  GI:23310725
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 5 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 728
AR213494/c
LOCUS       AR213494                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 5 from patent US 6403779.
ACCESSION   AR213494
VERSION     AR213494.1  GI:23310725
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 5 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 729
AR213495
LOCUS       AR213495                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 6 from patent US 6403779.
ACCESSION   AR213495
VERSION     AR213495.1  GI:23310726
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 6 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 730
AR213495/c
LOCUS       AR213495                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 6 from patent US 6403779.
ACCESSION   AR213495
VERSION     AR213495.1  GI:23310726
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 1 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 721
AR213491
LOCUS       AR213491                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 2 from patent US 6403779.
ACCESSION   AR213491
VERSION     AR213491.1  GI:23310722
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 2 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 722
AR213491/c
LOCUS       AR213491                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 2 from patent US 6403779.
ACCESSION   AR213491
VERSION     AR213491.1  GI:23310722
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 2 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 723
AR213492
LOCUS       AR213492                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 3 from patent US 6403779.
ACCESSION   AR213492
VERSION     AR213492.1  GI:23310723
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 3 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 724
AR213492/c
LOCUS       AR213492                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 3 from patent US 6403779.
ACCESSION   AR213492
VERSION     AR213492.1  GI:23310723
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 3 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 725
AR213493
LOCUS       AR213493                19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 4 from patent US 6403779.
ACCESSION   AR213493
VERSION     AR213493.1  GI:23310724
KEYWORDS    .
SOURCE      Unknown.
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 18 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 716
AR205801/c
LOCUS       AR205801                  19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 18 from patent US 6369209.
ACCESSION   AR205801
VERSION     AR205801.1  GI:21503476
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 18 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 717
AR205809
LOCUS       AR205809                  19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 26 from patent US 6369209.
ACCESSION   AR205809
VERSION     AR205809.1  GI:21503486
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 26 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 718
AR205809/c
LOCUS       AR205809                  19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 26 from patent US 6369209.
ACCESSION   AR205809
VERSION     AR205809.1  GI:21503486
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 26 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 719
AR213490
LOCUS       AR213490                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 1 from patent US 6403779.
ACCESSION   AR213490
VERSION     AR213490.1  GI:23310721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
            Prakash,T.P.
  TITLE     Regioselective synthesis of 2'-O-modified nucleosides
  JOURNAL   Patent: US 6403779-A 1 11-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 720
AR213490/c
LOCUS       AR213490                  19 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 1 from patent US 6403779.
ACCESSION   AR213490
VERSION     AR213490.1  GI:23310721
KEYWORDS    .
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VERSION     AR205798.1  GI:21503472
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 15 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 711
AR205799
LOCUS       AR205799                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 16 from patent US 6369209.
ACCESSION   AR205799
VERSION     AR205799.1  GI:21503473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 16 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 712
AR205799/c
LOCUS       AR205799                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 16 from patent US 6369209.
ACCESSION   AR205799
VERSION     AR205799.1  GI:21503473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 16 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 713
AR205800
LOCUS       AR205800                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 17 from patent US 6369209.
ACCESSION   AR205800
VERSION     AR205800.1  GI:21503474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 17 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 714
AR205800/c
LOCUS       AR205800                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 17 from patent US 6369209.
ACCESSION   AR205800
VERSION     AR205800.1  GI:21503474
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 17 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 715
AR205801
LOCUS       AR205801                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 18 from patent US 6369209.
ACCESSION   AR205801
VERSION     AR205801.1  GI:21503476
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 707
BD274449
LOCUS       BD274449                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274449
VERSION     BD274449.1  GI:33084217
KEYWORDS    JP 2002543215-A/26.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 26 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/26
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   2'-modified T linkage
            CC   2'-modified T linkage
            CC   2'-modified T linkage
            CC   2'-modified T linkage
            FH   Key             Location/Qualifiers
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19)
            FT   misc_feature    (19). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 708
BD274449/c
LOCUS       BD274449                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274449
VERSION     BD274449.1  GI:33084217
KEYWORDS    JP 2002543215-A/26.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 26 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/26
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   2'-modified T linkage
            CC   2'-modified T linkage
            CC   2'-modified T linkage
            CC   2'-modified T linkage
            FH   Key             Location/Qualifiers
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19)
            FT   misc_feature    (19). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 709
AR205798
LOCUS       AR205798                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 15 from patent US 6369209.
ACCESSION   AR205798
VERSION     AR205798.1  GI:21503472
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form conformational
            geometry
  JOURNAL   Patent: US 6369209-A 15 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 710
AR205798/c
LOCUS       AR205798                 19 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 15 from patent US 6369209.
ACCESSION   AR205798
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```
RESULT 704
BD274440/c
LOCUS       BD274440                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274440
VERSION     BD274440.1  GI:33084208
KEYWORDS    JP 2002543215-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 17 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/17
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   sub O linkage
            CC   3' - O-MOE linkage; sub O linkage
            CC   3' - O-MOE linkage; sub O linkage
            CC   3' - O-MOE linkage; sub O linkage
            CC   3' - O-MOE linkage
            FH   Key             Location/Qualifiers
            FT   misc_feature    (15). .(16)
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19)
            FT   misc_feature    (19). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 705
BD274441
LOCUS       BD274441                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274441
VERSION     BD274441.1  GI:33084209
KEYWORDS    JP 2002543215-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 18 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/18
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   sub O linkage
            CC   2'- O-MOE; sub O linkage
            CC   2'- O-MOE; sub O linkage
            CC   2'- O-MOE; sub O linkage
            CC   2'- O-MOE
            FH   Key             Location/Qualifiers
            FT   misc_feature    (15). .(16)
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19)
            FT   misc_feature    (19). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 706
BD274441/c
LOCUS       BD274441                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274441
VERSION     BD274441.1  GI:33084209
KEYWORDS    JP 2002543215-A/18.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 18 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/18
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   sub O linkage
            CC   2'- O-MOE; sub O linkage
            CC   2'- O-MOE; sub O linkage
            CC   2'- O-MOE; sub O linkage
            CC   2'- O-MOE
            FH   Key             Location/Qualifiers
            FT   misc_feature    (15). .(16)
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19)
            FT   misc_feature    (19). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
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RESULT 701
BD274439
LOCUS       BD274439                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274439
VERSION     BD274439.1  GI:33084207
KEYWORDS    JP 2002543215-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 16 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/16
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   2' - O-MOE linkage
            CC   2' - O-MOE linkage
            CC   2' - O-MOE linkage
            FH   Key             Location/Qualifiers
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 702
BD274439/c
LOCUS       BD274439                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274439
VERSION     BD274439.1  GI:33084207
KEYWORDS    JP 2002543215-A/16.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 16 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/16
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   2' - O-MOE linkage
            CC   2' - O-MOE linkage
            CC   2' - O-MOE linkage
            FH   Key             Location/Qualifiers
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 703
BD274440
LOCUS       BD274440                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274440
VERSION     BD274440.1  GI:33084208
KEYWORDS    JP 2002543215-A/17.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 17 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/17
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   sub O linkage
            CC   3' - O-MOE linkage; sub O linkage
            CC   3' - O-MOE linkage; sub O linkage
            CC   3' - O-MOE linkage; sub O linkage
            CC   3' - O-MOE linkage
            FH   Key             Location/Qualifiers
            FT   misc_feature    (15). .(16)
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19)
            FT   misc_feature    (19). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19
```

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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Mohan,V. and Boswell,H.
  TITLE     RNA targeted 2'-modified oligonucleotides that are conformationally
            preorganized
  JOURNAL   Patent: US 6271358-A 6 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 698
AR164173/c
LOCUS       AR164173                  19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 6 from patent US 6271358.
ACCESSION   AR164173
VERSION     AR164173.1  GI:16235162
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Mohan,V. and Boswell,H.
  TITLE     RNA targeted 2'-modified oligonucleotides that are conformationally
            preorganized
  JOURNAL   Patent: US 6271358-A 6 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 699
BD274438
LOCUS       BD274438                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274438
VERSION     BD274438.1  GI:33084206
KEYWORDS    JP 2002543215-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 15 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/15
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   3' - O-MOE linkage
            CC   3' - O-MOE linkage
            CC   3' - O-MOE linkage
            FH   Key             Location/Qualifiers
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 700
BD274438/c
LOCUS       BD274438                  19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry.
ACCESSION   BD274438
VERSION     BD274438.1  GI:33084206
KEYWORDS    JP 2002543215-A/15.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M. and Mohan,V.
  TITLE     Oligonucleotides having A-DNA form and B-DNA form confirmational
            geometry
  JOURNAL   Patent: JP 2002543215-A 15 17-DEC-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002543215-A/15
            PD   17-DEC-2002
            PF   03-MAY-2000 JP 2000615638
            PR   03-MAY-1999 US    09/303586
            PI   MUTHIAH MANOHARAN,VENKATRAMAN MOHAN
            PC   C07H21/02,A61K48/00,A61P35/00,A61P35/02,A61P43/00,C12N15/09,
            PC   C12N15/00
            CC   Oligonucleotide
            CC   3' - O-MOE linkage
            CC   3' - O-MOE linkage
            CC   3' - O-MOE linkage
            FH   Key             Location/Qualifiers
            FT   misc_feature    (16). .(17)
            FT   misc_feature    (17). .(18)
            FT   misc_feature    (18). .(19).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 44 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 693
AR141898
LOCUS       AR141898                19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 4 from patent US 6147200.
ACCESSION   AR141898
VERSION     AR141898.1  GI:15101414
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Kawasaki,A.M., Cook,P.Dan., Fraser,A.S. and
            Prakash,T.P.
  TITLE     2'-O-acetamido modified monomers and oligomers
  JOURNAL   Patent: US 6147200-A 4 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 694
AR141898/c
LOCUS       AR141898                19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 4 from patent US 6147200.
ACCESSION   AR141898
VERSION     AR141898.1  GI:15101414
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Kawasaki,A.M., Cook,P.Dan., Fraser,A.S. and
            Prakash,T.P.
  TITLE     2'-O-acetamido modified monomers and oligomers
  JOURNAL   Patent: US 6147200-A 4 14-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 695
AR153863
LOCUS       AR153863                19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 16 from patent US 6238624.
ACCESSION   AR153863
VERSION     AR153863.1  GI:15121916
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
  TITLE     Methods for transport in molecular biological analysis and
            diagnostics
  JOURNAL   Patent: US 6238624-A 16 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 696
AR153863/c
LOCUS       AR153863                19 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 16 from patent US 6238624.
ACCESSION   AR153863
VERSION     AR153863.1  GI:15121916
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
  TITLE     Methods for transport in molecular biological analysis and
            diagnostics
  JOURNAL   Patent: US 6238624-A 16 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 697
AR164173
LOCUS       AR164173                19 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 6 from patent US 6271358.
ACCESSION   AR164173
VERSION     AR164173.1  GI:16235162
KEYWORDS    .
SOURCE      Unknown.
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RESULT 687
AR135304
LOCUS       AR135304                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 33 from patent US 6194598.
ACCESSION   AR135304
VERSION     AR135304.1  GI:14124209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 33 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 688
AR135304/c
LOCUS       AR135304                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 33 from patent US 6194598.
ACCESSION   AR135304
VERSION     AR135304.1  GI:14124209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 33 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 689
AR135305
LOCUS       AR135305                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 34 from patent US 6194598.
ACCESSION   AR135305
VERSION     AR135305.1  GI:14124210
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 34 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 690
AR135305/c
LOCUS       AR135305                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 34 from patent US 6194598.
ACCESSION   AR135305
VERSION     AR135305.1  GI:14124210
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 34 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 691
AR135315
LOCUS       AR135315                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 44 from patent US 6194598.
ACCESSION   AR135315
VERSION     AR135315.1  GI:14124220
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 44 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 692
AR135315/c
LOCUS       AR135315                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 44 from patent US 6194598.
ACCESSION   AR135315
VERSION     AR135315.1  GI:14124220
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Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 19


RESULT 682
AR135297/c
LOCUS       AR135297                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 26 from patent US 6194598.
ACCESSION   AR135297
VERSION     AR135297.1  GI:14124202
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 26 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 683
AR135298
LOCUS       AR135298                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 27 from patent US 6194598.
ACCESSION   AR135298
VERSION     AR135298.1  GI:14124203
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 27 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 19


RESULT 684
AR135298/c
LOCUS       AR135298                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 27 from patent US 6194598.
ACCESSION   AR135298
VERSION     AR135298.1  GI:14124203
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 27 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 685
AR135302
LOCUS       AR135302                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 31 from patent US 6194598.
ACCESSION   AR135302
VERSION     AR135302.1  GI:14124207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 31 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTT 2184
              ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTT 19


RESULT 686
AR135302/c
LOCUS       AR135302                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 31 from patent US 6194598.
ACCESSION   AR135302
VERSION     AR135302.1  GI:14124207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 31 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1
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                    /organism="unknown"
                    /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 677
AR135295
LOCUS       AR135295                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 24 from patent US 6194598.
ACCESSION   AR135295
VERSION     AR135295.1  GI:14124200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 24 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 678
AR135295/c
LOCUS       AR135295                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 24 from patent US 6194598.
ACCESSION   AR135295
VERSION     AR135295.1  GI:14124200
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 24 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 679
AR135296
LOCUS       AR135296                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 25 from patent US 6194598.
ACCESSION   AR135296
VERSION     AR135296.1  GI:14124201
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 25 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 680
AR135296/c
LOCUS       AR135296                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 25 from patent US 6194598.
ACCESSION   AR135296
VERSION     AR135296.1  GI:14124201
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 25 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 681
AR135297
LOCUS       AR135297                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 26 from patent US 6194598.
ACCESSION   AR135297
VERSION     AR135297.1  GI:14124202
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 26 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 21 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 672
AR135292/c
LOCUS       AR135292                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 21 from patent US 6194598.
ACCESSION   AR135292
VERSION     AR135292.1  GI:14124197
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 21 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 673
AR135293
LOCUS       AR135293                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 22 from patent US 6194598.
ACCESSION   AR135293
VERSION     AR135293.1  GI:14124198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 22 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 674
AR135293/c
LOCUS       AR135293                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 22 from patent US 6194598.
ACCESSION   AR135293
VERSION     AR135293.1  GI:14124198
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 22 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 675
AR135294
LOCUS       AR135294                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6194598.
ACCESSION   AR135294
VERSION     AR135294.1  GI:14124199
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 23 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 676
AR135294/c
LOCUS       AR135294                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6194598.
ACCESSION   AR135294
VERSION     AR135294.1  GI:14124199
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 23 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
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ACCESSION   AR124857
VERSION     AR124857.1  GI:14110218
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 34 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 667
AR124867
LOCUS       AR124867                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 44 from patent US 6172209.
ACCESSION   AR124867
VERSION     AR124867.1  GI:14110228
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 44 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 668
AR124867/c
LOCUS       AR124867                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 44 from patent US 6172209.
ACCESSION   AR124867
VERSION     AR124867.1  GI:14110228
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 44 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 669
AR135291
LOCUS       AR135291                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 20 from patent US 6194598.
ACCESSION   AR135291
VERSION     AR135291.1  GI:14124196
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 20 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 670
AR135291/c
LOCUS       AR135291                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 20 from patent US 6194598.
ACCESSION   AR135291
VERSION     AR135291.1  GI:14124196
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     Aminooxy-modified oligonucleotide synthetic intermediates
  JOURNAL   Patent: US 6194598-A 20 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 671
AR135292
LOCUS       AR135292                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 21 from patent US 6194598.
ACCESSION   AR135292
VERSION     AR135292.1  GI:14124197
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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```
RESULT 661
AR124854
LOCUS       AR124854                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 31 from patent US 6172209.
ACCESSION   AR124854
VERSION     AR124854.1  GI:14110215
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 31 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 662
AR124854/c
LOCUS       AR124854                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 31 from patent US 6172209.
ACCESSION   AR124854
VERSION     AR124854.1  GI:14110215
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 31 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 663
AR124856
LOCUS       AR124856                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 33 from patent US 6172209.
ACCESSION   AR124856
VERSION     AR124856.1  GI:14110217
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 33 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 664
AR124856/c
LOCUS       AR124856                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 33 from patent US 6172209.
ACCESSION   AR124856
VERSION     AR124856.1  GI:14110217
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 33 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 665
AR124857
LOCUS       AR124857                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 34 from patent US 6172209.
ACCESSION   AR124857
VERSION     AR124857.1  GI:14110218
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 34 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 666
AR124857/c
LOCUS       AR124857                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 34 from patent US 6172209.
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  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 656
AR124848/c
LOCUS       AR124848                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 25 from patent US 6172209.
ACCESSION   AR124848
VERSION     AR124848.1  GI:14110209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 25 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 657
AR124849
LOCUS       AR124849                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 26 from patent US 6172209.
ACCESSION   AR124849
VERSION     AR124849.1  GI:14110210
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 26 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 658
AR124849/c
LOCUS       AR124849                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 26 from patent US 6172209.
ACCESSION   AR124849
VERSION     AR124849.1  GI:14110210
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 26 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 659
AR124850
LOCUS       AR124850                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 27 from patent US 6172209.
ACCESSION   AR124850
VERSION     AR124850.1  GI:14110211
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 27 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 660
AR124850/c
LOCUS       AR124850                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 27 from patent US 6172209.
ACCESSION   AR124850
VERSION     AR124850.1  GI:14110211
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 27 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1
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FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 651
AR124846
LOCUS       AR124846                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6172209.
ACCESSION   AR124846
VERSION     AR124846.1  GI:14110207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 23 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 652
AR124846/c
LOCUS       AR124846                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6172209.
ACCESSION   AR124846
VERSION     AR124846.1  GI:14110207
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 23 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 653
AR124847
LOCUS       AR124847                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 24 from patent US 6172209.
ACCESSION   AR124847
VERSION     AR124847.1  GI:14110208
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 24 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 654
AR124847/c
LOCUS       AR124847                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 24 from patent US 6172209.
ACCESSION   AR124847
VERSION     AR124847.1  GI:14110208
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 24 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 655
AR124848
LOCUS       AR124848                 19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 25 from patent US 6172209.
ACCESSION   AR124848
VERSION     AR124848.1  GI:14110209
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 25 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
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  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 20 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 646
AR124843/c
LOCUS       AR124843                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 20 from patent US 6172209.
ACCESSION   AR124843
VERSION     AR124843.1  GI:14110204
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 20 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 647
AR124844
LOCUS       AR124844                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 21 from patent US 6172209.
ACCESSION   AR124844
VERSION     AR124844.1  GI:14110205
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 21 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 648
AR124844/c
LOCUS       AR124844                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 21 from patent US 6172209.
ACCESSION   AR124844
VERSION     AR124844.1  GI:14110205
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 21 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 649
AR124845
LOCUS       AR124845                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 22 from patent US 6172209.
ACCESSION   AR124845
VERSION     AR124845.1  GI:14110206
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 22 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 650
AR124845/c
LOCUS       AR124845                  19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 22 from patent US 6172209.
ACCESSION   AR124845
VERSION     AR124845.1  GI:14110206
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
  TITLE     Aminooxy-modified oligonucleotides and methods for making same
  JOURNAL   Patent: US 6172209-A 22 09-JAN-2001;
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LOCUS       AR111959                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 33 from patent US 6127533.
ACCESSION   AR111959
VERSION     AR111959.1  GI:12828807
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 33 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 641
AR111960
LOCUS       AR111960                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 34 from patent US 6127533.
ACCESSION   AR111960
VERSION     AR111960.1  GI:12828808
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 34 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 642
AR111960/c
LOCUS       AR111960                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 34 from patent US 6127533.
ACCESSION   AR111960
VERSION     AR111960.1  GI:12828808
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 34 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 643
AR111970
LOCUS       AR111970                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 44 from patent US 6127533.
ACCESSION   AR111970
VERSION     AR111970.1  GI:12828818
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 44 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
             |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 644
AR111970/c
LOCUS       AR111970                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 44 from patent US 6127533.
ACCESSION   AR111970
VERSION     AR111970.1  GI:12828818
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 44 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
             |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 645
AR124843
LOCUS       AR124843                19 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 20 from patent US 6172209.
ACCESSION   AR124843
VERSION     AR124843.1  GI:14110204
KEYWORDS    .
SOURCE      Unknown.
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              ||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 635
AR111953
LOCUS       AR111953                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 27 from patent US 6127533.
ACCESSION   AR111953
VERSION     AR111953.1  GI:12828801
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 27 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 636
AR111953/c
LOCUS       AR111953                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 27 from patent US 6127533.
ACCESSION   AR111953
VERSION     AR111953.1  GI:12828801
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 27 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 637
AR111957
LOCUS       AR111957                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 31 from patent US 6127533.
ACCESSION   AR111957
VERSION     AR111957.1  GI:12828805
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 31 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 638
AR111957/c
LOCUS       AR111957                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 31 from patent US 6127533.
ACCESSION   AR111957
VERSION     AR111957.1  GI:12828805
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 31 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 639
AR111959
LOCUS       AR111959                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 33 from patent US 6127533.
ACCESSION   AR111959
VERSION     AR111959.1  GI:12828807
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 33 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 640
AR111959/c
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  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 630
AR111950/c
LOCUS       AR111950                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 24 from patent US 6127533.
ACCESSION   AR111950
VERSION     AR111950.1  GI:12828798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 24 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 631
AR111951
LOCUS       AR111951                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 25 from patent US 6127533.
ACCESSION   AR111951
VERSION     AR111951.1  GI:12828799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 25 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 632
AR111951/c
LOCUS       AR111951                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 25 from patent US 6127533.
ACCESSION   AR111951
VERSION     AR111951.1  GI:12828799
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 25 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 633
AR111952
LOCUS       AR111952                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 26 from patent US 6127533.
ACCESSION   AR111952
VERSION     AR111952.1  GI:12828800
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 26 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 634
AR111952/c
LOCUS       AR111952                  19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 26 from patent US 6127533.
ACCESSION   AR111952
VERSION     AR111952.1  GI:12828800
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 26 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
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  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 21 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 625
AR111948
LOCUS       AR111948                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 22 from patent US 6127533.
ACCESSION   AR111948
VERSION     AR111948.1  GI:12828796
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 22 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 626
AR111948/c
LOCUS       AR111948                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 22 from patent US 6127533.
ACCESSION   AR111948
VERSION     AR111948.1  GI:12828796
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 22 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 627
AR111949
LOCUS       AR111949                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 23 from patent US 6127533.
ACCESSION   AR111949
VERSION     AR111949.1  GI:12828797
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 23 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 628
AR111949/c
LOCUS       AR111949                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 23 from patent US 6127533.
ACCESSION   AR111949
VERSION     AR111949.1  GI:12828797
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 23 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 629
AR111950
LOCUS       AR111950                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 24 from patent US 6127533.
ACCESSION   AR111950
VERSION     AR111950.1  GI:12828798
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 24 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Leeds,J.M. and Cummins,L.L.
  TITLE     Fluorescence based nuclease assay
  JOURNAL   Patent: US 6127124-A 1 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 620
AR111371/c
LOCUS       AR111371                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 1 from patent US 6127124.
ACCESSION   AR111371
VERSION     AR111371.1  GI:12828219
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Leeds,J.M. and Cummins,L.L.
  TITLE     Fluorescence based nuclease assay
  JOURNAL   Patent: US 6127124-A 1 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 621
AR111946
LOCUS       AR111946                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 20 from patent US 6127533.
ACCESSION   AR111946
VERSION     AR111946.1  GI:12828794
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 20 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 622
AR111946/c
LOCUS       AR111946                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 20 from patent US 6127533.
ACCESSION   AR111946
VERSION     AR111946.1  GI:12828794
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 20 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 623
AR111947
LOCUS       AR111947                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 21 from patent US 6127533.
ACCESSION   AR111947
VERSION     AR111947.1  GI:12828795
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
  TITLE     2'-O-aminooxy-modified oligonucleotides
  JOURNAL   Patent: US 6127533-A 21 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 624
AR111947/c
LOCUS       AR111947                19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 21 from patent US 6127533.
ACCESSION   AR111947
VERSION     AR111947.1  GI:12828795
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
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            PF   23-JAN-2002 WO 2002JP000467
            PR   23-JAN-2001 JP 01P   014510
            PI   TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
            PC   C12P21/02,C12N15/53,C12N15/63,C12N1/21//(C12P21/02,C12R1:91),
            PC   (C12N15/53,C12R1:01),(C12N1/21,C12R1:01)
            CC   Process for producing cytochrome c
            FH   Key             Location/Qualifiers
            FT   source          1. .33
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 33;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAA 10


RESULT 615
A68209
LOCUS       A68209                   19 bp    DNA     linear   PAT 06-MAY-1999
DEFINITION  Sequence 4 from Patent WO9747636.
ACCESSION   A68209
VERSION     A68209.1  GI:4759376
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Collingwood,S.P., Moser,H.E., Altmann,K. and Douglas,M.E.
  TITLE     INTERMEDIATES FOR OLIGONUCLEOTIDE SYNTHESIS
  JOURNAL   Patent: WO 9747636-A 4 18-DEC-1997;
            CIBA GEIGY AG (CH)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 616
A68209/c
LOCUS       A68209                   19 bp    DNA     linear   PAT 06-MAY-1999
DEFINITION  Sequence 4 from Patent WO9747636.
ACCESSION   A68209
VERSION     A68209.1  GI:4759376
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Collingwood,S.P., Moser,H.E., Altmann,K. and Douglas,M.E.
  TITLE     INTERMEDIATES FOR OLIGONUCLEOTIDE SYNTHESIS
  JOURNAL   Patent: WO 9747636-A 4 18-DEC-1997;
            CIBA GEIGY AG (CH)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 617
AR048767
LOCUS       AR048767                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5821354.
ACCESSION   AR048767
VERSION     AR048767.1  GI:5971110
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Leclerc,G. and Martel,R.
  TITLE     Radiolabeled DNA oligonucleotide and method of preparation
  JOURNAL   Patent: US 5821354-A 1 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2184
              |||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 19


RESULT 618
AR048767/c
LOCUS       AR048767                 19 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5821354.
ACCESSION   AR048767
VERSION     AR048767.1  GI:5971110
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Leclerc,G. and Martel,R.
  TITLE     Radiolabeled DNA oligonucleotide and method of preparation
  JOURNAL   Patent: US 5821354-A 1 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity  100.0%;  Pred. No. 4e+02;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2786 AAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||
Db         19 AAAAAAAAAAAAAAAAAAA 1


RESULT 619
AR111371
LOCUS       AR111371                 19 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 1 from patent US 6127124.
ACCESSION   AR111371
VERSION     AR111371.1  GI:12828219
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ACCESSION   E04206
VERSION     E04206.1  GI:2172416
KEYWORDS    JP 1993001099-A/34.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Morita,K., Hasegawa,M., Yokoo,Y., Sato,M., Sekine,S., Sugimoto,S.,
            Koda,H., Mori,H. and Arima,T.
  TITLE     FUSED ANTIGENIC POLYPEPTIDE
  JOURNAL   Patent: JP 1993001099-A 34 08-JAN-1993;
            KYOWA HAKKO KOGYO CO LTD
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1993001099-A/34
            PD   08-JAN-1993
            PF   25-JUN-1991 JP 1991153031
            PI   MORITA KAZUKI, HASEGAWA MAMORU, YOKOO YOSHIHARU, SATO
            MORIYUKI, PI   SEKINE SUSUMU, SUGIMOTO SEIJI, KODA HAJIME, MORI
            HIDEJI, PI   ARIMA TERUMASA
            PC   C07K7/10,C07K13/00,C12N1/21,C12N15/62,C12N15/70,C12P21/02, PC
             C12Q1/68,
            PC
            G01N33/569,G01N33/576//A61K39/00,C12N15/51,(C12N1/21,C12R1:19), PC
             (C12P21/02,
            PC   C12R1:19),C07K99:00;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No.
FEATURES            Location/Qualifiers
     source         1. .29
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||| |||||||  |||
Db          4 TCCTTTTTTTTCTTTTTTCGTTT 27


RESULT 612
BD234356/c
LOCUS       BD234356                  32 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234356
VERSION     BD234356.1  GI:33044126
KEYWORDS    JP 2002532085-A/29.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 29 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/29
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .32
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .32
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 32;
  Best Local Similarity   87.5%;  Pred. No. 1.5e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAAAAAAAA 9


RESULT 613
BD171339/c
LOCUS       BD171339                  33 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Production method of cytochrome c.
ACCESSION   BD171339
VERSION     BD171339.1  GI:28412629
KEYWORDS    JP 2002218979-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Oku,T., Nishio,T. and Sato,T.
  TITLE     Production method of cytochrome c
  JOURNAL   Patent: JP 2002218979-A 2 06-AUG-2002;
            NIHON UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002218979-A/2
            PD   06-AUG-2002
            PF   23-JAN-2001 JP 2001014510
            PI   TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
            PC   C12N15/09,C12N1/21,C12P21/02//(C12N15/09,C12R1:91),(C12N1/21,
            PC   C12R1:01),
            PC   (C12P21/02,C12R1:01),C12N15/00,(C12N15/00,C12R1:91) CC
            Production method of cytochrome c
            FH   Key             Location/Qualifiers
            FT   source          1. .33
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .33
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 33;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAA 10


RESULT 614
BD173750/c
LOCUS       BD173750                  33 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Process for producing cytochrome c.
ACCESSION   BD173750
VERSION     BD173750.1  GI:28415083
KEYWORDS    WO 02059339-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Oku,T., Nishio,T. and Sato,T.
  TITLE     Process for producing cytochrome c
  JOURNAL   Patent: WO 02059339-A 2 01-AUG-2002;
            NIHON UNIVERSITY,TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
COMMENT     OS   Artificial Sequence
            PN   WO 02059339-A/2
            PD   01-AUG-2002
```

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  JOURNAL   Patent: EP 1207210-A 7 22-MAY-2002;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          2 AAAAAAAAAAAAAAAAAAAAAAAAA 25


RESULT 608
BD165919
LOCUS       BD165919                  29 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for melting curve analysis of repetitive PCR products.
ACCESSION   BD165919
VERSION     BD165919.1  GI:27871731
KEYWORDS    JP 2002191384-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dietmaier,W.
  TITLE     Method for melting curve analysis of repetitive PCR products
  JOURNAL   Patent: JP 2002191384-A 7 09-JUL-2002;
            F HOFFMANN LA ROCHE AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191384-A/7
            PD   09-JUL-2002
            PF   13-NOV-2001 JP 2001348017
            PR   15-NOV-2000 EP   00124897.0
            PI   WOLFGANG DIETMAIER
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Method for melting curve analysis of repetitive PCR products
            FH   Key             Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          2 AAAAAAAAAAAAAAAAAAAAAAAAA 25


RESULT 609
BD274324
LOCUS       BD274324                  29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION   BD274324
VERSION     BD274324.1  GI:33084092
KEYWORDS    JP 2002526030-A/291.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
  TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
  JOURNAL   Patent: JP 2002526030-A 291 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526030-A/291
            PD   20-AUG-2002
            PF   12-MAY-1999 JP 2000548510
            PR   12-MAY-1998 US    60/085092,12-MAY-1998 US    09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC   Description
            of Artificial Sequence: Novel Sequence CC   N is any nucleotide
            FH   Key             Location/Qualifiers
            FT   misc_feature    (28). .(29).
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAA 2801
              ||||  | ||||||||||||||||
Db          4 TAGACCTAAAAAAAAAAAAAAAAAA 27


RESULT 610
BD274342
LOCUS       BD274342                  29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION   BD274342
VERSION     BD274342.1  GI:33084110
KEYWORDS    JP 2002526030-A/309.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
  TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
  JOURNAL   Patent: JP 2002526030-A 309 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526030-A/309
            PD   20-AUG-2002
            PF   12-MAY-1999 JP 2000548510
            PR   12-MAY-1998 US    60/085092,12-MAY-1998 US    09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC   Description
            of Artificial Sequence: Novel Sequence CC   N is any nucleotide
            FH   Key             Location/Qualifiers
            FT   misc_feature    (28). .(29).
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 29;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAA 2801
              ||||  | ||||||||||||||||
Db          4 TAGACCTAAAAAAAAAAAAAAAAAA 27


RESULT 611
E04206
LOCUS       E04206                    29 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  single strand DNA sequence of Type C hepatitis virus.
```

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Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 604
BD175131/c
LOCUS       BD175131                  27 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Androgen receptor complex-associated protein.
ACCESSION   BD175131
VERSION     BD175131.1  GI:29120825
KEYWORDS    JP 2002262871-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Chan,T.Z.
  TITLE     Androgen receptor complex-associated protein
  JOURNAL   Patent: JP 2002262871-A 12 17-SEP-2002;
            VETERANS GENERAL HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002262871-A/12
            PD   17-SEP-2002
            PF   28-FEB-2001 JP 2001055192
            PI   TAI ZHAI CHAN
            PC   C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
            ,C12P21/02,C12Q1/68,
            PC   G01N33/15,G01N33/50,G01N33/566,C12N15/00,C12N5/00 CC   n =
            A,T,C or G
            CC   synthetically generated primer
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(27).
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 27;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 605
BD234339/c
LOCUS       BD234339                  28 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234339
VERSION     BD234339.1  GI:33044109
KEYWORDS    JP 2002532085-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 12 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/12
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .28
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 28;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 606
BD234335/c
LOCUS       BD234335                  28 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234335
VERSION     BD234335.1  GI:33044105
KEYWORDS    JP 2002532085-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 8 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/8
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .28
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 28;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||||
Db         28 AAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 607
AX430216
LOCUS       AX430216                  29 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 7 from Patent EP1207210.
ACCESSION   AX430216
VERSION     AX430216.1  GI:21655581
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dietmaier,W.
  TITLE     Method for melting curve analysis of repetitive pcr products
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```
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 600
E30823
LOCUS       E30823                    26 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Modified antibody Fab fragment.
ACCESSION   E30823
VERSION     E30823.1  GI:13017253
KEYWORDS    JP 1999341980-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Takashi,S., Izumi,I. and Nobuhiko,M.
  TITLE     Modified antibody Fab fragment
  JOURNAL   Patent: JP 1999341980-A 6 14-DEC-1999;
            TOYOBO CO LTD
COMMENT     OS   Unidentified
            PN   JP 1999341980-A/6
            PD   14-DEC-1999
            PF   02-JUN-1998 JP 1998152956
            PR
            PI   TAKASHI SAZU,IZUMI INOHARA,NOBUHIKO MAEKAWA
            PC   C12N1/21,C07K16/00,C07K17/08,C07K17/14,C12N15/09,G01N33/531,
            PC   G01N33/547//
            PC   C12P21/08,(C12N1/21,C12R1:19),C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 26;
  Best Local Similarity   87.5%;  Pred. No. 9.1e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTGAA 2195
              |||||||||||||||  || |||
Db          2 TTTTTTTTTTTTTTTATTTTCGAA 25


RESULT 601
AX327980/c
LOCUS       AX327980                  27 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 37 from Patent WO0190747.
ACCESSION   AX327980
VERSION     AX327980.1  GI:18098134
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rhode,P., Wittman,V., Weidanz,J.A., Burkhardt,M., Card,K.F.,
            Tal,R., Acevedo,J. and Wong,H.C.
  TITLE     Modulation of t-cell receptor interactions
  JOURNAL   Patent: WO 0190747-A 37 29-NOV-2001;
            Sunol Molecular Corporation (US)
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Primer"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 27;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 602
S64862S3
LOCUS       S64862S3                  27 bp    DNA     linear   PRI 17-DEC-1993
DEFINITION  alpha 1-theta 1 globin intergenic region {3' alpha 1-Alu 1 repeat}
            [Hylobates sp.=gibbons, Genomic, 27 nt, segment 3 of 5].
ACCESSION   S64864
VERSION     S64864.1  GI:415419
KEYWORDS    .
SEGMENT     3 of 5
SOURCE      Hylobates sp. (gibbon)
  ORGANISM  Hylobates sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Bailey,A.D. and Shen,C.K.
  TITLE     Sequential insertion of Alu family repeats into specific genomic
            sites of higher primates
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7205-7209 (1993)
  MEDLINE   93348242
   PUBMED   8394013
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 136653] from the original journal article.
            This sequence comes from Fig. 2A.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="Hylobates sp."
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9581"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 27;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 603
AX492939/c
LOCUS       AX492939                  27 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 16 from Patent EP1227150.
ACCESSION   AX492939
VERSION     AX492939.1  GI:23338609
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tai-Jay,C.
  TITLE     Androgen receptor complex-associated protein
  JOURNAL   Patent: EP 1227150-A 16 31-JUL-2002;
            Veterans General Hospital (TW)
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="synthetically generated primer"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 27;
  Best Local Similarity   87.5%;  Pred. No. 1e+03;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
RESULT 596
AX043563
LOCUS       AX043563                  25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 1129 from Patent WO0065088.
ACCESSION   AX043563
VERSION     AX043563.1  GI:11342171
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 1129 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="HLA-C Heterozygote Primer Sequence"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2175 TTTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||||| |||  |||||
Db          1 TTTTTTTTTTTTAGCTTGTAAAGT 24


RESULT 597
BD090045/c
LOCUS       BD090045                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD090045
VERSION     BD090045.1  GI:22635655
KEYWORDS    JP 2001321190-A/2289.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2289 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2289
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTT 2185
              | |||||||||||||| || ||||
Db         25 CACCTTTTTTTTTTTTCTTCTTTT 2


RESULT 598
I79496/c
LOCUS       I79496                    26 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 3 from patent US 5707807.
ACCESSION   I79496
VERSION     I79496.1  GI:3207786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 3 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 26;
  Best Local Similarity   87.5%;  Pred. No. 9.1e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 599
BD192375/c
LOCUS       BD192375                  26 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Reagents and methods useful for detecting diseases of the breast.
ACCESSION   BD192375
VERSION     BD192375.1  GI:33002114
KEYWORDS    JP 2002516576-A/14.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
            Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
            Russell,J.C., Scheffel,C.P., Stroupe,S.D. and Yu,H.
  TITLE     Reagents and methods useful for detecting diseases of the breast
  JOURNAL   Patent: JP 2002516576-A 14 04-JUN-2002;
            ABBOTT LABORATORIES
COMMENT     PN   JP 2002516576-A/14
            PD   04-JUN-2002
            PF   19-JUN-1998 JP 1999504891
            PR   20-JUN-1997 US    08/879354
            PI   PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA

            PI   N FRIEDMAN,
            PI   JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R  PI
             KLASS,
            PI   JON D KRATOCHVIL,JOHN C RUSSELL,CHRISTI P SCHEFFEL,STEPHEN D
            PI   STROUPE,
            PI   HONG YU
            PC   C12N15/12,C07K14/47,C12Q1/68,C12N15/85,C12N5/10,C07K16/18, PC
             G01N33/574
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10095"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 26;
  Best Local Similarity   87.5%;  Pred. No. 9.1e+02;
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```
LOCUS       BD187513                  25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Probe carrier, Method and Apparatus for producing Probe carrier.
ACCESSION   BD187513
VERSION     BD187513.1  GI:32997252
KEYWORDS    JP 2003014773-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Okamura,N., Okamoto,T. and Kameyama,M.
  TITLE     Probe carrier, Method and Apparatus for producing Probe carrier
  JOURNAL   Patent: JP 2003014773-A 3 15-JAN-2003;
            CANON INC
COMMENT     OS   Artificial Sequence
            PN   JP 2003014773-A/3
            PD   15-JAN-2003
            PF   28-MAR-2002 JP 2002093024
            PI   nobuyuki okamura,tadashi okamoto,makoto kameyama CC   Designed
            oligonucleotide to be hybridized with the designed CC
            oligonucleotide
            CC   'ttttttttttttttttttttttttt'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 593
BD187514/c
LOCUS       BD187514                  25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Probe carrier, Method and Apparatus for producing Probe carrier.
ACCESSION   BD187514
VERSION     BD187514.1  GI:32997253
KEYWORDS    JP 2003014773-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Okamura,N., Okamoto,T. and Kameyama,M.
  TITLE     Probe carrier, Method and Apparatus for producing Probe carrier
  JOURNAL   Patent: JP 2003014773-A 4 15-JAN-2003;
            CANON INC
COMMENT     OS   Artificial Sequence
            PN   JP 2003014773-A/4
            PD   15-JAN-2003
            PF   28-MAR-2002 JP 2002093024
            PI   nobuyuki okamura,tadashi okamoto,makoto kameyama CC   Designed
            oligonucleotide used as a probe to be stabilized CC   on a surface
            of a
            CC   carrier
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 594
BD204988/c
LOCUS       BD204988                  25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein array enabling site specification.
ACCESSION   BD204988
VERSION     BD204988.1  GI:33014758
KEYWORDS    JP 2002510505-A/23.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Protein array enabling site specification
  JOURNAL   Patent: JP 2002510505-A 23 09-APR-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002510505-A/23
            PD   09-APR-2002
            PF   31-MAR-1999 JP 2000542484
            PR   03-APR-1998 US    60/080686
            PI   ROBERT G KUIMELIS,RICHARD WAGNER
            PC   C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
              G01N33/68,
            PC   C12N15/00
            CC   Capture probe sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 595
I29929
LOCUS       I29929                    25 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 42 from patent US 5578468.
ACCESSION   I29929
VERSION     I29929.1  GI:1820720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Pickup,D.J., Patel,D. and Antczak,J.B.
  TITLE     Site-specific RNA cleavage
  JOURNAL   Patent: US 5578468-A 42 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          2 AAAACAAAAAAAAAAAAAAAAAAA 25
```

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REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
  TITLE     Hybridization assay signal enhancement
  JOURNAL   Patent: US 6103474-A 5 15-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 588
BD234336/c
LOCUS       BD234336                  25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234336
VERSION     BD234336.1  GI:33044106
KEYWORDS    JP 2002532085-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 9 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/9
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 589
I58009/c
LOCUS       I58009                    25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2 from patent US 5610287.
ACCESSION   I58009
VERSION     I58009.1  GI:2483073
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Nikiforov,T. and Knapp,M.R.
  TITLE     Method for immobilizing nucleic acid molecules
  JOURNAL   Patent: US 5610287-A 2 11-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 590
I96072/c
LOCUS       I96072                    25 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 2 from patent US 5734020.
ACCESSION   I96072
VERSION     I96072.1  GI:3940542
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Wong,Y.N.
  TITLE     Production and use of magnetic porous inorganic materials
  JOURNAL   Patent: US 5734020-A 2 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 591
AR288252/c
LOCUS       AR288252                  25 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 23 from patent US 6537749.
ACCESSION   AR288252
VERSION     AR288252.1  GI:31675536
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Addressable protein arrays
  JOURNAL   Patent: US 6537749-A 23 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 19.2;  DB 1;  Length 25;
  Best Local Similarity   87.5%;  Pred. No. 8.2e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         25 AAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 592
BD187513
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RESULT 583
AX750585/c
LOCUS       AX750585                  24 bp    DNA     linear   PAT 20-JUN-2003
DEFINITION  Sequence 11 from Patent WO0221134.
ACCESSION   AX750585
VERSION     AX750585.1  GI:32133003
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mack,D. and Gish,K.C.
  TITLE     Methods of diagnosing breast cancer and screening for modulators
  JOURNAL   Patent: WO 0221134-A 11 14-MAR-2002;
            EOS Biotechnology, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="T7-(dT)-24 primer"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 584
AX829247/c
LOCUS       AX829247                  24 bp    DNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 140 from Patent WO02059377.
ACCESSION   AX829247
VERSION     AX829247.1  GI:39838972
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mack,D.H., Gish,K.C. and Afar,D.
  TITLE     Methods of diagnosis of breast cancer, compositions and methods of
            screening for modulators of breast cancer
  JOURNAL   Patent: WO 02059377-A 140 01-AUG-2002;
            EOS Biotechnology, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence:T7-T24 oligo"
     modified_base   8. .24
                     /note="t at positions 8-24 may be present or absent"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 585
BD136714
LOCUS       BD136714                  24 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Quantitative assay of nucleic acid amplification product.
ACCESSION   BD136714
VERSION     BD136714.1  GI:23231659
KEYWORDS    JP 2002504350-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Patel,R. and Kurn,N.
  TITLE     Quantitative assay of nucleic acid amplification product
  JOURNAL   Patent: JP 2002504350-A 4 12-FEB-2002;
            DADE BEHRING INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002504350-A/4
            PD   12-FEB-2002
            PF   17-FEB-1999 JP 2000532556
            PR   18-FEB-1998 US    09/025639
            PI   RAJESH PATEL,NURITH KURN
            PC   C12Q1/68,C12N15/09,C12N15/00
            CC   Synthetic DNA Probe
            FH   Key             Location/Qualifiers
            FT   misc_binding    (1). .(24).
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 586
AR168453
LOCUS       AR168453                  24 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 82 from patent US 6287854.
ACCESSION   AR168453
VERSION     AR168453.1  GI:17904379
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Spurr,N.K., Gray,I.C. and Stewart,L.M.
  TITLE     Diagnosis of susceptibility to cancer and treatment thereof
  JOURNAL   Patent: US 6287854-A 82 11-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTT 2185
                |||   ||||||||||||||||||
Db          1 CTCGAGTTTTTTTTTTTTTTTTT 24


RESULT 587
AR105982/c
LOCUS       AR105982                  25 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 5 from patent US 6103474.
ACCESSION   AR105982
VERSION     AR105982.1  GI:12820047
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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           artificial sequences.
REFERENCE   1
  AUTHORS   Pease,J.S., Cromer,R., Patel,R., Kurn,N. and de Keczer,S.
  TITLE     Compositions for detection of multiple analytes
  JOURNAL   Patent: WO 0184157-A 1 08-NOV-2001;
            Dade Behring Marburg GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthesized"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 579
AX547294/c
LOCUS       AX547294                 24 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 433 from Patent WO02053141.
ACCESSION   AX547294
VERSION     AX547294.1  GI:25812438
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 433 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 580
AX547822/c
LOCUS       AX547822                 24 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 961 from Patent WO02053141.
ACCESSION   AX547822
VERSION     AX547822.1  GI:25812966
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 961 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 581
AX547823
LOCUS       AX547823                 24 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 962 from Patent WO02053141.
ACCESSION   AX547823
VERSION     AX547823.1  GI:25812967
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 962 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 582
AX684290/c
LOCUS       AX684290                 24 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 13 from Patent WO02059609.
ACCESSION   AX684290
VERSION     AX684290.1  GI:29371160
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mack,D.H., Gish,K.C. and Wilson,K.E.
  TITLE     Methods of diagnosing colorectal cancer and/or breast cancer,
            compositions, and methods of screening for colorectal cancer and/or
            breast cancer modulators
  JOURNAL   Patent: WO 02059609-A 13 01-AUG-2002;
            EOS Biotechnology, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="T7-(dT)-24 primer"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1
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                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 574
AX104770
LOCUS       AX104770                 24 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 962 from Patent WO0122972.
ACCESSION   AX104770
VERSION     AX104770.1  GI:13920967
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 962 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 575
AX354553
LOCUS       AX354553                 24 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 11 from Patent WO0173129.
ACCESSION   AX354553
VERSION     AX354553.1  GI:18619355
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Pollner,R.B.
  TITLE     Real time monitoring of PCR using loci
  JOURNAL   Patent: WO 0173129-A 11 04-OCT-2001;
            DADE BEHRING INC. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide attached to beads"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 576
AX355813/c
LOCUS       AX355813                 24 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 841 from Patent WO0197843.
ACCESSION   AX355813
VERSION     AX355813.1  GI:18620481
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 841 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 577
AX427163/c
LOCUS       AX427163                 24 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 12 from Patent WO0210374.
ACCESSION   AX427163
VERSION     AX427163.1  GI:21530544
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lin,S.L., Chuong,C.M. and Widelitz,R.B.
  TITLE     Gene silencing using mrna-cdna hybrids
  JOURNAL   Patent: WO 0210374-A 12 07-FEB-2002;
            UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Poly(dT)24 primer"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 578
AX428574
LOCUS       AX428574                 24 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from Patent WO0184157.
ACCESSION   AX428574
VERSION     AX428574.1  GI:21538485
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 569
AR232949
LOCUS       AR232949                 24 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6457426.
ACCESSION   AR232949
VERSION     AR232949.1  GI:27275296
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Cruson,I.
  TITLE     Front tube furrow opener attachment
  JOURNAL   Patent: US 6457426-A 1 01-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 570
AR340571
LOCUS       AR340571                 24 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 4 from patent US 6573054.
ACCESSION   AR340571
VERSION     AR340571.1  GI:33732217
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Patel,R. and Kurn,N.
  TITLE     Quantitative determination of nucleic acid amplification products
  JOURNAL   Patent: US 6573054-A 4 03-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 571
AR345020
LOCUS       AR345020                 24 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6582938.
ACCESSION   AR345020
VERSION     AR345020.1  GI:33741140
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Su,X., Dong,H. and Ryder,T.B.
  TITLE     Amplification of nucleic acids
  JOURNAL   Patent: US 6582938-A 1 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 572
AX104241/c
LOCUS       AX104241                 24 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 433 from Patent WO0122972.
ACCESSION   AX104241
VERSION     AX104241.1  GI:13920438
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 433 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 573
AX104769/c
LOCUS       AX104769                 24 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 961 from Patent WO0122972.
ACCESSION   AX104769
VERSION     AX104769.1  GI:13920966
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 961 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
```

```
RESULT 564
BD234330/c
LOCUS       BD234330                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234330
VERSION     BD234330.1  GI:33044100
KEYWORDS    JP 2002532085-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 3 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/3
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db         24 AAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 565
I24762
LOCUS       I24762                    24 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 25 from patent US 5545551.
ACCESSION   I24762
VERSION     I24762.1  GI:1604632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Johnson,E.M. and Bergmann,A.D.
  TITLE     Cloning and expression of pur protein
  JOURNAL   Patent: US 5545551-A 25 13-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 566
AR184443
LOCUS       AR184443                  24 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 11 from patent US 6346384.
ACCESSION   AR184443
VERSION     AR184443.1  GI:20230408
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Pollner,R.B.
  TITLE     Real-time monitoring of PCR using LOCI
  JOURNAL   Patent: US 6346384-A 11 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 567
AR202876
LOCUS       AR202876                  24 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 4 from patent US 6365346.
ACCESSION   AR202876
VERSION     AR202876.1  GI:21499117
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Patel,R. and Kurn,N.
  TITLE     Quantitative determination of nucleic acid amplification products
  JOURNAL   Patent: US 6365346-A 4 02-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
                ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 568
AR213697
LOCUS       AR213697                  24 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 4 from patent US 6406667.
ACCESSION   AR213697
VERSION     AR213697.1  GI:23310978
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Singh,S. and Ullman,E.F.
  TITLE     Chemiluminescent compositions for use in detection of multiple
            analytes
  JOURNAL   Patent: US 6406667-A 4 18-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
```

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  Best Local Similarity   95.0%;  Pred. No. 7.3e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||||
Db         24 BAAAAAAAAAAAAAAAAAAA 5


RESULT 559
AR010037
LOCUS       AR010037                 24 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 50 from patent US 5756684.
ACCESSION   AR010037
VERSION     AR010037.1  GI:3968842
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Johnson,E.M. and Bergemann,A.D.
  TITLE     Cloning and expression of PUR protein
  JOURNAL   Patent: US 5756684-A 50 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 560
AR034772
LOCUS       AR034772                 24 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 50 from patent US 5869622.
ACCESSION   AR034772
VERSION     AR034772.1  GI:5950377
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Johnson,E.M. and Bergemann,A.D.
  TITLE     Monoclonal antibodies to the pur protein
  JOURNAL   Patent: US 5869622-A 50 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 561
AR068465
LOCUS       AR068465                 24 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5853993.
ACCESSION   AR068465
VERSION     AR068465.1  GI:6000672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dellinger,D.J., Dahm,S.C. and Troll,M.A.
  TITLE     Signal enhancement method and kit
  JOURNAL   Patent: US 5853993-A 1 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 562
AR105984
LOCUS       AR105984                 24 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 7 from patent US 6103474.
ACCESSION   AR105984
VERSION     AR105984.1  GI:12820049
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
  TITLE     Hybridization assay signal enhancement
  JOURNAL   Patent: US 6103474-A 7 15-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24


RESULT 563
AR107972
LOCUS       AR107972                 24 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 1 from patent US 6110682.
ACCESSION   AR107972
VERSION     AR107972.1  GI:12823459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dellinger,D.J., Dahm,S.C. and Troll,M.A.
  TITLE     Signal enhancement method and kit
  JOURNAL   Patent: US 6110682-A 1 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
  Best Local Similarity   87.5%;  Pred. No. 7.3e+02;
  Matches   21;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAA 24
```

```
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 17 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              |||||      ||||||||||||||||||
Db         29 TTTTTGGGAGATTTTTTTTTTTTTTTTT 1


RESULT 555
AX394620/c
LOCUS       AX394620                 29 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 18 from Patent EP1186673.
ACCESSION   AX394620
VERSION     AX394620.1  GI:21065733
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 18 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              |||||||      ||||||||||||||||
Db         29 TTTTTTTGGGAGATTTTTTTTTTTTTTTT 1


RESULT 556
AX838502
LOCUS       AX838502                 32 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 2 from Patent WO03076654.
ACCESSION   AX838502
VERSION     AX838502.1  GI:39922105
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Palecek,E. and Kosak,H.
  TITLE     Method for identifying, quantifying and/or characterizing an
            analyte
  JOURNAL   Patent: WO 03076654-A 2 18-SEP-2003;
            November Aktiengesellschaft Gesellschaft fuer Molekulare Medizin
            (DE)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen Sequenz:
                     Willkuerliche Sequenz"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 32;
  Best Local Similarity   95.2%;  Pred. No. 1.4e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||
Db         11 TCAAAAAAAAAAAAAAAAAA 31


RESULT 557
AX583623/c
LOCUS       AX583623                 22 bp    DNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 3 from Patent WO02074988.
ACCESSION   AX583623
VERSION     AX583623.1  GI:27655433
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mir,K.
  TITLE     Arrays and methods of use
  JOURNAL   Patent: WO 02074988-A 3 26-SEP-2002;
            THE CHANCELLOR, MASTERS AND SCHOLARS OF THE UNIVERSITY OF OXFORD
            (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide primer (Oligo-dT"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 22;
  Best Local Similarity   95.0%;  Pred. No. 5.7e+02;
  Matches   19;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              :||||||||||||||||||
Db         21 BAAAAAAAAAAAAAAAAAAA 2


RESULT 558
AX391871/c
LOCUS       AX391871                 24 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 21 from Patent WO0216618.
ACCESSION   AX391871
VERSION     AX391871.1  GI:19700451
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Basten,D., Dekker,P.J., Schuurhuizen,P.W., Schaap,P.J. and
            Visser,J.
  TITLE     Aminopeptidase
  JOURNAL   Patent: WO 0216618-A 21 28-FEB-2002;
            DSM N.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="RT reaction primer"

  Query Match             0.7%;  Score 19.2;  DB 1;  Length 24;
```

```
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Reimholz,R. and Ploeger,F.
  TITLE     Method for identifying peptides that can be specifically cleaved
            and the use of peptide sequences of this type
  JOURNAL   Patent: WO 0216574-A 10 28-FEB-2002;
            Xzillion GmbH & CO.KG (DE)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Puromycin-Linker-RNA-Teil"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||||
Db          8 TGCAAAAAAAAAAAAAAAAAA 28


RESULT 550
AR162868
LOCUS       AR162868                 29 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6258943.
ACCESSION   AR162868
VERSION     AR162868.1  GI:16230214
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Fong,T.Ming., Huang,R.-R.C. and Strader,C.D.
  TITLE     Human neurokinin-3 receptor
  JOURNAL   Patent: US 6258943-A 8 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||    ||  ||||||||||||||||
Db          1 TTTTGCGGCCGCTTTTTTTTTTTTTTTT 29


RESULT 551
AR194018
LOCUS       AR194018                 29 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 8 from patent US 6348330.
ACCESSION   AR194018
VERSION     AR194018.1  GI:20240610
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Fong,T.Ming., Huang,R.-R.C. and Strader,C.D.
  TITLE     Method for measuring human neurokinin-3 receptor ligand binding
  JOURNAL   Patent: US 6348330-A 8 19-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||    ||  ||||||||||||||||
Db          1 TTTTGCGGCCGCTTTTTTTTTTTTTTTT 29


RESULT 552
AR409905
LOCUS       AR409905                 29 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 18 from patent US 6635422.
ACCESSION   AR409905
VERSION     AR409905.1  GI:40161040
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 18 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              |||||||    ||||||| |||| |||||
Db          1 TTTTTTTAAATTTTTTATTTCTTTTT 29


RESULT 553
AX181697/c
LOCUS       AX181697                 29 bp    DNA     linear   PAT 07-AUG-2001
DEFINITION  Sequence 54 from Patent WO0146231.
ACCESSION   AX181697
VERSION     AX181697.1  GI:15133035
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burgess,C.E.
  TITLE     Novel proteins and nucleic acids encoding same
  JOURNAL   Patent: WO 0146231-A 54 28-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 29;
  Best Local Similarity   79.3%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||| || |||| |||| |||||  ||||
Db         29 CTTTATTCTTTTGTTTTGTTTTATTTTTG 1


RESULT 554
AX394619/c
LOCUS       AX394619                 29 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 17 from Patent EP1186673.
ACCESSION   AX394619
VERSION     AX394619.1  GI:21065732
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6297425-A 19 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 545
AR173356
LOCUS       AR173356                 28 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 19 from patent US 6303846.
ACCESSION   AR173356
VERSION     AR173356.1  GI:17912847
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Scelonge,C.J. and Bidney,D.L.
  TITLE     Gene encoding oxalate decarboxylase from aspergillus phoenices
  JOURNAL   Patent: US 6303846-A 19 16-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 546
I87998
LOCUS       I87998                   28 bp    DNA     linear   PAT 10-AUG-1998
DEFINITION  Sequence 9 from patent US 5716820.
ACCESSION   I87998
VERSION     I87998.1  GI:3407938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J., Rood,T. and Wang,X.
  TITLE     Fumonisin detoxification enzymes
  JOURNAL   Patent: US 5716820-A 9 10-FEB-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 547
AR340907
LOCUS       AR340907                 28 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 9 from patent US 6573075.
ACCESSION   AR340907
VERSION     AR340907.1  GI:33732850
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 6573075-A 9 03-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 548
AX029525
LOCUS       AX029525                 28 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 9 from Patent EP0981953.
ACCESSION   AX029525
VERSION     AX029525.1  GI:10190261
KEYWORDS    .
SOURCE      Exophiala spinifera
  ORGANISM  Exophiala spinifera
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Chaetothyriomycetes;
            Chaetothyriales; Herpotrichiellaceae; mitosporic
            Herpotrichiellaceae; Exophiala.
REFERENCE   1
  AUTHORS   Duvick,J., Maddox,J.R., Rood,T.A. and Wang,X.
  TITLE     Transgenic plants transformed with fumonisin detoxifying enzymes
  JOURNAL   Patent: EP 0981953-A 9 01-MAR-2000;
            PIONEER HI BRED INT (US)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Exophiala spinifera"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:91928"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 549
AX391845
LOCUS       AX391845                 28 bp    RNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 10 from Patent WO0216574.
ACCESSION   AX391845
VERSION     AX391845.1  GI:19700427
KEYWORDS    .
SOURCE      synthetic construct
```

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RESULT 539
AR068449
LOCUS       AR068449                 28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5853991.
ACCESSION   AR068449
VERSION     AR068449.1  GI:6000656
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA subtractive cloning method
  JOURNAL   Patent: US 5853991-A 13 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 540
AR068450
LOCUS       AR068450                 28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5853991.
ACCESSION   AR068450
VERSION     AR068450.1  GI:6000657
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA subtractive cloning method
  JOURNAL   Patent: US 5853991-A 14 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 541
AR068451
LOCUS       AR068451                 28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5853991.
ACCESSION   AR068451
VERSION     AR068451.1  GI:6000658
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA subtractive cloning method
  JOURNAL   Patent: US 5853991-A 15 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 542
AR150988
LOCUS       AR150988                 28 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from patent US 6229071.
ACCESSION   AR150988
VERSION     AR150988.1  GI:15115579
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J., Maddox,J.R., Rood,T.A. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 6229071-A 9 08-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 543
AR156058
LOCUS       AR156058                 28 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 9 from patent US 6239330.
ACCESSION   AR156058
VERSION     AR156058.1  GI:15124111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J., Maddox,J.R. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 6239330-A 9 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27


RESULT 544
AR172065
LOCUS       AR172065                 28 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 19 from patent US 6297425.
ACCESSION   AR172065
VERSION     AR172065.1  GI:17911015
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RESULT 534
AX513052/c
LOCUS       AX513052                  27 bp    DNA     linear   PAT 03-OCT-2002
DEFINITION  Sequence 42 from Patent WO02062135.
ACCESSION   AX513052
VERSION     AX513052.1  GI:23504143
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Egelrud,T. and Hansson,L.
  TITLE     Scce modified transgenic mammals and their use as models of human
            disease
  JOURNAL   Patent: WO 02062135-A 42 15-AUG-2002;
            Egelrud, Torbjorn (SE) ; Hansson, Lennart (SE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="5 -RACE cDNA synthesis primer."

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 27;
  Best Local Similarity   84.0%;  Pred. No. 9.3e+02;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              :||   ||||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 535
AR022650
LOCUS       AR022650                  28 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 9 from patent US 5792931.
ACCESSION   AR022650
VERSION     AR022650.1  GI:3976712
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Duvick,J., Rood,T., Maddox,J.R. and Wang,X.
  TITLE     Fumonisin detoxification compositions and methods
  JOURNAL   Patent: US 5792931-A 9 11-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27

RESULT 536
AR055108
LOCUS       AR055108                  28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 13 from patent US 5837468.
ACCESSION   AR055108
VERSION     AR055108.1  GI:5980685
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA substractive cloning method
  JOURNAL   Patent: US 5837468-A 13 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27

RESULT 537
AR055109
LOCUS       AR055109                  28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 14 from patent US 5837468.
ACCESSION   AR055109
VERSION     AR055109.1  GI:5980686
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA substractive cloning method
  JOURNAL   Patent: US 5837468-A 14 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27

RESULT 538
AR055110
LOCUS       AR055110                  28 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5837468.
ACCESSION   AR055110
VERSION     AR055110.1  GI:5980687
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Wang,X., Duvick,J.P. and Briggs,S.P.
  TITLE     PCR-based cDNA substractive cloning method
  JOURNAL   Patent: US 5837468-A 15 17-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 28;
  Best Local Similarity   95.2%;  Pred. No. 1e+03;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||| ||||||||||||||||||
Db          7 TCCGTTTTTTTTTTTTTTTT 27
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  TITLE     Genes and proteins predictive and therapeutic for stroke,
            hypertension, diabetes and obesity
  JOURNAL   Patent: US 6486299-A 43 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 8.4e+02;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              :||   ||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 530
AR263647/c
LOCUS       AR263647                  26 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 6 from patent US 6331413.
ACCESSION   AR263647
VERSION     AR263647.1  GI:28075580
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Adler,D.A. and Sheppard,P.O.
  TITLE     Secreted salivary ZSIG63 Polypeptide
  JOURNAL   Patent: US 6331413-A 6 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 8.4e+02;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              :||   ||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 531
AX814950/c
LOCUS       AX814950                  26 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 36 from Patent WO03064691.
ACCESSION   AX814950
VERSION     AX814950.1  GI:39104088
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 36 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"
     misc_feature    26
                     /note="v is a, c or g"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 8.4e+02;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              :||   ||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 532
BD062456/c
LOCUS       BD062456                  26 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A human 2-19 protein homologue, Z219A.
ACCESSION   BD062456
VERSION     BD062456.1  GI:22608059
KEYWORDS    JP 2001507946-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Conklin,D.C. and Blumberg,H.
  TITLE     A human 2-19 protein homologue, Z219A
  JOURNAL   Patent: JP 2001507946-A 4 19-JUN-2001;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001507946-A/4
            PD   19-JUN-2001
            PF   06-OCT-1998 JP 1999522287
            PR   06-OCT-1997 US    60/061712
            PI   DARRELL C CONKLIN,HAL BLUMBERG
            PC   C12N15/12,C12N15/62,C12N5/10,C07K14/47,C07K16/18,C12Q1/68, PC
             A01K67/027
            CC   Oligonucleotide primer ZC7231
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 8.4e+02;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              :||   ||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 533
AR013918
LOCUS       AR013918                  26 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5773223.
ACCESSION   AR013918
VERSION     AR013918.1  GI:3971372
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Shyamala,V. and Olson,P.Tekamp.
  TITLE     Endothelin B.sub.1, (ETB.sub.1) receptor polypeptide and its
            encoding nucleic acid methods, and uses thereof
  JOURNAL   Patent: US 5773223-A 3 30-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   95.2%;  Pred. No. 8.4e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              | ||||||||||||||||||
Db          6 TACTTTTTTTTTTTTTTTTT 26
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  Best Local Similarity   87.0%;  Pred. No. 6.7e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAA 2188
              ||| |||||||||||||||||  |
Db         24 TTTNTTTTTTTTTTTTTTTTNCA 2

RESULT 526
BD056964/c
LOCUS       BD056964                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sets of labeled energy transfer fluorescent primers and their use
            in multi component analysis.
ACCESSION   BD056964
VERSION     BD056964.1  GI:22602570
KEYWORDS    JP 2001509271-A/1.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ju,J.
  TITLE     Sets of labeled energy transfer fluorescent primers and their use
            in multi component analysis
  JOURNAL   Patent: JP 2001509271-A 1 10-JUL-2001;
            INCYTE PHARMACEUTICALS INC
COMMENT     PN   JP 2001509271-A/1
            PD   10-JUL-2001
            PF   12-DEC-1997 JP 1998534358
            PR   15-JAN-1997 US    08/784162
            PI   JINGYUE JU
            PC   G01N21/78,C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .25
                        /organism="Arabidopsis thaliana"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:3702"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 25;
  Best Local Similarity   95.2%;  Pred. No. 7.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db         24 TAAAAAAAAAAAAAAAAAAAA 4

RESULT 527
AX708814
LOCUS       AX708814                  25 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 30 from Patent WO02095071.
ACCESSION   AX708814
VERSION     AX708814.1  GI:29564541
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plasterk,R.H.
  TITLE     Means and methods for identifying genes and proteins involved in
            the prevention and/or repair of a replication error
  JOURNAL   Patent: WO 02095071-A 30 28-NOV-2002;
            Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES                Location/Qualifiers
     source             1. .25
                        /organism="synthetic construct"
                        /mol_type="unassigned DNA"
                        /db_xref="taxon:32630"
                        /note="sequence to demonstrate the principle of how to
                        detect somatic repeat instability~##N# stands for any
                        number of nucleotides seleted from A, C, T or G#"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 25;
  Best Local Similarity   87.0%;  Pred. No. 7.6e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2804
              ||  |||||||||||||||| |
Db          1 ATGNAAAAAAAAAAAAAAAANA 23

RESULT 528
BD237566/c
LOCUS       BD237566                  26 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Genes and proteins predicting and treating fit, hypertension,
            diabetes and obesity.
ACCESSION   BD237566
VERSION     BD237566.1  GI:33047336
KEYWORDS    JP 2002525115-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Shimkets,R.A.
  TITLE     Genes and proteins predicting and treating fit, hypertension,
            diabetes and obesity
  JOURNAL   Patent: JP 2002525115-A 1 13-AUG-2002;
            CURAGEN CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002525115-A/1
            PD   13-AUG-2002
            PF   28-SEP-1999 JP 2000572365
            PR   28-SEP-1998 US    09/161939
            PI   RICHARD A SHIMKETS
            PC   C12N15/09,A01K67/027,A61K31/7088,A61K38/00,A61K39/395,A61K39/
            PC   395,
            PC   A61K39/395,A61K48/00,A61P3/04,A61P3/06,A61P9/10,A61P9/12, PC
            A61P43/00,
            PC   C07K14/47,C07K16/18,C12N9/10,C12N9/88,C12Q1/25,C12Q1/52 PC
            ,C12Q1/68,G01N33/15,
            PC   G01N33/50,C12N15/00,A61K37/02
            CC   Description of Artificial Sequence: oligo(dT)<25>V FH   Key
                     Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
     source             1. .26
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 26;
  Best Local Similarity   84.0%;  Pred. No. 8.4e+02;
  Matches   21;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              :||   ||||||||||||||||||||
Db         26 BAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 529
AR257336/c
LOCUS       AR257336                  26 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 43 from patent US 6486299.
ACCESSION   AR257336
VERSION     AR257336.1  GI:27307233
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Shimkets,R.A.
```

```
Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db         21 TCAAAAAAAAAAAAAAAAAAA 1


RESULT 522
AX825158
LOCUS       AX825158                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 56 from Patent WO03072818.
ACCESSION   AX825158
VERSION     AX825158.1  GI:39750887
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 56 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTTGT 21


RESULT 523
AR431308
LOCUS       AR431308                 24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 2 from patent US 6651008.
ACCESSION   AR431308
VERSION     AR431308.1  GI:40193276
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 2 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 24;
  Best Local Similarity   95.2%;  Pred. No. 6.7e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||| ||||||||||||
Db          2 TTTTTTTATTTTTTTTTTTT 22


RESULT 524
AX708815
LOCUS       AX708815                 24 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 31 from Patent WO02095071.
ACCESSION   AX708815
VERSION     AX708815.1  GI:29564542
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plasterk,R.H.
  TITLE     Means and methods for identifying genes and proteins involved in
            the prevention and/or repair of a replication error
  JOURNAL   Patent: WO 02095071-A 31 28-NOV-2002;
            Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence to demonstrate the principle of how to
                     detect somatic repeat instability~##N# stands for any
                     number of nucleotides selected from A, C, T or G#"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 24;
  Best Local Similarity   87.0%;  Pred. No. 6.7e+02;
  Matches   20;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAA 2804
              ||  |||||||||||||||| ||
Db          1 ATGNAAAAAAAAAAAAAAAANAA 23


RESULT 525
AX708815/c
LOCUS       AX708815                 24 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 31 from Patent WO02095071.
ACCESSION   AX708815
VERSION     AX708815.1  GI:29564542
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plasterk,R.H.
  TITLE     Means and methods for identifying genes and proteins involved in
            the prevention and/or repair of a replication error
  JOURNAL   Patent: WO 02095071-A 31 28-NOV-2002;
            Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence to demonstrate the principle of how to
                     detect somatic repeat instability~##N# stands for any
                     number of nucleotides selected from A, C, T or G#"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 24;
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VERSION     AX825150.1  GI:39750879
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 48 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTCTT 21


RESULT 520
AX825155
LOCUS       AX825155                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 53 from Patent WO03072818.
ACCESSION   AX825155
VERSION     AX825155.1  GI:39750884
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 53 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTGA 21


RESULT 521
AX825155/c
LOCUS       AX825155                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 53 from Patent WO03072818.
ACCESSION   AX825155
VERSION     AX825155.1  GI:39750884
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 53 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||||
Db         21 TGGAAAAAAAAAAAAAAAAAA 1


RESULT 517
AX825147
LOCUS       AX825147                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 45 from Patent WO03072818.
ACCESSION   AX825147
VERSION     AX825147.1  GI:39750876
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 45 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTCTA 21


RESULT 518
AX825147/c
LOCUS       AX825147                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 45 from Patent WO03072818.
ACCESSION   AX825147
VERSION     AX825147.1  GI:39750876
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 45 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
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                     /mod_base=OTHER
     modified_base   12
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||||
Db         21 TAGAAAAAAAAAAAAAAAAAA 1


RESULT 519
AX825150
LOCUS       AX825150                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 48 from Patent WO03072818.
ACCESSION   AX825150
```

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                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTA 21


RESULT 514
AX825134
LOCUS       AX825134                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 32 from Patent WO03072818.
ACCESSION   AX825134
VERSION     AX825134.1  GI:39750863
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 32 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGTT 21


RESULT 515
AX825139/c
LOCUS       AX825139                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 37 from Patent WO03072818.
ACCESSION   AX825139
VERSION     AX825139.1  GI:39750868
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 37 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2803
              | ||||||||||||||||||
Db         21 TCGAAAAAAAAAAAAAAAAA 1


RESULT 516
AX825143/c
LOCUS       AX825143                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 41 from Patent WO03072818.
ACCESSION   AX825143
VERSION     AX825143.1  GI:39750872
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 41 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2803
              || ||||||||||||||||||
Db         21 TTCAAAAAAAAAAAAAAAAAA 1


RESULT 511
AX825121
LOCUS       AX825121                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 19 from Patent WO03072818.
ACCESSION   AX825121
VERSION     AX825121.1  GI:39750850
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 19 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTGAC 21


RESULT 512
AX825127/c
LOCUS       AX825127                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 25 from Patent WO03072818.
ACCESSION   AX825127
VERSION     AX825127.1  GI:39750856
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 25 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||||
Db         21 TGCAAAAAAAAAAAAAAAAAA 1


RESULT 513
AX825131
LOCUS       AX825131                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 29 from Patent WO03072818.
ACCESSION   AX825131
VERSION     AX825131.1  GI:39750860
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 29 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
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  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTATC 21


RESULT 508
AX825118
LOCUS       AX825118                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 16 from Patent WO03072818.
ACCESSION   AX825118
VERSION     AX825118.1  GI:39750847
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 16 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTATT 21


RESULT 509
AX825119
LOCUS       AX825119                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 17 from Patent WO03072818.
ACCESSION   AX825119
VERSION     AX825119.1  GI:39750848
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 17 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTGAA 21


RESULT 510
AX825119/c
LOCUS       AX825119                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 17 from Patent WO03072818.
ACCESSION   AX825119
VERSION     AX825119.1  GI:39750848
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 17 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
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DEFINITION  Sequence 12 from Patent WO03072818.
ACCESSION   AX825114
VERSION     AX825114.1  GI:39750843
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 12 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTTACT 21


RESULT 506
AX825115
LOCUS       AX825115                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 13 from Patent WO03072818.
ACCESSION   AX825115
VERSION     AX825115.1  GI:39750844
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 13 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTATA 21


RESULT 507
AX825117
LOCUS       AX825117                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 15 from Patent WO03072818.
ACCESSION   AX825117
VERSION     AX825117.1  GI:39750846
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 15 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
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  JOURNAL   Patent: WO 03072818-A 7 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTAGC 21


RESULT 503
AX825111/c
LOCUS       AX825111                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 9 from Patent WO03072818.
ACCESSION   AX825111
VERSION     AX825111.1  GI:39750840
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 9 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||||
Db         21 TGTAAAAAAAAAAAAAAAAAA 1


RESULT 504
AX825113
LOCUS       AX825113                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 11 from Patent WO03072818.
ACCESSION   AX825113
VERSION     AX825113.1  GI:39750842
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 11 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTACC 21


RESULT 505
AX825114
LOCUS       AX825114                  21 bp    DNA     linear   PAT 11-DEC-2003
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RESULT 499
AX825137
LOCUS       AX825137                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 35 from Patent WO03072818.
ACCESSION   AX825137
VERSION     AX825137.1  GI:39750866
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 35 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
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                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTCAC 21


RESULT 500
AX825162
LOCUS       AX825162                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 60 from Patent WO03072818.
ACCESSION   AX825162
VERSION     AX825162.1  GI:39750891
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 60 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTCT 21


RESULT 501
AR241831
LOCUS       AR241831                21 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 119 from patent US 6472154.
ACCESSION   AR241831
VERSION     AR241831.1  GI:27287643
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 119 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||| |||||||||
Db          1 TTTTTTTTTTATTTTTTTT 21


RESULT 502
AX825109
LOCUS       AX825109                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 7 from Patent WO03072818.
ACCESSION   AX825109
VERSION     AX825109.1  GI:39750838
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
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           artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 61 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              | ||||||||||||||||||||
Db         21 TAAAAAAAAAAAAAAAAAAAA 1


RESULT 497
AX825103/c
LOCUS       AX825103                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 1 from Patent WO03072818.
ACCESSION   AX825103
VERSION     AX825103.1  GI:39750832
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 1 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              || ||||||||||||||||||||
Db         21 TTTAAAAAAAAAAAAAAAAAA 1


RESULT 498
AX825106/c
LOCUS       AX825106                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 4 from Patent WO03072818.
ACCESSION   AX825106
VERSION     AX825106.1  GI:39750835
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 4 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              ||| ||||||||||||||||||
Db         21 ATTAAAAAAAAAAAAAAAAAA 1
```

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                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTCAA 21


RESULT 494
AX825151/c
LOCUS       AX825151                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 49 from Patent WO03072818.
ACCESSION   AX825151
VERSION     AX825151.1  GI:39750880
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 49 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2803
              || ||||||||||||||||||
Db         21 TTAAAAAAAAAAAAAAAAAAA 1


RESULT 495
AX825159
LOCUS       AX825159                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 57 from Patent WO03072818.
ACCESSION   AX825159
VERSION     AX825159.1  GI:39750888
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 57 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 4.6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTCA 21


RESULT 496
AX825163/c
LOCUS       AX825163                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 61 from Patent WO03072818.
ACCESSION   AX825163
VERSION     AX825163.1  GI:39750892
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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  Best Local Similarity   84.6%;  Pred. No. 1.9e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         38 AAAAAAAAAAAAAAAAAAAAAAAAAAA 13


RESULT 489
A48799
LOCUS       A48799                   40 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 6 from Patent WO9603528.
ACCESSION   A48799
VERSION     A48799.1  GI:2302466
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Petrik,J., Allain,J. and Pearson,G.J.
  TITLE     OLIGONUCLEOTIDES AND THEIR USE
  JOURNAL   Patent: WO 9603528-A 6 08-FEB-1996;
            LYNXVALE LTD (GB)
COMMENT     Other publication AU 3118395 960222.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 40;
  Best Local Similarity   84.6%;  Pred. No. 2.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 490
AR232955
LOCUS       AR232955                 40 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6457426.
ACCESSION   AR232955
VERSION     AR232955.1  GI:27275302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Cruson,I.
  TITLE     Front tube furrow opener attachment
  JOURNAL   Patent: US 6457426-A 7 01-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 40;
  Best Local Similarity   84.6%;  Pred. No. 2.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 491
AR309630/c
LOCUS       AR309630                 41 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9 from patent US 6555657.
ACCESSION   AR309630
VERSION     AR309630.1  GI:31701680
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Christensen,T.
  TITLE     Isolated transcription factor for an alpha-amylase promoter in
            filamentous fungi
  JOURNAL   Patent: US 6555657-A 9 29-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 41;
  Best Local Similarity   84.6%;  Pred. No. 2.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         41 AAAAAAAAAAAAAAAAAAAAAAAAAAA 16


RESULT 492
AX225198/c
LOCUS       AX225198                 43 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 7 from Patent WO0161033.
ACCESSION   AX225198
VERSION     AX225198.1  GI:15555219
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schouten,J.P.
  TITLE     Multiplex ligatable probe amplification
  JOURNAL   Patent: WO 0161033-A 7 23-AUG-2001;
            Schouten, Johannes Petrus (NL)
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 43;
  Best Local Similarity   84.6%;  Pred. No. 2.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         43 AAAAAAAAAAAAAAAAAAAAAAAAAAA 18


RESULT 493
AX825135
LOCUS       AX825135                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 33 from Patent WO03072818.
ACCESSION   AX825135
VERSION     AX825135.1  GI:39750864
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 33 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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  AUTHORS   Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
            Grilley,M., Watkins,M. and Hillyard,D.R.
  TITLE     Contryphan peptides
  JOURNAL   Patent: US 6153738-A 26 28-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 33;
  Best Local Similarity   84.6%;  Pred. No. 1.4e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAAAA 8


RESULT 485
A63578/c
LOCUS       A63578                    34 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 19 from Patent WO9720924.
ACCESSION   A63578
VERSION     A63578.1  GI:3717233
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
            AGENTS
  JOURNAL   Patent: WO 9720924-A 19 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 34;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         34 ACAAAAAAAAAAAAAAAAAAAAAAAA 9


RESULT 486
I29931
LOCUS       I29931                    37 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 44 from patent US 5578468.
ACCESSION   I29931
VERSION     I29931.1  GI:1820722
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 37)
  AUTHORS   Pickup,D.J., Patel,D. and Antczak,J.B.
  TITLE     Site-specific RNA cleavage
  JOURNAL   Patent: US 5578468-A 44 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 37;
  Best Local Similarity   84.6%;  Pred. No. 1.8e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db          2 AAAAAAAAAAAAAAAAAAAAAAAAAA 27


RESULT 487
AX106972/c
LOCUS       AX106972                  37 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 25 from Patent WO0125442.
ACCESSION   AX106972
VERSION     AX106972.1  GI:13922521
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
  TITLE     Dna polymerase lambda and uses thereof
  JOURNAL   Patent: WO 0125442-A 25 12-APR-2001;
            CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="poly dT"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 37;
  Best Local Similarity   84.6%;  Pred. No. 1.8e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         37 AAAAAAAAAAAAAAAAAAAAAAAAAA 12


RESULT 488
E50766/c
LOCUS       E50766                    38 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Vector expressing full-length gene of RNA virus and utilization
            thereof.
ACCESSION   E50766
VERSION     E50766.1  GI:18628191
KEYWORDS    JP 2000152793-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Obara,M., Obara,K., Tabira,K., Matsuzaki,J. and Om,H.
  TITLE     Vector expressing full-length gene of RNA virus and utilization
  JOURNAL   Patent: JP 2000152793-A 19 06-JUN-2000;
            TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, CHUGAI
            PHARMACEUT CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000152793-A/19
            PD   06-JUN-2000
            PF   24-JUN-1999 JP 1999178347
            PR
            PI   MICHINORI OBARA,KYOKO OBARA,KAZUNARI TABIRA,JUNICHI MATSUZAKI,
            PI   HIROSHI OMORI
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/70,C12N15/00,C12N5/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .38
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 38;
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RESULT 480
AX267026
LOCUS       AX267026                30 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 15 from Patent WO0173001.
ACCESSION   AX267026
VERSION     AX267026.1  GI:16515811
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Seidman,M.M. and Majumdar,A.
  TITLE     Establishment of cellular manipulations which enhance
            oligo-mediated gene targeting
  JOURNAL   Patent: WO 0173001-A 15 04-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTT 2181
              |||||||| ||||| ||| |||||| |
Db          5 TTTTTTCTTCTTTTCTTTCTTTTTCT 30


RESULT 481
I29892/c
LOCUS       I29892                  32 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 5 from patent US 5578468.
ACCESSION   I29892
VERSION     I29892.1  GI:1820683
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Pickup,D.J., Patel,D. and Antczak,J.B.
  TITLE     Site-specific RNA cleavage
  JOURNAL   Patent: US 5578468-A 5 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 32;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACTTT 2192
              |||||||||||||||||| | || | |
Db         32 TTTTTTTTTTTTTTTTTATAAAATCT 7


RESULT 482
BD011883/c
LOCUS       BD011883                33 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  Detection kit for SRSV.
ACCESSION   BD011883
VERSION     BD011883.1  GI:22092072
KEYWORDS    WO 0079280-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Takeda,N., Natori,K., Miyamura,T., Kunio, Kamata, Sato,T. and
            Sato,S.
  TITLE     Detection kit for SRSV
  JOURNAL   Patent: WO 0079280-A 13 28-DEC-2000;
            JAPAN AS REPRESENTED BY DIRECTOR GE YOSHIHIKO HIROSE,MITSUAKI
            MORIGUCHI,KIMIYASU ISOBE DISEASES, DENKA SEIKEN CO LTD,NAOKAZU
            TAKEDA,KATSURO NATORI,TATSUO MIYAMURA, KUNIO KAMATA,TOSHINORI
            SATO,SEIYA SATO
COMMENT     OS   Artificial Sequence
            PN   WO 0079280-A/13
            PD   28-DEC-2000
            PF   22-JUN-2000 WO 2000JP004095
            PR   22-JUN-1999 JP 99P   175928
            PI   NAOKAZU TAKEDA,KATSURO NATORI,TATSUO MIYAMURA,KUNIO PI
            KAMATA,TOSHINORI  SATO,
            PI   SEIYA SATO
            PC   G01N33/569,C12N15/40
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 33;
  Best Local Similarity   84.6%;  Pred. No. 1.4e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAAAA 8


RESULT 483
AR099615/c
LOCUS       AR099615                33 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 26 from patent US 6077934.
ACCESSION   AR099615
VERSION     AR099615.1  GI:12809381
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
            Grilley,M., Watkins,M. and Hillyard,D.R.
  TITLE     Contryphan peptides
  JOURNAL   Patent: US 6077934-A 26 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 33;
  Best Local Similarity   84.6%;  Pred. No. 1.4e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAAAA 8


RESULT 484
AR120128/c
LOCUS       AR120128                33 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 26 from patent US 6153738.
ACCESSION   AR120128
VERSION     AR120128.1  GI:14102827
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
```

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                  ||| | |||||||||||||||| || |
Db          30 CTTATGTTTTTTTTTTTTTTTGAATT 5


RESULT 475
I59848/c
LOCUS       I59848                    30 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 85 from patent US 5654414.
ACCESSION   I59848
VERSION     I59848.1  GI:2478480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Beck,J.J. and Friedrich,L.B.
  TITLE     Chemically inducible promoter of a cucumber chitinase/lysozyme gene
  JOURNAL   Patent: US 5654414-A 85 05-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTTAACT 2190
                ||| | |||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTTGAATT 5


RESULT 476
I75175/c
LOCUS       I75175                    30 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 85 from patent US 5689044.
ACCESSION   I75175
VERSION     I75175.1  GI:3011316
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
  TITLE     Chemically inducible promoter of a plant PR-1 gene
  JOURNAL   Patent: US 5689044-A 85 18-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTTAACT 2190
                ||| | |||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTTGAATT 5


RESULT 477
AR409723/c
LOCUS       AR409723                  30 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 85 from patent US 6632981.
ACCESSION   AR409723
VERSION     AR409723.1  GI:40160700
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Meins,F. Jr., Shinshi,H., Wenzler,H.C., Hofsteenge,J., Ryals,J.A.
            and Sperisen,C.
  TITLE     DNA sequences encoding polypeptides having beta-1,3-glucanase
            activity
  JOURNAL   Patent: US 6632981-A 85 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTTAACT 2190
                ||| | |||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTTGAATT 5


RESULT 478
AR028195
LOCUS       AR028195                  30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 44 from patent US 5858661.
ACCESSION   AR028195
VERSION     AR028195.1  GI:5940168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Shiloh,Y.
  TITLE     Ataxia-telangiectasia gene and its genomic organization
  JOURNAL   Patent: US 5858661-A 44 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTT 2178
                |||||| |||| ||| |||| |||||
Db          5 GATTTTCTTCTTCTTGTTTTGTTTTT 30


RESULT 479
AR138598
LOCUS       AR138598                  30 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 123 from patent US 6200749.
ACCESSION   AR138598
VERSION     AR138598.1  GI:14480943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Shiloh,Y.
  TITLE     Mutated forms of the ataxia-telangiectasia gene and method to
            screen for a partial A-T phenotype
  JOURNAL   Patent: US 6200749-A 123 13-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTT 2178
                |||||| |||| ||| |||| |||||
Db          5 GATTTTCTTCTTCTTGTTTTGTTTTT 30
```

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RESULT 470
AR038488/c
LOCUS       AR038488                  30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 85 from patent US 5804693.
ACCESSION   AR038488
VERSION     AR038488.1  GI:5957205
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Gaffney,T.D., Ryals,J.A., Friedrich,L.B., Uknes,S.J., Ward,E.R.,
            Kessmann,H. and Vernooij,B.T.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL   Patent: US 5804693-A 85 08-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||| | |||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTGAATT 5


RESULT 471
AR064630/c
LOCUS       AR064630                  30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 85 from patent US 5847258.
ACCESSION   AR064630
VERSION     AR064630.1  GI:5993938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Moyer,M.B., Payne,G.B. and Ward,E.R.
  TITLE     DNA encoding .beta.-1,3-glucanases
  JOURNAL   Patent: US 5847258-A 85 08-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||| | |||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTGAATT 5


RESULT 472
AR067555/c
LOCUS       AR067555                  30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 85 from patent US 5851766.
ACCESSION   AR067555
VERSION     AR067555.1  GI:5998777
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A. and Harms,C.
  TITLE     Process for isolating chemically regulatable DNA sequences
  JOURNAL   Patent: US 5851766-A 85 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||| | |||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTGAATT 5


RESULT 473
I38507/c
LOCUS       I38507                    30 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 85 from patent US 5614395.
ACCESSION   I38507
VERSION     I38507.1  GI:2084561
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
            Friedrich,L.B., Harms,C., Meins,F. Jr., Montoya,A. deceased,
            Moyer,M.B., Neuhaus,J.-M., Payne,G.B., Sperisen,C., Stinson,J.R.,
            Uknes,S.J., Ward,E.R. and Williams,S.C.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL   Patent: US 5614395-A 85 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||| | |||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTGAATT 5


RESULT 474
I56982/c
LOCUS       I56982                    30 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 85 from patent US 5650505.
ACCESSION   I56982
VERSION     I56982.1  GI:2477395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
            Friedrich,L.B., Harms,C., Meins,F. Jr., Montoya,A. deceased,
            Moyer,M.B., Neuhaus,J.-M., Payne,G.B., Sperisen,C., Stinson,J.R.,
            Uknes,S.J., Ward,E.R. and Williams,S.C.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL   Patent: US 5650505-A 85 22-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
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              | ||   ||||||||||||||||||||
Db          4 ACAAAAAAAAAAAAAAAAAAAAAAAA 29


RESULT 465
AR127791
LOCUS       AR127791                  30 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 12 from patent US 6180777.
ACCESSION   AR127791
VERSION     AR127791.1  GI:14114386
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Horn,T.
  TITLE     Synthesis of branched nucleic acids
  JOURNAL   Patent: US 6180777-A 12 30-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          4 ACAAAAAAAAAAAAAAAAAAAAAAAA 29


RESULT 466
I28373
LOCUS       I28373                    30 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 12 from patent US 5571677.
ACCESSION   I28373
VERSION     I28373.1  GI:1819149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 12 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          4 ACAAAAAAAAAAAAAAAAAAAAAAAA 29


RESULT 467
AR016852/c
LOCUS       AR016852                  30 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 85 from patent US 5777200.
ACCESSION   AR016852
VERSION     AR016852.1  GI:3973129
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Alexander,D.C., Goodman,R.M. and Stinson,J.R.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL   Patent: US 5777200-A 85 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||| | ||||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTGAATT 5


RESULT 468
AR020878/c
LOCUS       AR020878                  30 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 85 from patent US 5789214.
ACCESSION   AR020878
VERSION     AR020878.1  GI:3975493
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
  TITLE     Method of inducing gene transcription in a plant
  JOURNAL   Patent: US 5789214-A 85 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||| | ||||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTGAATT 5


RESULT 469
AR027201/c
LOCUS       AR027201                  30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 85 from patent US 5856154.
ACCESSION   AR027201
VERSION     AR027201.1  GI:5938041
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Alexander,D.C., Goodman,R.M. and Ward,E.R.
  TITLE     Method of protecting plants from oomycete pathogens
  JOURNAL   Patent: US 5856154-A 85 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||| | ||||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTGAATT 5
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LOCUS       BD132851                30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Methods of nucleic acid detection.
ACCESSION   BD132851
VERSION     BD132851.1  GI:23227796
KEYWORDS    JP 2002509443-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
  TITLE     Methods of nucleic acid detection
  JOURNAL   Patent: JP 2002509443-A 2 26-MAR-2002;
            GEN PROBE INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002509443-A/2
            PD   26-MAR-2002
            PF   30-OCT-1998 JP 1999526687
            PR   31-OCT-1997 US    60/063969
            PI   WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
            C12Q1/68
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 462
BD181358/c
LOCUS       BD181358                30 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION   BD181358
VERSION     BD181358.1  GI:30792276
KEYWORDS    JP 2002327130-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
  TITLE     Novel fluorescent colorant and method of assaying nucleic acid
  JOURNAL   Patent: JP 2002327130-A 1 15-NOV-2002;
            TOSOH CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002327130-A/1
            PD   15-NOV-2002
            PF   11-JAN-2002 JP 2002005267
            PI   TAKUMI TOKUNAGA,TAKAHIKO ISHIGURO,RYUICHI HORIE PC
            C09B23/00,C07D417/14,C07H21/04,C09K11/06,C12N15/09,C12Q1/68, PC
            G01N33/58,
            PC   C12N15/00
            CC   dT30mer
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 463
BD181359
LOCUS       BD181359                30 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION   BD181359
VERSION     BD181359.1  GI:30792277
KEYWORDS    JP 2002327130-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
  TITLE     Novel fluorescent colorant and method of assaying nucleic acid
  JOURNAL   Patent: JP 2002327130-A 2 15-NOV-2002;
            TOSOH CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002327130-A/2
            PD   15-NOV-2002
            PF   11-JAN-2002 JP 2002005267
            PI   TAKUMI TOKUNAGA,TAKAHIKO ISHIGURO,RYUICHI HORIE PC
            C09B23/00,C07D417/14,C07H21/04,C09K11/06,C12N15/09,C12Q1/68, PC
            G01N33/58,
            PC   C12N15/00
            CC   dA30mer
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 464
AR051244
LOCUS       AR051244                30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5830658.
ACCESSION   AR051244
VERSION     AR051244.1  GI:5974608
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 12 03-NOV-1998;
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
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```
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 457
AX474673/c
LOCUS       AX474673                 30 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1 from Patent EP1223226.
ACCESSION   AX474673
VERSION     AX474673.1  GI:22214013
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
  TITLE     Novel fluorescent dye and method of measuring nucleic acid
  JOURNAL   Patent: EP 1223226-A 1 17-JUL-2002;
            Tosoh Corporation (JP)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificial"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 458
AX474674
LOCUS       AX474674                 30 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 2 from Patent EP1223226.
ACCESSION   AX474674
VERSION     AX474674.1  GI:22214014
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
  TITLE     Novel fluorescent dye and method of measuring nucleic acid
  JOURNAL   Patent: EP 1223226-A 2 17-JUL-2002;
            Tosoh Corporation (JP)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificial"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 459
AX521609/c
LOCUS       AX521609                 30 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 115 from Patent WO0222874.
ACCESSION   AX521609
VERSION     AX521609.1  GI:23572654
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Utermohlen,J.G. and Connaughton,J.
  TITLE     Oligonucleotides for labeling oligonucleotide probes and proteins
  JOURNAL   Patent: WO 0222874-A 115 21-MAR-2002;
            VENTANA MEDICAL SYSTEMS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide probe"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 460
BD105776
LOCUS       BD105776                 30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Conjugates of biologically stable polymers and polynucleotides for
            treating systemic lupus erythematosus.
ACCESSION   BD105776
VERSION     BD105776.1  GI:22651350
KEYWORDS    JP 2001354569-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Conrad,M.J. and Coutts,S.
  TITLE     Conjugates of biologically stable polymers and polynucleotides for
            treating systemic lupus erythematosus
  JOURNAL   Patent: JP 2001354569-A 1 25-DEC-2001;
            LA JOLLA PHARMACEUTICAL CO
COMMENT     OS   Artificial Sequence
            PN   JP 2001354569-A/1
            PD   25-DEC-2001
            PF   04-APR-2001 JP 2001106534
            PR   16-JAN-1990 US       466138,13-MAR-1990 US       494118 PI
            MICHAEL J CONRAD,STEPHEN COUTTS
            PC   A61K31/7088,A61K47/48,A61P37/02,C07K14/00,C12N15/00,C12N15/00
            CC   Synthetic Construct
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 461
BD132851/c
```

```
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 453
E04638/c
LOCUS       E04638                    30 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION  Synthesized Oligoribonucleotides of more than 20 mers.
ACCESSION   E04638
VERSION     E04638.1  GI:5708508
KEYWORDS    JP 1992330093-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Tanimura,H. and Imada,M.
  TITLE     PRODUCTION OF OLIGORIBONUCLEOTIDE
  JOURNAL   Patent: JP 1992330093-A 2 18-NOV-1992;
            TAKEDA CHEM IND LTD
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1992330093-A/2
            PD   18-NOV-1992
            PF   07-JUN-1991 JP 1991136086
            PR   20-JUL-1990 JP 90P   190762
            PI   TANIMURA HIROSHI, IMADA MICHI
            PC   C07H21/02;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   misc_feature    1. .30
            FT                   /note='suitably selected protection of RNA  FT
                              units
            FT                   facilitates 20 or more-mer oligonucleotides'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 454
I84450
LOCUS       I84450                    30 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 9 from patent US 5695936.
ACCESSION   I84450
VERSION     I84450.1  GI:3021970
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Mandrand,B., Cros,P., Delair,T., Charles,M.-H., Erout,M.-N. and
            Pichot,C.
  TITLE     Reagent and method for the detection of a nucleotide sequence with
            signal amplification
  JOURNAL   Patent: US 5695936-A 9 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 455
AX104902/c
LOCUS       AX104902                  30 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1094 from Patent WO0122972.
ACCESSION   AX104902
VERSION     AX104902.1  GI:13921099
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1094 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 456
AX104903
LOCUS       AX104903                  30 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1095 from Patent WO0122972.
ACCESSION   AX104903
VERSION     AX104903.1  GI:13921100
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1095 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 30;
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                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 448
A43784
LOCUS       A43784                    30 bp    DNA     linear   PAT 06-MAR-1997
DEFINITION  Sequence 9 from Patent WO9508000.
ACCESSION   A43784
VERSION     A43784.1  GI:2298962
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Mandrand,B., Cros,P., Delair,T., Charles,M., Erout,M. and Pichot,C.
  TITLE     REAGENT AND METHOD FOR THE DETECTION OF A NUCLEOTIDE SEQUENCE WITH
            SIGNAL AMPLIFICATION
  JOURNAL   Patent: WO 9508000-A 9 23-MAR-1995;
            BIO MERIEUX (FR)
COMMENT     Other publication CA 2149315 950323
            Other publication FR 2710075 950324.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 449
A62991/c
LOCUS       A62991                    30 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 3 from Patent WO9720068.
ACCESSION   A62991
VERSION     A62991.1  GI:3716863
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  JOURNAL   Patent: WO 9720068-A 3 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 450
A62995
LOCUS       A62995                    30 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 7 from Patent WO9720068.
ACCESSION   A62995
VERSION     A62995.1  GI:3716867
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  JOURNAL   Patent: WO 9720068-A 7 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 451
AR179066/c
LOCUS       AR179066                  30 bp    DNA     linear   PAT 16-MAY-2002
DEFINITION  Sequence 3 from patent US 6326143.
ACCESSION   AR179066
VERSION     AR179066.1  GI:20220621
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Orum,H. and Seeger,C.
  TITLE     Method for generating multiple double stranded nucleic acids
  JOURNAL   Patent: US 6326143-A 3 04-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 452
AR179070
LOCUS       AR179070                  30 bp    DNA     linear   PAT 16-MAY-2002
DEFINITION  Sequence 7 from patent US 6326143.
ACCESSION   AR179070
VERSION     AR179070.1  GI:20220625
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Orum,H. and Seeger,C.
  TITLE     Method for generating multiple double stranded nucleic acids
  JOURNAL   Patent: US 6326143-A 7 04-DEC-2001;
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            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Linker"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 444
AX052994
LOCUS       AX052994                 29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 10 from Patent WO0071749.
ACCESSION   AX052994
VERSION     AX052994.1  GI:12227096
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 10 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Puromycin-Linker"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 445
AX353685
LOCUS       AX353685                 29 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 5 from Patent WO0204656.
ACCESSION   AX353685
VERSION     AX353685.1  GI:18618749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wagner,P. and Polakowski,T.
  TITLE     Bio-probes and use thereof
  JOURNAL   Patent: WO 0204656-A 5 17-JAN-2002;
            Xzillion GmbH & CO.KG (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Linker mit Puromycin am 3'-Ende"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 446
AX662302
LOCUS       AX662302                 29 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 41 from Patent WO02059293.
ACCESSION   AX662302
VERSION     AX662302.1  GI:29163186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Forster,A.C. and Blacklow,S.C.
  TITLE     Process and compositions for peptide, protein and peptidomimetic
            synthesis
  JOURNAL   Patent: WO 02059293-A 41 01-AUG-2002;
            Forster, Anthony C. (US) ; Blacklow, Stephen C. (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="FROM SYNTHETIC DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 447
BD204968
LOCUS       BD204968                 29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein array enabling site specification.
ACCESSION   BD204968
VERSION     BD204968.1  GI:33014738
KEYWORDS    JP 2002510505-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Protein array enabling site specification
  JOURNAL   Patent: JP 2002510505-A 3 09-APR-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002510505-A/3
            PD   09-APR-2002
            PF   31-MAR-1999 JP 2000542484
            PR   03-APR-1998 US    60/080686
            PI   ROBERT G KUIMELIS,RICHARD WAGNER
            PC   C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
              G01N33/68,
            PC   C12N15/00
            CC   Oligonucleotide used for attaching puromycin
            FH   Key             Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
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RESULT 439
BD238387
LOCUS       BD238387                  29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238387
VERSION     BD238387.1  GI:33048157
KEYWORDS    JP 2002536025-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 5 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/5
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US    09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 440
AR279813
LOCUS       AR279813                  29 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518018.
ACCESSION   AR279813
VERSION     AR279813.1  GI:29714958
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 8 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 441
AR288232
LOCUS       AR288232                  29 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6537749.
ACCESSION   AR288232
VERSION     AR288232.1  GI:31675516
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Addressable protein arrays
  JOURNAL   Patent: US 6537749-A 3 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 442
AX048408/c
LOCUS       AX048408                  29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 7 from Patent WO0071747.
ACCESSION   AX048408
VERSION     AX048408.1  GI:12225572
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 7 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAAAAAAAAAAAA 4


RESULT 443
AX048409
LOCUS       AX048409                  29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 8 from Patent WO0071747.
ACCESSION   AX048409
VERSION     AX048409.1  GI:12225573
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 8 30-NOV-2000;
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DEFINITION  Sequence 911 from Patent WO0122972.
ACCESSION   AX104719
VERSION     AX104719.1  GI:13920916
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 911 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 435
AX355814/c
LOCUS       AX355814                  27 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 842 from Patent WO0197843.
ACCESSION   AX355814
VERSION     AX355814.1  GI:18620482
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 842 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide~phosphorothioate
                     backbone"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 436
AX547772/c
LOCUS       AX547772                  27 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 911 from Patent WO02053141.
ACCESSION   AX547772
VERSION     AX547772.1  GI:25812916
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 911 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 437
AR162080
LOCUS       AR162080                  29 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6258558.
ACCESSION   AR162080
VERSION     AR162080.1  GI:16229144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Method for selection of proteins using RNA-protein fusions
  JOURNAL   Patent: US 6258558-A 8 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 438
AR166605
LOCUS       AR166605                  29 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6281344.
ACCESSION   AR166605
VERSION     AR166605.1  GI:16241997
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Nucleic acid-protein fusion molecules and libraries
  JOURNAL   Patent: US 6281344-A 8 28-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
             | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26
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  TITLE     Monoclonal antibodies to the pur protein
  JOURNAL   Patent: US 5869622-A 15 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTT 2184
              | ||| |  ||||||||||||||||||
Db          1 TATCTGCAGTTTTTTTTTTTTTTTT 26


RESULT 430
AR098647/c
LOCUS       AR098647                 26 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 5 from patent US 6077668.
ACCESSION   AR098647
VERSION     AR098647.1  GI:12808413
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kool,E.T.
  TITLE     Highly sensitive multimeric nucleic acid probes
  JOURNAL   Patent: US 6077668-A 5 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||| ||||||   ||||
Db         26 TTTTTTTTTTTTGTTTTTTTTTTTG 1


RESULT 431
I24758
LOCUS       I24758                   26 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 21 from patent US 5545551.
ACCESSION   I24758
VERSION     I24758.1  GI:1604628
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Johnson,E.M. and Bergmann,A.D.
  TITLE     Cloning and expression of pur protein
  JOURNAL   Patent: US 5545551-A 21 13-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTT 2184
              | ||| |  ||||||||||||||||||
Db          1 TATCTGCAGTTTTTTTTTTTTTTTT 26


RESULT 432
AR204721/c
LOCUS       AR204721                 26 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 5 from patent US 6368802.
ACCESSION   AR204721
VERSION     AR204721.1  GI:21502120
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kool,E.T.
  TITLE     Circular DNA vectors for synthesis of RNA and DNA
  JOURNAL   Patent: US 6368802-A 5 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||| ||||||   ||||
Db         26 TTTTTTTTTTTTGTTTTTTTTTTTG 1


RESULT 433
E04985
LOCUS       E04985                   27 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence of 3'terminal fragment of ITR.
ACCESSION   E04985
VERSION     E04985.1  GI:2173180
KEYWORDS    JP 1993103673-A/79.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Sengu,K.Y. and Ito,S.
  TITLE     REPLICATION OF DNA
  JOURNAL   Patent: JP 1993103673-A 79 27-APR-1993;
            ARIZONA BOARD OF REGENTS
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1993103673-A/79
            PD   27-APR-1993
            PF   26-AUG-1991 JP 1991240525
            PI   SENGU KUU YUU, ITO SUMIYOSHI
            PC   C12N15/10,C12N15/11//C12Q1/68;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   misc_feature    1. .27
            FT                   /note='3'terminal fragment of ITR'.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 434
AX104719/c
LOCUS       AX104719                 27 bp    DNA     linear   PAT 30-APR-2001
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```
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 425
AX427154/c
LOCUS       AX427154                  26 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 3 from Patent WO0210374.
ACCESSION   AX427154
VERSION     AX427154.1  GI:21530535
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lin,S.L., Chuong,C.M. and Widelitz,R.B.
  TITLE     Gene silencing using mrna-cdna hybrids
  JOURNAL   Patent: WO 0210374-A 3 07-FEB-2002;
            UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Poly(dT)-26mer primer"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 426
AX528804/c
LOCUS       AX528804                  26 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 53 from Patent WO02059357.
ACCESSION   AX528804
VERSION     AX528804.1  GI:25172859
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Pedersen,M.L.
  TITLE     Assay and kit for analyzing gene expression
  JOURNAL   Patent: WO 02059357-A 53 01-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 427
A63569
LOCUS       A63569                    26 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 10 from Patent WO9720924.
ACCESSION   A63569
VERSION     A63569.1  GI:3717224
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
            AGENTS
  JOURNAL   Patent: WO 9720924-A 10 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTT 2181
              |||||| |  ||||||| ||||||||
Db          1 TTTTTTTGTTTTTTTGTTTTTTT 26


RESULT 428
AR010003
LOCUS       AR010003                  26 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 15 from patent US 5756684.
ACCESSION   AR010003
VERSION     AR010003.1  GI:3968808
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Johnson,E.M. and Bergemann,A.D.
  TITLE     Cloning and expression of PUR protein
  JOURNAL   Patent: US 5756684-A 15 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTT 2184
              | ||| |  ||||||||||||||||||
Db          1 TATCTGCAGTTTTTTTTTTTTTTTT 26


RESULT 429
AR034738
LOCUS       AR034738                  26 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 15 from patent US 5869622.
ACCESSION   AR034738
VERSION     AR034738.1  GI:5950343
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Johnson,E.M. and Bergemann,A.D.
```

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                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
              || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 420
I79494/c
LOCUS       I79494                  26 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 1 from patent US 5707807.
ACCESSION   I79494
VERSION     I79494.1  GI:3207784
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 1 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
              || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 421
AR263648/c
LOCUS       AR263648                26 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 7 from patent US 6331413.
ACCESSION   AR263648
VERSION     AR263648.1  GI:28075581
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Adler,D.A. and Sheppard,P.O.
  TITLE     Secreted salivary ZSIG63 Polypeptide
  JOURNAL   Patent: US 6331413-A 7 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
              || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 422
AR374073/c
LOCUS       AR374073                26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 38 from patent US 6605272.
ACCESSION   AR374073
VERSION     AR374073.1  GI:40076645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Methods of using zalpha11 ligand
  JOURNAL   Patent: US 6605272-A 38 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
              || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 423
AX106717/c
LOCUS       AX106717                26 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 9 from Patent WO0125444.
ACCESSION   AX106717
VERSION     AX106717.1  GI:13922378
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Presnell,S.R., Novak,J.E. and Gao,Z.
  TITLE     Human phosphodiesterase zcytor13
  JOURNAL   Patent: WO 0125444-A 9 12-APR-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC7764b"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
              || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 424
AR137712/c
LOCUS       AR137712                26 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 5 from patent US 6197554.
ACCESSION   AR137712
VERSION     AR137712.1  GI:14479221
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.
  TITLE     Method for generating full-length cDNA library from single cells
  JOURNAL   Patent: US 6197554-A 5 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .26
```

```
  AUTHORS   Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
  TITLE     Support for immobilizing nucleotide and process for producing the
  JCURNAL   Patent: WO 0155365-A 2 02-AUG-2001;
            TOYO KOHAN CO LTD,MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,
            KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0155365-A/2
            PD   02-AUG-2001
            PF   24-JAN-2001 WO 2001JP000443
            PR   27-JAN-2000 JP 00P   019301
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,KOJIRO  PI
            TAKAHASHI
            PC   C12N15/10,C07H21/04//G01N33/50,C12Q1/68
            CC   Support for immobilizing nucleotide and process for producing
            CC            the same
            FH   Key             Location/Qualifiers
            FT   source          1. .27
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 19.8;  DB 1;  Length 27;
  Best Local Similarity   91.3%;  Pred. No. 8e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||| || |
Db         23 TTTTTTTTTTTTTTTTTGAATT 1


RESULT 417
BD161932/c
LOCUS       BD161932                  27 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate.
ACCESSION   BD161932
VERSION     BD161932.1  GI:27867690
KEYWORDS    JP 2002191369-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
  TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate
  JOURNAL   Patent: JP 2002191369-A 9 09-JUL-2002;
            TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   JP 2002191369-A/9
            PD   09-JUL-2002
            PF   27-DEC-2000 JP 2000399573
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
            C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC   Method for
            carrying out thermal cycle of PCR using DNA- CC
            immobilized
            CC   substrate
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .27
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 19.8;  DB 1;  Length 27;
  Best Local Similarity   91.3%;  Pred. No. 8e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||| || |
Db         23 TTTTTTTTTTTTTTTTTGAATT 1


RESULT 418
AR174581/c
LOCUS       AR174581                  26 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 38 from patent US 6307024.
ACCESSION   AR174581
VERSION     AR174581.1  GI:17914901
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 38 23-OCT-2001;
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 7.8e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
              || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 419
BD248974/c
LOCUS       BD248974                  26 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel cytokine ZALPHA11 ligand.
ACCESSION   BD248974
VERSION     BD248974.1  GI:33058744
KEYWORDS    JP 2002537839-A/35.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Novel cytokine ZALPHA11 ligand
  JOURNAL   Patent: JP 2002537839-A 35 12-NOV-2002;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002537839-A/35
            PD   12-NOV-2002
            PF   09-MAR-2000 JP 2000603382
            PR   09-MAR-1999 US    09/264908,11-MAR-1999 US    09/265992 PR
            01-JUL-1999 US    60/142013
            PI   JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C  PI
            FOSTER,
            PI   RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
            PI   STACEY R DILLON,ANGELA K HAMMOND
            PC   C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
            PC   C07K14/53,
            PC   C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
             A61K37/02
            CC   Oligonucleotide primer ZC7764a
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .26
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```
ACCESSION   BD244864
VERSION     BD244864.1  GI:33054634
KEYWORDS    JP 2002532063-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 9 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/9
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 25;
  Best Local Similarity   91.3%;  Pred. No. 6.4e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAA 2188
             ||||||| ||||| |||||||||
Db         23 TTTTTTTCTTTTTGTTTTTTAA 1


RESULT 413
AX043282
LOCUS       AX043282                25 bp    DNA     linear   PAT 23-NOV-2000
DEFINITION  Sequence 848 from Patent WO0065088.
ACCESSION   AX043282
VERSION     AX043282.1  GI:11341890
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ulfendahl,P.J. and Wong,K.C.
  TITLE     Primers for identifying typing or classifying nucleic acids
  JOURNAL   Patent: WO 0065088-A 848 02-NOV-2000;
            Amersham Pharmacia Biotech AB (SE)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="DQA1 Heterozygote Primer Sequence"

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 25;
  Best Local Similarity   91.3%;  Pred. No. 6.4e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTGA 2194
             |||||||||||||||  |||||
Db          1 TTTTTTTTTTTTTTAGATTTGA 23


RESULT 414
AX338547
LOCUS       AX338547                26 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3 from Patent WO0188192.
ACCESSION   AX338547
VERSION     AX338547.1  GI:18128947
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Nicolaides,N.C., Sass,P.M., Grasso,L., Vogelstein,B. and
            Kinzler,K.W.
  TITLE     A method for generating hypermutable organisms
  JOURNAL   Patent: WO 0188192-A 3 22-NOV-2001;
            The Johns Hopkins UNiversity School of Medicine (US) ; Morphotek
            Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Sass, Philip, M. (US) ;
            Grasso, Luigi (US) ; Vogelstein, Bert (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Recombinant DNA"

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 26;
  Best Local Similarity   91.3%;  Pred. No. 7.2e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAA 2804
              || | ||||||||||||||||||
Db          1 ATGGCAAAAAAAAAAAAAAAAA 23


RESULT 415
AX711956/c
LOCUS       AX711956                27 bp    DNA     linear   PAT 12-MAY-2003
DEFINITION  Sequence 35 from Patent WO02103060.
ACCESSION   AX711956
VERSION     AX711956.1  GI:29787747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tuvemo,H.T., Frisk,G.E. and Yin,H.
  TITLE     Enterovirus nucleic acids
  JOURNAL   Patent: WO 02103060-A 35 27-DEC-2002;
            Innoventus Project AB (SE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 27;
  Best Local Similarity   81.5%;  Pred. No. 8e+02;
  Matches   22;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2804
              :| ||   ||||||||||||||||||
Db         27 BAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 416
BD097128/c
LOCUS       BD097128                27 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Support for immobilizing nucleotide and process for producing the
            same.
ACCESSION   BD097128
VERSION     BD097128.1  GI:22642702
KEYWORDS    WO 0155365-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
```

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          probe with a target
          CC             nucleic
          CC   acid.
          FH   Key             Location/Qualifiers
          FT   source          1. .30
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTCTTTTTTTT 29


RESULT 409
BD166129
LOCUS       BD166129                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166129
VERSION     BD166129.1  GI:27871941
KEYWORDS    JP 2002191372-A/109.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 109 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/109
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid,
            CC   and the base sequence was used as that of the probe. FH   Key
                   Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTGTTTTTTTT 29


RESULT 410
AR431313/c
LOCUS       AR431313                24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6651008.
ACCESSION   AR431313
VERSION     AR431313.1  GI:40193281
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 7 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 19.8;  DB 1;  Length 24;
  Best Local Similarity   91.3%;  Pred. No. 5.7e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2803
              ||| |||||||||||| ||||||
Db         24 AATAGAAAAAAAAAAACAAAAAA 2


RESULT 411
AX338548
LOCUS       AX338548                25 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4 from Patent WO0188192.
ACCESSION   AX338548
VERSION     AX338548.1  GI:18128948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Nicolaides,N.C., Sass,P.M., Grasso,L., Vogelstein,B. and
            Kinzler,K.W.
  TITLE     A method for generating hypermutable organisms
  JOURNAL   Patent: WO 0188192-A 4 22-NOV-2001;
            The Johns Hopkins UNiversity School of Medicine (US) ; Morphotek
            Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Sass, Philip, M. (US) ;
            Grasso, Luigi (US) ; Vogelstein, Bert (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Recombinant DNA"

  Query Match              0.7%;  Score 19.8;  DB 1;  Length 25;
  Best Local Similarity   91.3%;  Pred. No. 6.4e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
              || | ||||||||||||||||||
Db          1 ATGGCAAAAAAAAAAAAAAAAAA 23


RESULT 412
BD244864/c
LOCUS       BD244864                25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
```

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BD166028
LOCUS       BD166028                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166028
VERSION     BD166028.1  GI:27871840
KEYWORDS    JP 2002191372-A/8.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 8 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/8
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTT 29


RESULT 407
BD166032
LOCUS       BD166032                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166032
VERSION     BD166032.1  GI:27871844
KEYWORDS    JP 2002191372-A/12.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 12 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/12
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTCTTTTTTTTT 29


RESULT 408
BD166033
LOCUS       BD166033                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166033
VERSION     BD166033.1  GI:27871845
KEYWORDS    JP 2002191372-A/13.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 13 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/13
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
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            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTCTTTTTTTT 29


RESULT 404
BD166026
LOCUS       BD166026                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166026
VERSION     BD166026.1  GI:27871838
KEYWORDS    JP 2002191372-A/6.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 6 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/6
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 405
BD166027
LOCUS       BD166027                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166027
VERSION     BD166027.1  GI:27871839
KEYWORDS    JP 2002191372-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 7 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/7
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 406
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     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTT 29


RESULT 401
BD145028
LOCUS       BD145028                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145028
VERSION     BD145028.1  GI:27850786
KEYWORDS    JP 2002119291-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 9 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/9
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTT 29


RESULT 402
BD145032
LOCUS       BD145032                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145032
VERSION     BD145032.1  GI:27850790
KEYWORDS    JP 2002119291-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 13 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/13
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTCTTTTTTTTT 29


RESULT 403
BD145033
LOCUS       BD145033                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145033
VERSION     BD145033.1  GI:27850791
KEYWORDS    JP 2002119291-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 14 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/14
            PD   23-APR-2002
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ACCESSION   BD145025
VERSION     BD145025.1  GI:27850783
KEYWORDS    JP 2002119291-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 6 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/6
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .30
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 399
BD145026
LOCUS       BD145026                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145026
VERSION     BD145026.1  GI:27850784
KEYWORDS    JP 2002119291-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 7 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/7
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
     source         1. .30
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 400
BD145027
LOCUS       BD145027                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145027
VERSION     BD145027.1  GI:27850785
KEYWORDS    JP 2002119291-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 8 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/8
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES            Location/Qualifiers
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            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 5 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/5
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
             | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTGTTTTTTTT 29


RESULT 396
BD107500
LOCUS       BD107500                30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107500
VERSION     BD107500.1  GI:23202318
KEYWORDS    JP 2002000275-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 9 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/9
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
             | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTCTTTTTTTT 29


RESULT 397
BD107501
LOCUS       BD107501                30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107501
VERSION     BD107501.1  GI:23202319
KEYWORDS    JP 2002000275-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 10 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/10
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
             | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTCTTTTTTTT 29


RESULT 398
BD145025
LOCUS       BD145025                30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
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            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTTT 29


RESULT 393
BD107494
LOCUS       BD107494                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107494
VERSION     BD107494.1  GI:23202312
KEYWORDS    JP 2002000275-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 3 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/3
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTTT 29


RESULT 394
BD107495
LOCUS       BD107495                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107495
VERSION     BD107495.1  GI:23202313
KEYWORDS    JP 2002000275-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 4 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/4
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTTT 29


RESULT 395
BD107496
LOCUS       BD107496                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107496
VERSION     BD107496.1  GI:23202314
KEYWORDS    JP 2002000275-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
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FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
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                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTGTTTTTTTT 29


RESULT 390
BD072873
LOCUS       BD072873                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072873
VERSION     BD072873.1  GI:22618476
KEYWORDS    JP 2001286300-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 11 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/11
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTCTTTTTTTT 29


RESULT 391
BD072874
LOCUS       BD072874                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072874
VERSION     BD072874.1  GI:22618477
KEYWORDS    JP 2001286300-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 12 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/12
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                       examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                      labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTCTTTTTTTT 29


RESULT 392
BD107493
LOCUS       BD107493                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107493
VERSION     BD107493.1  GI:23202311
KEYWORDS    JP 2002000275-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 2 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/2
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KEYWORDS    JP 2001286300-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JCURNAL   Patent: JP 2001286300-A 5 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/5
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTTT 29


RESULT 388
BD072868
LOCUS       BD072868                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072868
VERSION     BD072868.1  GI:22618471
KEYWORDS    JP 2001286300-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 6 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/6
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTTT 29


RESULT 389
BD072869
LOCUS       BD072869                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072869
VERSION     BD072869.1  GI:22618472
KEYWORDS    JP 2001286300-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 7 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/7
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
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REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 8 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTT 29


RESULT 384
AR264928
LOCUS       AR264928                30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 12 from patent US 6492121.
ACCESSION   AR264928
VERSION     AR264928.1  GI:29693315
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 12 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTCTTTTTTTTT 29


RESULT 385
AR264929
LOCUS       AR264929                30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 13 from patent US 6492121.
ACCESSION   AR264929
VERSION     AR264929.1  GI:29693316
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 13 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTCTTTTTTTTT 29


RESULT 386
BD072866
LOCUS       BD072866                30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072866
VERSION     BD072866.1  GI:22618469
KEYWORDS    JP 2001286300-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 4 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/4
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542,  PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                    labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC                nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||
Db          2 TATATATTTTTTTTGTTTTTTTTTTT 29


RESULT 387
BD072867
LOCUS       BD072867                30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072867
VERSION     BD072867.1  GI:22618470
```

```
RESULT 379
BD274339/c
LOCUS       BD274339                  29 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION   BD274339
VERSION     BD274339.1  GI:33084107
KEYWORDS    JP 2002526030-A/306.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
  TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
  JOURNAL   Patent: JP 2002526030-A 306 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526030-A/306
            PD   20-AUG-2002
            PF   12-MAY-1999 JP 2000548510
            PR   12-MAY-1998 US    60/085092,12-MAY-1998 US    09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC   Description
            of Artificial Sequence: Novel Sequence FH   Key
            Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="synthetic construct"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 29;
  Best Local Similarity   82.1%;  Pred. No. 9e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              |||||||||||||||||| | ||  | |
Db         29 TTTTTTTTTTTTTTTTTTCAGTTCTACA 2


RESULT 380
AR264921
LOCUS       AR264921                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6492121.
ACCESSION   AR264921
VERSION     AR264921.1  GI:29693308
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 5 10-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 381
AR264922
LOCUS       AR264922                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 6 from patent US 6492121.
ACCESSION   AR264922
VERSION     AR264922.1  GI:29693309
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 6 10-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 382
AR264923
LOCUS       AR264923                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 7 from patent US 6492121.
ACCESSION   AR264923
VERSION     AR264923.1  GI:29693310
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 7 10-DEC-2002;
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 9.8e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 383
AR264924
LOCUS       AR264924                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6492121.
ACCESSION   AR264924
VERSION     AR264924.1  GI:29693311
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 20;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
             ||||||||||||||||||||
Db         20 GAAAAAAAAAAAAAAAAAAA 1


RESULT 375
AX708814/c
LOCUS       AX708814                  25 bp    DNA     linear   PAT 04-APR-2003
DEFINITION  Sequence 30 from Patent WO02095071.
ACCESSION   AX708814
VERSION     AX708814.1  GI:29564541
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plasterk,R.H.
  TITLE     Means and methods for identifying genes and proteins involved in
            the prevention and/or repair of a replication error
  JOURNAL   Patent: WO 02095071-A 30 28-NOV-2002;
            Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="sequence to demonstrate the principle of how to
                     detect somatic repeat instability~##N# stands for any
                     number of nucleotides seleted from A, C, T or G#"

  Query Match              0.7%;  Score 20;  DB 1;  Length 25;
  Best Local Similarity   95.2%;  Pred. No. 5.9e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
             ||| ||||||||||||||||||
Db         25 TTTNTTTTTTTTTTTTTTTT 5


RESULT 376
AR142409
LOCUS       AR142409                  27 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 16 from patent US 6174992.
ACCESSION   AR142409
VERSION     AR142409.1  GI:15102709
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Ni,J., Yu,G.-L. and Gentz,R.
  TITLE     Human endometrial specific steroid-binding factor I, II and III
  JOURNAL   Patent: US 6174992-A 16 16-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 20;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTT 2183
             ||||||||||||||||||||
Db          8 CCTTTTTTTTTTTTTTTTTT 27


RESULT 377
AR182555
LOCUS       AR182555                  27 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 16 from patent US 6338948.
ACCESSION   AR182555
VERSION     AR182555.1  GI:20225762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Ni,J., Yu,G.-L. and Gentz,R.
  TITLE     Human endometrial specific steroid-binding factor I, II and III
  JOURNAL   Patent: US 6338948-A 16 15-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 20;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTT 2183
             ||||||||||||||||||||
Db          8 CCTTTTTTTTTTTTTTTTTT 27


RESULT 378
BD274321/c
LOCUS       BD274321                  29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION   BD274321
VERSION     BD274321.1  GI:33084089
KEYWORDS    JP 2002526030-A/288.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
  TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
  JOURNAL   Patent: JP 2002526030-A 288 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526030-A/288
            PD   20-AUG-2002
            PF   12-MAY-1999 JP 2000548510
            PR   12-MAY-1998 US    60/085092,12-MAY-1998 US    09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC   Description
            of Artificial Sequence: Novel Sequence FH   Key
            Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 29;
  Best Local Similarity   82.1%;  Pred. No. 9e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
             |||||||||||||||||| | ||  | |
Db         29 TTTTTTTTTTTTTTTTTTCAGTTCTACA 2
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                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         21 GAAAAAAAAAAAAAAAAAAA 2

RESULT 372
BD087491/c
LOCUS       BD087491                  21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis.
ACCESSION   BD087491
VERSION     BD087491.1  GI:22633101
KEYWORDS    JP 2001525193-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
            Edman,C.F.
  TITLE     Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis
  JOURNAL   Patent: JP 2001525193-A 2 11-DEC-2001;
            NANOGEN INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001525193-A/2
            PD   11-DEC-2001
            PF   01-DEC-1998 JP 2000524303
            PR   05-DEC-1997 US    08/986065
            PI   RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I  PI
            NERENBERG,
            PI   MICHAEL J HELLER,CARL F EDMAN
            PC   C12Q1/68,C12N15/09,C12N15/00
            CC   Description of Artificial Sequence: Synthesized with u at 3'
            CC            terminus to
            CC   provide ribonucleic acid base for reactivity; Poly A sequence
            CC            for reduced
            CC   secondary structure
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 373
AR241846/c
LOCUS       AR241846                  24 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 134 from patent US 6472154.
ACCESSION   AR241846
VERSION     AR241846.1  GI:27287658
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 134 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 5.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         24 GAAAAAAAAAAAAAAAAAAA 5

RESULT 374
E13209/c
LOCUS       E13209                    24 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  DNA probe.
ACCESSION   E13209
VERSION     E13209.1  GI:3252014
KEYWORDS    JP 1997149799-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Kanbara,H., Okano,K. and Uematsu,K.
  TITLE     ANALYSIS OR DETECTION OF NUCLEIC ACID AND ANALYSER OR INSPECTION
            DEVICE OF NUCLEIC ACID
  JOURNAL   Patent: JP 1997149799-A 1 10-JUN-1997;
            HITACHI LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997149799-A/1
            PD   10-JUN-1997
            PF   30-NOV-1995 JP 1995311949
            PI   KANBARA HIDEKI, OKANO KAZUNOBU, UEMATSU KAZUMUNE PC
            C12Q1/68,C07H21/04,C12M1/00,C12N15/09,C12Q1/44,C12Q1/48, PC
            G01N27/447,
            PC   G01N27/447,G01N33/50;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .24
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .24
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                     /mod_base=OTHER
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                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         20 GAAAAAAAAAAAAAAAAAAA 1


RESULT 369
AX825164
LOCUS       AX825164                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 62 from Patent WO03072818.
ACCESSION   AX825164
VERSION     AX825164.1  GI:39750893
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 62 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 370
AX825165
LOCUS       AX825165                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 63 from Patent WO03072818.
ACCESSION   AX825165
VERSION     AX825165.1  GI:39750894
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 63 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 371
AX825165/c
LOCUS       AX825165                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 63 from Patent WO03072818.
ACCESSION   AX825165
VERSION     AX825165.1  GI:39750894
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 63 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTA 20


RESULT 366
AX825160/c
LOCUS       AX825160                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 58 from Patent WO03072818.
ACCESSION   AX825160
VERSION     AX825160.1  GI:39750889
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 58 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match              0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         20 GAAAAAAAAAAAAAAAAAAA 1


RESULT 367
AX825161/c
LOCUS       AX825161                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 59 from Patent WO03072818.
ACCESSION   AX825161
VERSION     AX825161.1  GI:39750890
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 59 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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                     /note="LNA-T (Locked Nucleic Acid)"
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  Query Match              0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         20 GAAAAAAAAAAAAAAAAAAA 1


RESULT 368
AX825162/c
LOCUS       AX825162                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 60 from Patent WO03072818.
ACCESSION   AX825162
VERSION     AX825162.1  GI:39750891
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 60 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
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Db         20 TGAAAAAAAAAAAAAAAAA 1


RESULT 363
AX825152
LOCUS       AX825152                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 50 from Patent WO03072818.
ACCESSION   AX825152
VERSION     AX825152.1  GI:39750881
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 50 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTA 20


RESULT 364
AX825153
LOCUS       AX825153                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 51 from Patent WO03072818.
ACCESSION   AX825153
VERSION     AX825153.1  GI:39750882
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 51 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTA 20


RESULT 365
AX825154
LOCUS       AX825154                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 52 from Patent WO03072818.
ACCESSION   AX825154
VERSION     AX825154.1  GI:39750883
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 52 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 34 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||||
Db         20 TGAAAAAAAAAAAAAAAAAA 1


RESULT 361
AX825137/c
LOCUS       AX825137                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 35 from Patent WO03072818.
ACCESSION   AX825137
VERSION     AX825137.1  GI:39750866
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 35 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
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     modified_base   15
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                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
              ||||||||||||||||||||
Db         20 TGAAAAAAAAAAAAAAAAAA 1


RESULT 362
AX825138/c
LOCUS       AX825138                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 36 from Patent WO03072818.
ACCESSION   AX825138
VERSION     AX825138.1  GI:39750867
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 36 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
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     modified_base   12
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     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2803
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                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
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     modified_base   12
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                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTAA 20


RESULT 358
AX825104
LOCUS       AX825104                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 2 from Patent WO03072818.
ACCESSION   AX825104
VERSION     AX825104.1  GI:39750833
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 2 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTAA 20


RESULT 359
AX825106
LOCUS       AX825106                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 4 from Patent WO03072818.
ACCESSION   AX825106
VERSION     AX825106.1  GI:39750835
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 4 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTAA 20


RESULT 360
AX825136/c
LOCUS       AX825136                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 34 from Patent WO03072818.
ACCESSION   AX825136
VERSION     AX825136.1  GI:39750865
KEYWORDS    .
```

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          CC   Description of Artificial Sequence:primer
          FH   Key             Location/Qualifiers
          FT   source          1. .20
          FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 354
BD218101/c
LOCUS       BD218101                  20 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Compositions derived from mycobacterium vaccae and methods for
            their use.
ACCESSION   BD218101
VERSION     BD218101.1  GI:33027871
KEYWORDS    JP 2002514385-A/26.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tan,P., Watson,J., Visser,E.S., Skinner,M.A. and Prestid,R.L.
  TITLE     Compositions derived from mycobacterium vaccae and methods for
            their
  JOURNAL   Patent: JP 2002514385-A 26 21-MAY-2002;
            GENESIS RESEARCH AND DEVELOPMENT CORP LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002514385-A/26
            PD   21-MAY-2002
            PF   23-DEC-1998 JP 2000525553
            PR   23-DEC-1997 US    08/997362,23-DEC-1997 US    08/997080 PR
            23-DEC-1997 US    08/996624,11-JUN-1998 US    09/095855 PR
            17-SEP-1998 US    09/156181,04-DEC-1998 US    09/205426 PI   PAUL
            TAN,JAMES WATSON,ELIZABETH S VISSER,MARGOT A SKINNER,ROSS
            PI   L PRESTIDGE
            PC   C12N15/09,A61K31/711,A61K39/04,A61K48/00,A61P11/00,A61P11/06,
            PC   A61P17/00,
            PC   A61P17/06,A61P31/00,A61P31/06,A61P37/04,C07K14/35,C07K16/12,
            PC   C07K19/00,
            PC   C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/02,G01N33/569, PC
            G01N33/68//
            PC   (C12N15/09,C12R1:32),C12N15/00,C12N5/00,(C12N15/00,C12R1:32)
            CC   Made in a lab
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 355
AR153849/c
LOCUS       AR153849                  21 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6238624.
ACCESSION   AR153849
VERSION     AR153849.1  GI:15121902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
  TITLE     Methods for transport in molecular biological analysis and
            diagnostics
  JOURNAL   Patent: US 6238624-A 2 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 356
I36166/c
LOCUS       I36166                    21 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 2 from patent US 5605662.
ACCESSION   I36166
VERSION     I36166.1  GI:2086679
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Heller,M.J. and Tu,E.
  TITLE     Active programmable electronic devices for molecular biological
            analysis and diagnostics
  JOURNAL   Patent: US 5605662-A 2 25-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 357
AX825103
LOCUS       AX825103                  21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 1 from Patent WO03072818.
ACCESSION   AX825103
VERSION     AX825103.1  GI:39750832
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 1 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
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Db          1 TTTTTTTTTTTTTTTTTTT 20


RESULT 350
AX741052/c
LOCUS       AX741052                  20 bp    DNA     linear   PAT 10-MAY-2003
DEFINITION  Sequence 26 from Patent WO03027328.
ACCESSION   AX741052
VERSION     AX741052.1  GI:30523913
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
  TITLE     Methods, kits and compositions pertaining to the suppression of
            detectable probe binding to randomly distributed repeat sequences
            in genomic nucleic acid
  JOURNAL   Patent: WO 03027328-A 26 03-APR-2003;
            Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule:Synthetic
                     Oligomer Sequence~Synthetic Probe Sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 351
BD008523/c
LOCUS       BD008523                  20 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Compounds and methods for treatment and diagnosis of Mycobacterial
            infections.
ACCESSION   BD008523
VERSION     BD008523.1  GI:18636896
KEYWORDS    JP 2001503969-A/26.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tan,P., Hiyama,J., Visser,E.S., Skinner,M.A., Scott,L.M. and
            Prestidge,R.L.
  TITLE     Compounds and methods for treatment and diagnosis of Mycobacterial
            infections
  JOURNAL   Patent: JP 2001503969-A 26 27-MAR-2001;
            GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT     OS   Unidentified
            PN   JP 2001503969-A/26
            PD   27-MAR-2001
            PF   28-AUG-1997 JP 1998511516
            PR
            PI   PAUL TAN,JUN HIYAMA,ELIZABETH S VISSER,MARGOT A SKINNER, PI
            LINDA M SCOTT,
            PI   ROSS L PRESTIDGE
            PC   A61K39/04,A61K35/74,C07K14/35,C12N15/63
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 352
BD080522
LOCUS       BD080522                  20 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Ribonucleoside-derivative and method for preparing the same.
ACCESSION   BD080522
VERSION     BD080522.1  GI:22626125
KEYWORDS    JP 2001515087-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Pitsch,S., Weiss,P.A. and Jenny,L.
  TITLE     Ribonucleoside-derivative and method for preparing the same
  JOURNAL   Patent: JP 2001515087-A 1 18-SEP-2001;
            STEFAN PITSCH,PATRICK A WEISS,LUZI JENNY
COMMENT     OS   Artificial Sequence
            PN   JP 2001515087-A/1
            PD   18-SEP-2001
            PF   17-AUG-1998 JP 2000509723
            PR   18-AUG-1997 CH      1931/97
            PI   STEFAN PITSCH,PATRICK A WEISS,LUZI JENNY
            PC   C07H19/06,C07F7/18,C07H19/16,C07H21/02,C07H23/00 CC
            Description of Artificial Sequence:synthetic polynucleotide FH
            Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 20


RESULT 353
BD107450
LOCUS       BD107450                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method of detecting single base polymorphism.
ACCESSION   BD107450
VERSION     BD107450.1  GI:23202268
KEYWORDS    JP 2002034599-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Segawa,M., Takarada,H., Aono,T. and Yoshiga,S.
  TITLE     Method of detecting single base polymorphism
  JOURNAL   Patent: JP 2002034599-A 9 05-FEB-2002;
            TOYOBO CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002034599-A/9
            PD   05-FEB-2002
            PF   26-JUL-2000 JP 2000225354
            PI   MASAYA SEGAWA,HIROSHI TAKARADA,TOSHIYA AONO,SATOKO YOSHIGA PC
             C12Q1/68,C12N15/09,C12N15/00
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  JOURNAL   Patent: WO 0246472-A 55 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 346
AX556139/c
LOCUS       AX556139                 20 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 70 from Patent WO0246472.
ACCESSION   AX556139
VERSION     AX556139.1  GI:25899521
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 70 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 347
AX664307/c
LOCUS       AX664307                 20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 5 from Patent WO0246398.
ACCESSION   AX664307
VERSION     AX664307.1  GI:29164237
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Willson,R.C. and Murphy,J.C.
  TITLE     Nucleic acid separation using immobilized metal affinity
            chromatography
  JOURNAL   Patent: WO 0246398-A 5 13-JUN-2002;
            The University of Houston System (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 348
AX664308
LOCUS       AX664308                 20 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 6 from Patent WO0246398.
ACCESSION   AX664308
VERSION     AX664308.1  GI:29164238
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Willson,R.C. and Murphy,J.C.
  TITLE     Nucleic acid separation using immobilized metal affinity
            chromatography
  JOURNAL   Patent: WO 0246398-A 6 13-JUN-2002;
            The University of Houston System (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotide Sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 349
AX741040
LOCUS       AX741040                 20 bp    DNA     linear   PAT 10-MAY-2003
DEFINITION  Sequence 14 from Patent WO03027328.
ACCESSION   AX741040
VERSION     AX741040.1  GI:30523901
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kirtsen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
  TITLE     Methods, kits and compositions pertaining to the suppression of
            detectable probe binding to randomly distributed repeat sequences
            in genomic nucleic acid
  JOURNAL   Patent: WO 03027328-A 14 03-APR-2003;
            Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule:Synthetic
                     Oligomer Sequence~Synthetic Probe Sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
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Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 341
AX465326/c
LOCUS       AX465326                 20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 70 from Patent WO0218643.
ACCESSION   AX465326
VERSION     AX465326.1  GI:21899689
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0218643-A 70 07-MAR-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 342
AX547087
LOCUS       AX547087                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 226 from Patent WO02053141.
ACCESSION   AX547087
VERSION     AX547087.1  GI:25812231
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 226 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 343
AX547417
LOCUS       AX547417                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 556 from Patent WO02053141.
ACCESSION   AX547417
VERSION     AX547417.1  GI:25812561
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 556 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 344
AX547421/c
LOCUS       AX547421                 20 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 560 from Patent WO02053141.
ACCESSION   AX547421
VERSION     AX547421.1  GI:25812565
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 560 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 345
AX556124/c
LOCUS       AX556124                 20 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 55 from Patent WO0246472.
ACCESSION   AX556124
VERSION     AX556124.1  GI:25899506
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
```

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            cancer
  JOURNAL   Patent: WO 0197843-A 838 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 337
AX355811
LOCUS       AX355811                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 839 from Patent WO0197843.
ACCESSION   AX355811
VERSION     AX355811.1  GI:18620479
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 839 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphodiester backbone"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 338
AX440125/c
LOCUS       AX440125                  20 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 55 from Patent WO0173123.
ACCESSION   AX440125
VERSION     AX440125.1  GI:21664936
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0173123-A 55 04-OCT-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 339
AX440140/c
LOCUS       AX440140                  20 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 70 from Patent WO0173123.
ACCESSION   AX440140
VERSION     AX440140.1  GI:21664951
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0173123-A 70 04-OCT-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 340
AX465311/c
LOCUS       AX465311                  20 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 55 from Patent WO0218643.
ACCESSION   AX465311
VERSION     AX465311.1  GI:21899674
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0218643-A 55 07-MAR-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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                    ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 332
AX104368/c
LOCUS       AX104368                  20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 560 from Patent WO0122972.
ACCESSION   AX104368
VERSION     AX104368.1  GI:13920565
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 560 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
                ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 333
AX196224/c
LOCUS       AX196224                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 55 from Patent WO0151665.
ACCESSION   AX196224
VERSION     AX196224.1  GI:15386427
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0151665-A 55 19-JUL-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
                ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 334
AX196239/c
LOCUS       AX196239                  20 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 70 from Patent WO0151665.
ACCESSION   AX196239
VERSION     AX196239.1  GI:15386442
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0151665-A 70 19-JUL-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
                ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 335
AX354974/c
LOCUS       AX354974                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 2 from Patent WO0197843.
ACCESSION   AX354974
VERSION     AX354974.1  GI:18619641
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 2 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphodiester backbone"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
                ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 336
AX355810
LOCUS       AX355810                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 838 from Patent WO0197843.
ACCESSION   AX355810
VERSION     AX355810.1  GI:18620478
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
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           CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
           FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"
     misc_feature    1
                     /note="modified with digoxigenin"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 328
AX045787
LOCUS       AX045787                 20 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 17 from Patent WO0067023.
ACCESSION   AX045787
VERSION     AX045787.1  GI:11344154
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Noll,B.O., Schetter,C. and Krieg,A.M.
  TITLE     Screening for immunostimulatory dna functional modifyers
  JOURNAL   Patent: WO 0067023-A 17 09-NOV-2000;
            CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
            FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"
     misc_feature    1. .20
                     /note="phosphorothioate backbone"
     misc_feature    1
                     /note="modified with digoxigenin"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 329
AX045790
LOCUS       AX045790                 20 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 20 from Patent WO0067023.
ACCESSION   AX045790
VERSION     AX045790.1  GI:11344157
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Noll,B.O., Schetter,C. and Krieg,A.M.
  TITLE     Screening for immunostimulatory dna functional modifyers
  JOURNAL   Patent: WO 0067023-A 20 09-NOV-2000;
            CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
            FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 330
AX104034
LOCUS       AX104034                 20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 226 from Patent WO0122972.
ACCESSION   AX104034
VERSION     AX104034.1  GI:13920231
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 226 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 331
AX104364
LOCUS       AX104364                 20 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 556 from Patent WO0122972.
ACCESSION   AX104364
VERSION     AX104364.1  GI:13920561
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 556 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
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                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 323
AR365970/c
LOCUS       AR365970                  20 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 83 from patent US 6328978.
ACCESSION   AR365970
VERSION     AR365970.1  GI:34598223
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watson,J.D., Tan,P.L.J. and Prestidge,R.
  TITLE     Methods for the treatment of immunologically-mediated skin
            disorders
  JOURNAL   Patent: US 6328978-A 83 11-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 324
AR382312/c
LOCUS       AR382312                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 55 from patent US 6610491.
ACCESSION   AR382312
VERSION     AR382312.1  GI:40090724
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6610491-A 55 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 325
AR429653/c
LOCUS       AR429653                  20 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 55 from patent US 6645721.
ACCESSION   AR429653
VERSION     AR429653.1  GI:40189949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6645721-A 55 11-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 326
AX004876
LOCUS       AX004876                  20 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 5 from Patent WO9910527.
ACCESSION   AX004876
VERSION     AX004876.1  GI:9928276
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bayer,E. and Schewitz,J.
  TITLE     Method for isolating anionic organic substances from aqueous
            systems using cationic polymer nanoparticles
  JOURNAL   Patent: WO 9910527-A 5 04-MAR-1999;
            SUEDDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="phosphorthioate oligonucleotide"

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 20


RESULT 327
AX045779
LOCUS       AX045779                  20 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 9 from Patent WO0067023.
ACCESSION   AX045779
VERSION     AX045779.1  GI:11344146
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Noll,B.O., Schetter,C. and Krieg,A.M.
  TITLE     Screening for immunostimulatory dna functional modifyers
  JOURNAL   Patent: WO 0067023-A 9 09-NOV-2000;
```

```
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 318
AR222466/c
LOCUS       AR222466                 20 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 26 from patent US 6429300.
ACCESSION   AR222466
VERSION     AR222466.1  GI:23329997
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 26 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 319
AR236083
LOCUS       AR236083                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6462184.
ACCESSION   AR236083
VERSION     AR236083.1  GI:27279782
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6462184-A 1 08-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 20


RESULT 320
AR274394/c
LOCUS       AR274394                 20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 55 from patent US 6506564.
ACCESSION   AR274394
VERSION     AR274394.1  GI:29706840
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6506564-A 55 14-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 321
AR343047
LOCUS       AR343047                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 10 from patent US 6576752.
ACCESSION   AR343047
VERSION     AR343047.1  GI:33738375
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Manoharan,M., Lonnberg,H., Salo,H. and Virta,P.
  TITLE     Aminooxy functionalized oligomers
  JOURNAL   Patent: US 6576752-A 10 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 20


RESULT 322
AR344936/c
LOCUS       AR344936                 20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 55 from patent US 6582921.
ACCESSION   AR344936
VERSION     AR344936.1  GI:33741017
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            thereof
  JOURNAL   Patent: US 6582921-A 55 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
```

```
VERSION     AR154115.1  GI:15122168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Huang,Z. and Szostak,J.W.
  TITLE     Simple and efficient method to label and modify 3'-termini of RNA
            using DNA polymerase and a synthetic template with defined overhang
            nucleotides
  JOURNAL   Patent: US 6238865-A 14 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 314
AR164658/c
LOCUS       AR164658                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 13 from patent US 6274321.
ACCESSION   AR164658
VERSION     AR164658.1  GI:16237754
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Blumberg,B.
  TITLE     High throughput functional screening of cDNAs
  JOURNAL   Patent: US 6274321-A 13 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 315
E12676
LOCUS       E12676                    20 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Anti-HTLV-1 antisense oligonucleotide.
ACCESSION   E12676
VERSION     E12676.1  GI:3251508
KEYWORDS    JP 1997052898-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Mizuguchi,M., Kurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.
  TITLE     ANTI-HTLV-I ANTI-SENSE OLIGONUCLEOTIDE
  JOURNAL   Patent: JP 1997052898-A 10 25-FEB-1997;
            SOYAKU GIJUTSU KENKYUSHO:KK
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1997052898-A/10
            PD   25-FEB-1997
            PF   09-AUG-1995 JP 1995224606
            PI   MIZUGUCHI MASATSUGU, KUROSAKI NAOKO, MAKINO KEISUKE, PI
            KOYANAGI YOSHIO,
            PI   YAMAMOTO NAOKI
            PC   C07H21/04//A61K31/70;
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            CC   anti-sense: Yes;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .20
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 316
I36180
LOCUS       I36180                    20 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 16 from patent US 5605662.
ACCESSION   I36180
VERSION     I36180.1  GI:2086693
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Heller,M.J. and Tu,E.
  TITLE     Active programmable electronic devices for molecular biological
            analysis and diagnostics
  JOURNAL   Patent: US 5605662-A 16 25-FEB-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 317
AR213738/c
LOCUS       AR213738                  20 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 83 from patent US 6406704.
ACCESSION   AR213738
VERSION     AR213738.1  GI:23311025
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tan,P., Visser,E., Prestidge,R. and Watson,J.D.
  TITLE     Compounds and methods for treatment and diagnosis of mycobacterial
            infections
  JOURNAL   Patent: US 6406704-A 83 18-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
```

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AR093312/c
LOCUS       AR093312                20 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 83 from patent US 6001361.
ACCESSION   AR093312
VERSION     AR093312.1  GI:10020062
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tan,P., Hiyama,J., Visser,E., Skinner,M., Scott,L. and Prestidge,R.
  TITLE     Mycobacterium vaccae antigens
  JOURNAL   Patent: US 6001361-A 83 14-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 309
AR118970
LOCUS       AR118970                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 96 from patent US 6150092.
ACCESSION   AR118970
VERSION     AR118970.1  GI:14100880
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
  TITLE     Antisense nucleic acid compound targeted to VEGF
  JOURNAL   Patent: US 6150092-A 96 21-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 310
AR121692/c
LOCUS       AR121692                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 83 from patent US 6160093.
ACCESSION   AR121692
VERSION     AR121692.1  GI:14105268
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Visser,E.
  TITLE     Compounds and methods for treatment and diagnosis of mycobacterial
            infections
  JOURNAL   Patent: US 6160093-A 83 12-DEC-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 311
AR123335/c
LOCUS       AR123335                20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 1 from patent US 6169176.
ACCESSION   AR123335
VERSION     AR123335.1  GI:14108301
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bruice,T.C. and Dev,A.P.
  TITLE     Deoxynucleic alkyl thiourea compounds and uses thereof
  JOURNAL   Patent: US 6169176-A 1 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 312
AR141070
LOCUS       AR141070                20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6207819.
ACCESSION   AR141070
VERSION     AR141070.1  GI:14483566
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Manoharan,M. and Maier,M.A.
  TITLE     Compounds, processes and intermediates for synthesis of mixed
            backbone oligomeric compounds
  JOURNAL   Patent: US 6207819-A 1 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 313
AR154115
LOCUS       AR154115                20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 14 from patent US 6238865.
ACCESSION   AR154115
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Db         31 TTTTTTTTTTTTTTTTTTCAGTTCG 7


RESULT 303
AR279820/c
LOCUS       AR279820                  33 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 15 from patent US 6518018.
ACCESSION   AR279820
VERSION     AR279820.1  GI:29714965
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 15 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 33;
  Best Local Similarity   88.0%;  Pred. No. 1.2e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTG 2193
             |||||||||||||||||| | || |
Db         31 TTTTTTTTTTTTTTTTTTCAGTTCG 7


RESULT 304
AR064875
LOCUS       AR064875                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5849480.
ACCESSION   AR064875
VERSION     AR064875.1  GI:5995091
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cros,P., Kurfurst,R., Battail,N. and Piga,N.
  TITLE     Process and device for assaying a hapten
  JOURNAL   Patent: US 5849480-A 5 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 305
AR080000/c
LOCUS       AR080000                  20 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 83 from patent US 5968524.
ACCESSION   AR080000
VERSION     AR080000.1  GI:10006735
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Watson,J.D. and Tan,P.L.J.
  TITLE     Methods and compounds for the treatment of immunologically-mediated
            psoriasis
  JOURNAL   Patent: US 5968524-A 83 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 306
AR085926/c
LOCUS       AR085926                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 83 from patent US 5985287.
ACCESSION   AR085926
VERSION     AR085926.1  GI:10012692
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Tan,P., Skinner,M. and Prestidge,R.
  TITLE     Compounds and methods for treatment and diagnosis of mycobacterial
            infections
  JOURNAL   Patent: US 5985287-A 83 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 307
AR087520
LOCUS       AR087520                  20 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from patent US 5986084.
ACCESSION   AR087520
VERSION     AR087520.1  GI:10014283
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Pitsch,S., Weiss,P.A. and Jenny,L.
  TITLE     Ribonucleoside-derivative and method for preparing the same
  JOURNAL   Patent: US 5986084-A 1 16-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 308
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6518045-A 23 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||   ||||||||||||||||||
Db          6 TCTCGAGTTTTTTTTTTTTTTTTT 30


RESULT 299
AR322431
LOCUS       AR322431                30 bp    mRNA    linear   PAT 17-AUG-2003
DEFINITION  Sequence 23 from patent US 6566097.
ACCESSION   AR322431
VERSION     AR322431.1  GI:33708184
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6566097-A 23 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||   ||||||||||||||||||
Db          6 TCTCGAGTTTTTTTTTTTTTTTTT 30


RESULT 300
AR409723
LOCUS       AR409723                30 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 85 from patent US 6632981.
ACCESSION   AR409723
VERSION     AR409723.1  GI:40160700
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Meins,F. Jr., Shinshi,H., Wenzler,H.C., Hofsteenge,J., Ryals,J.A.
            and Sperisen,C.
  TITLE     DNA sequences encoding polypeptides having beta-1,3-glucanase
            activity
  JOURNAL   Patent: US 6632981-A 85 14-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 301
AR222454
LOCUS       AR222454                32 bp    RNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 14 from patent US 6429300.
ACCESSION   AR222454
VERSION     AR222454.1  GI:23329985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 14 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 32;
  Best Local Similarity   88.0%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||  ||||||||||||||||||
Db          5 GGATGCAAAAAAAAAAAAAAAAAAA 29


RESULT 302
BD238394/c
LOCUS       BD238394                33 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238394
VERSION     BD238394.1  GI:33048164
KEYWORDS    JP 2002536025-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 12 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/12
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US    09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
            FT   source          1. .33
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 33;
  Best Local Similarity   88.0%;  Pred. No. 1.2e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||||||| | || |
```

```
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
            Friedrich,L.B., Harms,C., Meins,F. Jr., Montoya,A. deceased,
            Moyer,M.B., Neuhaus,J.-M., Payne,G.B., Sperisen,C., Stinson,J.R.,
            Uknes,S.J., Ward,E.R. and Williams,S.C.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL   Patent: US 5614395-A 85 25-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| |||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAAACATA 28


RESULT 294
I56982
LOCUS       I56982                    30 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 85 from patent US 5650505.
ACCESSION   I56982
VERSION     I56982.1  GI:2477395
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Alexander,D.C., Beck,J.J., Duesing,J.H., Goodman,R.M.,
            Friedrich,L.B., Harms,C., Meins,F. Jr., Montoya,A. deceased,
            Moyer,M.B., Neuhaus,J.-M., Payne,G.B., Sperisen,C., Stinson,J.R.,
            Uknes,S.J., Ward,E.R. and Williams,S.C.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL   Patent: US 5650505-A 85 22-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| |||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAAACATA 28


RESULT 295
I59848
LOCUS       I59848                    30 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 85 from patent US 5654414.
ACCESSION   I59848
VERSION     I59848.1  GI:2478480
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Beck,J.J. and Friedrich,L.B.
  TITLE     Chemically inducible promoter of a cucumber chitinase/lysozyme gene
  JOURNAL   Patent: US 5654414-A 85 05-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| |||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAAACATA 28


RESULT 296
I75175
LOCUS       I75175                    30 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 85 from patent US 5689044.
ACCESSION   I75175
VERSION     I75175.1  GI:3011316
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
  TITLE     Chemically inducible promoter of a plant PR-1 gene
  JOURNAL   Patent: US 5689044-A 85 18-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| |||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAAACATA 28


RESULT 297
AR242448
LOCUS       AR242448                  30 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 23 from patent US 6472509.
ACCESSION   AR242448
VERSION     AR242448.1  GI:27288865
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Imamura,T., Maeda,H., Fujiyasu,T., Imagawa,Y. and Tokiyoshi,S.
  TITLE     Feline cytokine protein
  JOURNAL   Patent: US 6472509-A 23 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="mRNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||   ||||||||||||||||||
Db          6 TCTCGAGTTTTTTTTTTTTTTTTT 30


RESULT 298
AR280216
LOCUS       AR280216                  30 bp    mRNA    linear   PAT 10-APR-2003
DEFINITION  Sequence 23 from patent US 6518045.
ACCESSION   AR280216
VERSION     AR280216.1  GI:29715606
```

```
ACCESSION   AR020878
VERSION     AR020878.1  GI:3975493
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Friedrich,L.B., Uknes,S.J. and Ward,E.R.
  TITLE     Method of inducing gene transcription in a plant
  JOURNAL   Patent: US 5789214-A 85 04-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 289
AR027201
LOCUS       AR027201                 30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 85 from patent US 5856154.
ACCESSION   AR027201
VERSION     AR027201.1  GI:5938041
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Alexander,D.C., Goodman,R.M. and Ward,E.R.
  TITLE     Method of protecting plants from oomycete pathogens
  JOURNAL   Patent: US 5856154-A 85 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 290
AR038488
LOCUS       AR038488                 30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 85 from patent US 5804693.
ACCESSION   AR038488
VERSION     AR038488.1  GI:5957205
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Gaffney,T.D., Ryals,J.A., Friedrich,L.B., Uknes,S.J., Ward,E.R.,
            Kessmann,H. and Vernooij,B.T.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL   Patent: US 5804693-A 85 08-SEP-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 291
AR064630
LOCUS       AR064630                 30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 85 from patent US 5847258.
ACCESSION   AR064630
VERSION     AR064630.1  GI:5993938
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Moyer,M.B., Payne,G.B. and Ward,E.R.
  TITLE     DNA encoding .beta.-1,3-glucanases
  JOURNAL   Patent: US 5847258-A 85 08-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 292
AR067555
LOCUS       AR067555                 30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 85 from patent US 5851766.
ACCESSION   AR067555
VERSION     AR067555.1  GI:5998777
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A. and Harms,C.
  TITLE     Process for isolating chemically regulatable DNA sequences
  JOURNAL   Patent: US 5851766-A 85 22-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 293
I38507
LOCUS       I38507                   30 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 85 from patent US 5614395.
ACCESSION   I38507
VERSION     I38507.1  GI:2084561
KEYWORDS    .
SOURCE      Unknown.
```

```
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||   ||||||||||||||||||
Db          2 TCTCGAGTTTTTTTTTTTTTTTTT 26


RESULT 284
I06459
LOCUS       I06459                   28 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 2 from Patent WO 9001065.
ACCESSION   I06459
VERSION     I06459.1  GI:589700
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Fry,K., Larrick,J. and Tam,A.
  TITLE     RNA AND DNA AMPLIFICATION TECHNIQUES
  JOURNAL   Patent: WO 9001065-A 2 08-FEB-1990;
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 28;
  Best Local Similarity   88.0%;  Pred. No. 7.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTTT 2186
              |||   ||||||||||||||||||
Db          3 CTCGAGTTTTTTTTTTTTTTTTTT 27


RESULT 285
AX184127
LOCUS       AX184127                 28 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1880 from Patent WO0142511.
ACCESSION   AX184127
VERSION     AX184127.1  GI:15135467
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE     Ibd-related polymorphisms
  JOURNAL   Patent: WO 0142511-A 1880 14-JUN-2001;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Ellipsis
            Biotherapeutics Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 28;
  Best Local Similarity   84.6%;  Pred. No. 7.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTT 2175
              ||| ||||||||||  |  ||||||||
Db          3 ATTAATTTTTTTCTTCCNTTTTTTT 28


RESULT 286
BD183015/c
LOCUS       BD183015                 28 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  New functional nucleic acids targeting NS3 protease and helicase of
            hepatitis C virus.
ACCESSION   BD183015
VERSION     BD183015.1  GI:31875215
KEYWORDS    JP 2002345475-A/26.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Nishikawa,S., Fukuda,K., Funaji,K., Uragami,S. and Seki,S.
  TITLE     New functional nucleic acids targeting NS3 protease and helicase of
            hepatitis C virus
  JOURNAL   Patent: JP 2002345475-A 26 03-DEC-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            MITSUBISHI GAS CHEMICAL CO INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002345475-A/26
            PD   03-DEC-2002
            PF   25-MAY-2001 JP 2001156957
            PI   SATOSHI NISHIKAWA,KOTARO FUKUDA,KOHEI FUNAJI,SADAJI URAGAMI,
            PI   SATOSHI SEKIYA
            PC   C12N15/09,A61K31/7105,A61K31/711,A61K35/76,A61K48/00,A61P1/16,
            PC   A61P31/14,
            PC   A61P43/00,C12N9/99,C12Q1/06,C12N15/00
            CC   Description of Artificial Sequence: Synthetic DNA FH   Key
                    Location/Qualifiers
            FT   source          1. .28
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 28;
  Best Local Similarity   88.0%;  Pred. No. 7.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTT 2179
              ||  | ||||||||||||||||||||
Db         25 TTCCTCTCTCCTTTTTTTTTTTTT 1


RESULT 287
AR016852
LOCUS       AR016852                 30 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 85 from patent US 5777200.
ACCESSION   AR016852
VERSION     AR016852.1  GI:3973129
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Ryals,J.A., Alexander,D.C., Goodman,R.M. and Stinson,J.R.
  TITLE     Chemically regulatable and anti-pathogenic DNA sequences and uses
            thereof
  JOURNAL   Patent: US 5777200-A 85 07-JUL-1998;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 9.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 288
AR020878
LOCUS       AR020878                 30 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 85 from patent US 5789214.
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LOCUS       E33560                    26 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Stress-responsive gene promoter.
ACCESSION   E33560
VERSION     E33560.1  GI:18624133
KEYWORDS    JP 2000078977-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Tsujimoto,Y., Izawa,S., Inoue,Y., Kimura,H. and Sato,N.
  TITLE     Stress-responsive gene promoter
  JOURNAL   Patent: JP 2000078977-A 5 21-MAR-2000;
            MARUHA CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2000078977-A/5
            PD   21-MAR-2000
            PF   04-SEP-1998 JP 1998251390
            PR
            PI   YOSHIYUKI TSUJIMOTO,SHINGO IZAWA,YOSHIHARU INOUE,HIKARU
            KIMURA,
            PI   NOBUYUKI SATO
            PC   C12N15/09,C12N1/19,C12P21/02//(C12N15/09,C12R1:865),(C12N1/19,
            PC   C12R1:865),
            PC   (C12P21/02,C12R1:865),C12N15/00,(C12N15/00,C12R1:865) CC
            FH   Key             Location/Qualifiers
            FT   source          1. .36
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAAC 2189
             | ||||||||||||  |||||| ||
Db          1 CATTTTTTTTTTTATTTTTTGAC 25


RESULT 281
AR410280
LOCUS       AR410280                  26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 59 from patent US 6635459.
ACCESSION   AR410280
VERSION     AR410280.1  GI:40161559
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Sarkanen,S. and Ford,J.D.
  TITLE     Nucleotide sequences encoding pinoresinol/lariciresinol reductase
            proteins and their methods of use
  JOURNAL   Patent: US 6635459-A 59 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
             ||||   ||||||||||||||||||
Db          2 TCTCGAGTTTTTTTTTTTTTTTTT 26


RESULT 282
AX191907
LOCUS       AX191907                  26 bp    DNA     linear   PAT 15-AUG-2001
DEFINITION  Sequence 59 from Patent WO0149833.
ACCESSION   AX191907
VERSION     AX191907.1  GI:15210057
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Ford,J.D. and Sarkanen,S.
  TITLE     Recombinant pinoresinol/lariciresinol reductase, recombinant
            dirigent protein, and methods of use
  JOURNAL   Patent: WO 0149833-A 59 12-JUL-2001;
            Washington State University Research Foundation (US) ; REGENTS OF
            THE UNIVERSITY OF MINNESOTA (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide"
     misc_feature    1. .26
                     /note="cDNA synthesis linker primer"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
             ||||   ||||||||||||||||||
Db          2 TCTCGAGTTTTTTTTTTTTTTTTT 26


RESULT 283
BD064385
LOCUS       BD064385                  26 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Recombinant pinoresinol/lariciresinol reductases,recombinant
            dirigent proteins and methods of use.
ACCESSION   BD064385
VERSION     BD064385.1  GI:22609988
KEYWORDS    JP 2001507931-A/26.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lewis,N.G., Davin,L.B., Kostova,A.T.D., Fujita,M., Gang,D.R. and
            Sarkanen,S.
  TITLE     Recombinant pinoresinol/lariciresinol reductases,recombinant
            dirigent proteins and methods of use
  JOURNAL   Patent: JP 2001507931-A 26 19-JUN-2001;
            WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
COMMENT     PN   JP 2001507931-A/26
            PD   19-JUN-2001
            PF   07-NOV-1997 JP 1998521816
            PR   08-NOV-1996 US    60/030522,31-JUL-1997 US    60/054380 PI
            NORMAN G LEWIS,LAURENCE B DAVIN,ALBENA T DINKOVA KOSTOVA, PI
            MASAYUKI FUJITA,
            PI   DAVID R GANG,SIMO SARKANEN
            PC   C12N9/02,C12N15/53,C12N15/29
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   'cDNA synthesis linker primer'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
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     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 276
AR374074/c
LOCUS       AR374074                  26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 39 from patent US 6605272.
ACCESSION   AR374074
VERSION     AR374074.1  GI:40076646
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Methods of using zalpha11 ligand
  JOURNAL   Patent: US 6605272-A 39 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 277
AR404597/c
LOCUS       AR404597                  26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6627748.
ACCESSION   AR404597
VERSION     AR404597.1  GI:40153233
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Ju,J., Li,Z., Tong,A. and Russo,J.J.
  TITLE     Combinatorial fluorescence energy transfer tags and their
            applications for multiplex genetic analyses
  JOURNAL   Patent: US 6627748-A 1 30-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 278
BD007174/c
LOCUS       BD007174                  26 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method and composition for capturing multiple polynucleotide.
ACCESSION   BD007174
VERSION     BD007174.1  GI:18635545
KEYWORDS    JP 2001503973-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   OGneill,R.A., Chen,J.C., Chiesa,C. and Fry,G.
  TITLE     Method and composition for capturing multiple polynucleotide
  JOURNAL   Patent: JP 2001503973-A 2 27-MAR-2001;
            THE PERKIN ELMAR CORP
COMMENT     OS   Unidentified
            PN   JP 2001503973-A/2
            PD   27-MAR-2001
            PF   02-OCT-1997 JP 1998516839
            PR   04-OCT-1996 US    60/027832,12-JUN-1997 US    08/873437 PI
            ROGER A O'NEILL,JAR CAIN CHEN,CLAUDIA CHIESA,GEORGE FRY PC
            C12Q1/68,C12N15/09,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 279
AR144828
LOCUS       AR144828                  26 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 59 from patent US 6210942.
ACCESSION   AR144828
VERSION     AR144828.1  GI:15106695
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lewis,N.G., Davin,L.B., Dinkova-Kostova,A.T., Fujita,M., Gang,D.R.,
            Sarkanen,S. and Ford,J.D.
  TITLE     Recombinant pinoresinol/lariciresinol reductase, recombinant
            dirigent protein, and methods of use
  JOURNAL   Patent: US 6210942-A 59 03-APR-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||   ||||||||||||||||||
Db          2 TCTCGAGTTTTTTTTTTTTTTTTT 26


RESULT 280
E33560
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  TITLE     A method for generating hypermutable organisms
  JOURNAL   Patent: WO 0188192-A 4 22-NOV-2001;
            The Johns Hopkins UNiversity School of Medicine (US) ; Morphotek
            Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Sass, Philip, M. (US) ;
            Grasso, Luigi (US) ; Vogelstein, Bert (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Recombinant DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||||||  | |
Db         25 TTTTTTTTTTTTTTTTTTTTGCCAT 1


RESULT 272
AR174582/c
LOCUS       AR174582                 26 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 39 from patent US 6307024.
ACCESSION   AR174582
VERSION     AR174582.1  GI:17914902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 39 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 273
BD248975/c
LOCUS       BD248975                 26 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel cytokine ZALPHA11 ligand.
ACCESSION   BD248975
VERSION     BD248975.1  GI:33058745
KEYWORDS    JP 2002537839-A/36.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Novel cytokine ZALPHA11 ligand
  JOURNAL   Patent: JP 2002537839-A 36 12-NOV-2002;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002537839-A/36
            PD   12-NOV-2002
            PF   09-MAR-2000 JP 2000603382
            PR   09-MAR-1999 US    09/264908,11-MAR-1999 US    09/265992 PR
            01-JUL-1999 US    60/142013
            PI   JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C  PI
            FOSTER,
            PI   RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
            PI   STACEY R DILLON,ANGELA K HAMMOND
            PC   C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
            PC   C07K14/53,
            PC   C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
             A61K37/02
            CC   Oligonucleotide primer ZC7764b
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 274
I79495/c
LOCUS       I79495                   26 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 2 from patent US 5707807.
ACCESSION   I79495
VERSION     I79495.1  GI:3207785
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 2 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 6.1e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 275
AR279358/c
LOCUS       AR279358                 26 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 2 from patent US 6514699.
ACCESSION   AR279358
VERSION     AR279358.1  GI:29714110
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   O'Neill,R.A., Chen,J.-K., Chiesa,C. and Fry,G.
  TITLE     Multiplex polynucleotide capture methods and compositions
  JOURNAL   Patent: US 6514699-A 2 04-FEB-2003;
FEATURES             Location/Qualifiers
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            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || ||||| |  ||||||||||||||
Db          1 ATATATATTTTTTTTGTTTTTTTTTTTTTT 30


RESULT 268
BD166025
LOCUS       BD166025                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166025
VERSION     BD166025.1  GI:27871837
KEYWORDS    JP 2002191372-A/5.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 5 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/5
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                  labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || ||||| |  ||||||||||||||
Db          1 ATATATATTTTTTTTGTTTTTTTTTTTTTT 30


RESULT 269
AX583623
LOCUS       AX583623                 22 bp    DNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 3 from Patent WO02074988.
ACCESSION   AX583623
VERSION     AX583623.1  GI:27655433
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mir,K.
  TITLE     Arrays and methods of use
  JOURNAL   Patent: WO 02074988-A 3 26-SEP-2002;
            THE CHANCELLOR, MASTERS AND SCHOLARS OF THE UNIVERSITY OF OXFORD
            (GB)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic oligonucleotide primer (Oligo-dT"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 22;
  Best Local Similarity   95.2%;  Pred. No. 3.8e+02;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTV 21


RESULT 270
I29929/c
LOCUS       I29929                   25 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 42 from patent US 5578468.
ACCESSION   I29929
VERSION     I29929.1  GI:1820720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Pickup,D.J., Patel,D. and Antczak,J.B.
  TITLE     Site-specific RNA cleavage
  JOURNAL   Patent: US 5578468-A 42 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||||||  ||||
Db         25 TTTTTTTTTTTTTTTTTTTGTTTTG 1


RESULT 271
AX338548/c
LOCUS       AX338548                 25 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 4 from Patent WO0188192.
ACCESSION   AX338548
VERSION     AX338548.1  GI:18128948
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Nicolaides,N.C., Sass,P.M., Grasso,L., Vogelstein,B. and
            Kinzler,K.W.
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RESULT 265
BD072865
LOCUS       BD072865                 30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072865
VERSION     BD072865.1  GI:22618468
KEYWORDS    JP 2001286300-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 3 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/3
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || |||||  |  ||||||||||||||
Db          1 ATATATATTTTTTTTGTTTTTTTTTTTTTT 30


RESULT 266
BD107492
LOCUS       BD107492                 30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107492
VERSION     BD107492.1  GI:23202310
KEYWORDS    JP 2002000275-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 1 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/1
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC              nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || |||||  |  ||||||||||||||
Db          1 ATATATATTTTTTTTGTTTTTTTTTTTTTT 30


RESULT 267
BD145024
LOCUS       BD145024                 30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145024
VERSION     BD145024.1  GI:27850782
KEYWORDS    JP 2002119291-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 5 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/5
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
```

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ACCESSION   AR261539
VERSION     AR261539.1  GI:28072607
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Chetverin,A.B. and Kramer,F.R.
  TITLE     Oligonucleotide arrays and their use for sorting, isolating,
            sequencing, and manipulating nucleic acids
  JOURNAL   Patent: US 6322971-A 6 27-NOV-2001;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 24;
  Best Local Similarity   95.5%;  Pred. No. 4.5e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||||
Db          1 TTTAAAAAAAAAAAAAAAAAAA 22


RESULT 261
AR431312
LOCUS       AR431312                 24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 6 from patent US 6651008.
ACCESSION   AR431312
VERSION     AR431312.1  GI:40193280
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 6 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 24;
  Best Local Similarity   95.5%;  Pred. No. 4.5e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||| |||
Db          1 CTTTTTTTTTTTTTTTTGTTT 22


RESULT 262
A79651
LOCUS       A79651                   30 bp    DNA     linear   PAT 20-OCT-1999
DEFINITION  Sequence 2 from Patent EP0780479.
ACCESSION   A79651
VERSION     A79651.1  GI:6092605
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Fritton,H.D. and Hinzpeter,M.D.
  TITLE     METHOD FOR QUANTITATIVE DETERMINATION OF SPECIFIC NUCLEIC ACID
            SEQUENCES
  JOURNAL   Patent: EP 0780479-A 2 25-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   95.5%;  Pred. No. 8.4e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTTCA 22


RESULT 263
AR264920
LOCUS       AR264920                 30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 4 from patent US 6492121.
ACCESSION   AR264920
VERSION     AR264920.1  GI:29693307
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 4 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTT 2179
              ||  || ||||| |  ||||||||||||||
Db          1 ATATATATTTTTTTGTTTTTTTTTTTTTT 30


RESULT 264
AX394621/c
LOCUS       AX394621                 30 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 19 from Patent EP1186673.
ACCESSION   AX394621
VERSION     AX394621.1  GI:21065734
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 19 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 8.4e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
              ||||||      ||||||||||||||||||
Db         30 TTTTTTGGGAGATTTTTTTTTTTTTTTT 1
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HSA241944/c
LOCUS       HSA241944                29 bp    DNA     linear   PRI 24-FEB-2000
DEFINITION  Homo sapiens gp130 gene, partial, intron 14 splice acceptor site.
ACCESSION   AJ241944
VERSION     AJ241944.1  GI:7105900
KEYWORDS    gp130 gene; splice acceptor site.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szalai,C., Toth,S. and Falus,A.
  TITLE     Exon-intron organization of the human gp130 gene
  JOURNAL   Gene 243 (1-2), 161-166 (2000)
  MEDLINE   20156380
   PUBMED   10675624
REFERENCE   2  (bases 1 to 29)
  AUTHORS   Szalai,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-APR-1999) Szalai C., Heim Pal Pediatric Hospital
            Budapest, Budapest POBOX 66, H-1958 Hungary
COMMENT     Related sequence M57230.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /map="5q11"
     gene            1. .29
                     /gene="gp130"
     intron          1. .24
                     /gene="gp130"
                     /note="splice acceptor site"
                     /number=14
     exon            25. .29
                     /gene="gp130"
                     /number=15

  Query Match             0.7%;  Score 20.6;  DB 1;  Length 29;
  Best Local Similarity   85.2%;  Pred. No. 7.1e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||  | ||||||||||||||||||||
Db         29 TTGAGCTTAAAAAAAAAAAAAAAAAAA 3


RESULT 257
A08914
LOCUS       A08914                   31 bp    DNA     linear   PAT 02-SEP-1993
DEFINITION  H.sapiens (haplotype 3, allele MS32, isolate Mormon, serial number
            2) minisatellite sequence.
ACCESSION   A08914
VERSION     A08914.1  GI:411836
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Jeffreys,A.J.
  TITLE     Extended nucleotide sequences
  JOURNAL   Patent: EP 0370719-A 97 30-MAY-1990;
            IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 20.6;  DB 1;  Length 31;
  Best Local Similarity   85.2%;  Pred. No. 8.5e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||  | ||||||||||||||||||||
Db         1 TAAAAAAAAAAAAAAAAAAAAAAAAAA 27


RESULT 258
AR365237
LOCUS       AR365237                 33 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 1 from patent US 5478746.
ACCESSION   AR365237
VERSION     AR365237.1  GI:34428753
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Cohen,J.I., Purcell,R.H., Feinstone,S.M. and Ticehurst,J.R.
  TITLE     cDNA encoding attenuated cell culture adapted hepatitis A virus
            genome
  JOURNAL   Patent: US 5478746-A 1 26-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.6;  DB 1;  Length 33;
  Best Local Similarity   85.2%;  Pred. No. 1e+03;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||  | ||||||||||||||||||||
Db         2 TAAAAAAAAAAAAAAAAAAAAAAAAAA 28


RESULT 259
AX495372
LOCUS       AX495372                 36 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1137 from Patent WO02059256.
ACCESSION   AX495372
VERSION     AX495372.1  GI:23340982
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 1137 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 20.6;  DB 1;  Length 36;
  Best Local Similarity   85.2%;  Pred. No. 1.2e+03;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | |  | ||||||||||||||||||||
Db         2 TACAGGTAAAAAAAAAAAAAAAAAAAA 28


RESULT 260
AR261539
LOCUS       AR261539                 24 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 6 from patent US 6322971.
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```
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
             | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1


RESULT 252
AX196220/c
LOCUS       AX196220                 32 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 51 from Patent WO0151665.
ACCESSION   AX196220
VERSION     AX196220.1  GI:15386423
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0151665-A 51 19-JUL-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
             | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1


RESULT 253
AX440121/c
LOCUS       AX440121                 32 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 51 from Patent WO0173123.
ACCESSION   AX440121
VERSION     AX440121.1  GI:21664932
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0173123-A 51 04-OCT-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
             | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1


RESULT 254
AX465307/c
LOCUS       AX465307                 32 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 51 from Patent WO0218643.
ACCESSION   AX465307
VERSION     AX465307.1  GI:21899670
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0218643-A 51 07-MAR-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
             | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1


RESULT 255
AX556120/c
LOCUS       AX556120                 32 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 51 from Patent WO0246472.
ACCESSION   AX556120
VERSION     AX556120.1  GI:25899502
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 51 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
             | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1


RESULT 256
```

```
  Query Match              0.7%;  Score 20.8;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 5.4e+02;
  Matches   22;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              |:||   ||||||||||||||||||||
Db         27 ARAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 247
AR274390/c
LOCUS       AR274390                  32 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 51 from patent US 6506564.
ACCESSION   AR274390
VERSION     AR274390.1  GI:29706836
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6506564-A 51 14-JAN-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1

RESULT 248
AR344932/c
LOCUS       AR344932                  32 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 51 from patent US 6582921.
ACCESSION   AR344932
VERSION     AR344932.1  GI:33741013
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            thereof
  JOURNAL   Patent: US 6582921-A 51 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1

RESULT 249
AR382308/c
LOCUS       AR382308                  32 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 51 from patent US 6610491.
ACCESSION   AR382308
VERSION     AR382308.1  GI:40090720
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6610491-A 51 26-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 8.6e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1

RESULT 250
AR409897
LOCUS       AR409897                  32 bp    RNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 10 from patent US 6635422.
ACCESSION   AR409897
VERSION     AR409897.1  GI:40161032
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Keene,J.D., Tenenbaum,S.A. and Carson,C.C.
  TITLE     Methods for isolating and characterizing endogenous mRNA-protein
            (mRNP) complexes
  JOURNAL   Patent: US 6635422-A 10 21-OCT-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match              0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   78.1%;  Pred. No. 8.6e+02;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | ||||| | ||||||||||||||  | ||| |
Db          1 TATTTTTTTCTTTTTTTTTTTGGTCTTTAT 32

RESULT 251
AR429649/c
LOCUS       AR429649                  32 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 51 from patent US 6645721.
ACCESSION   AR429649
VERSION     AR429649.1  GI:40189945
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R. and Taton,T.A.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: US 6645721-A 51 11-NOV-2003;
FEATURES             Location/Qualifiers
```

```
            FH   Key             Location/Qualifiers
            FT   misc_binding    1. .24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 24;
  Best Local Similarity   91.7%;  Pred. No. 3.8e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||||| || |
Db          1 TTTTTTTTTTTTTTTTTTGAAAT 24


RESULT 243
BD196419/c
LOCUS       BD196419                 24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Prostatic cancer gene.
ACCESSION   BD196419
VERSION     BD196419.1  GI:33006189
KEYWORDS    JP 2002516657-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
  TITLE     Prostatic cancer gene
  JOURNAL   Patent: JP 2002516657-A 8 11-JUN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516657-A/8
            PD   11-JUN-2002
            PF   22-DEC-1998 JP 2000525562
            PR   22-DEC-1997 US    08/996306,09-SEP-1998 US    60/099658 PI
            DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
            C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
            ,C12N15/00,C12N5/00,
            PC   C12N5/00,C12N15/00
            CC   primer oligonucleotide PGRT32
            FH   Key             Location/Qualifiers
            FT   misc_binding    1. .24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 24;
  Best Local Similarity   91.7%;  Pred. No. 3.8e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              | || ||||||||||||||||||
Db         24 ATTTCAAAAAAAAAAAAAAAAAA 1


RESULT 244
AR241865/c
LOCUS       AR241865                 27 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 153 from patent US 6472154.
ACCESSION   AR241865
VERSION     AR241865.1  GI:27287677
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 153 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 27;
  Best Local Similarity   91.7%;  Pred. No. 5.4e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2804
              || | ||||||||||||||||||
Db         27 AAATAAAAAAAAAAAAAAAAAAA 4


RESULT 245
AR214918/c
LOCUS       AR214918                 27 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 18 from patent US 6410235.
ACCESSION   AR214918
VERSION     AR214918.1  GI:23312859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Weindel,K. and Brand,J.
  TITLE     DNA detection by means of a strand reassociation complex
  JOURNAL   Patent: US 6410235-A 18 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 5.4e+02;
  Matches   22;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2804
              |:||   ||||||||||||||||||
Db         27 ARAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 246
AX009609/c
LOCUS       AX009609                 27 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 18 from Patent EP0962536.
ACCESSION   AX009609
VERSION     AX009609.1  GI:9996841
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            tuberculosis complex.
REFERENCE   1
  AUTHORS   Brand,J. and Weindel,K.D.
  TITLE     Dna detection by a strand reassociation complex
  JOURNAL   Patent: EP 0962536-A 18 08-DEC-1999;
            ROCHE DIAGNOSTICS GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Mycobacterium tuberculosis"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1773"
     misc_signal     1
                     /note="Phosphate linked to biotin via Aminolinker"
     misc_signal     27
                     /note="Y means incorporation of
                     Aminolinker-phosphoramidite subsequently estered with 3-O
                     carboxymethyl digoxigenin"
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LOCUS       AR432384                32 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 7 from patent US 6653280.
ACCESSION   AR432384
VERSION     AR432384.1  GI:40194661
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
  TITLE     Antifungal polypeptide AlyAFP from Alyssum and methods for
            controlling plant pathogenic fungi
  JOURNAL   Patent: US 6653280-A 7 25-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||
Db         12 TCCTTTTTTTTTTTTTTTTT 32


RESULT 239
AX287571/c
LOCUS       AX287571                45 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 14 from Patent WO0177390.
ACCESSION   AX287571
VERSION     AX287571.1  GI:17049337
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 14 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"

  Query Match             0.7%;  Score 21;  DB 1;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||||
Db         37 TGAAAAAAAAAAAAAAAAAAA 17


RESULT 240
AX287575/c
LOCUS       AX287575                45 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 18 from Patent WO0177390.
ACCESSION   AX287575
VERSION     AX287575.1  GI:17049341
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 18 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"

  Query Match             0.7%;  Score 21;  DB 1;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+03;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||||
Db         37 TGAAAAAAAAAAAAAAAAAAA 17


RESULT 241
AR431307/c
LOCUS       AR431307                24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6651008.
ACCESSION   AR431307
VERSION     AR431307.1  GI:40193275
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 1 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 24;
  Best Local Similarity   91.7%;  Pred. No. 3.8e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              |||  ||||||||||||||||||||
Db         24 AATAAAAAAAAAAAAAAAAAAAAA 1


RESULT 242
BD196419
LOCUS       BD196419                24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Prostatic cancer gene.
ACCESSION   BD196419
VERSION     BD196419.1  GI:33006189
KEYWORDS    JP 2002516657-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
  TITLE     Prostatic cancer gene
  JOURNAL   Patent: JP 2002516657-A 8 11-JUN-2002;
            GENSET
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002516657-A/8
            PD   11-JUN-2002
            PF   22-DEC-1998 JP 2000525562
            PR   22-DEC-1997 US    08/996306,09-SEP-1998 US    60/099658 PI
            DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
            C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
            C12N1/19,
            PC   C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
            ,C12N15/00,C12N5/00,
            PC   C12N5/00,C12N15/00
            CC   primer oligonucleotide PGRT32
```

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  JOURNAL   Patent: EP 1207210-A 4 22-MAY-2002;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   82.8%;  Pred. No. 7.9e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAAAAA 2804
              | || ||   ||||||||||||||||||
Db          4 GGTAAAAAAAAAAAAAAAAAAAAAAAAAA 32


RESULT 234
BD165916
LOCUS       BD165916                32 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for melting curve analysis of repetitive PCR products.
ACCESSION   BD165916
VERSION     BD165916.1  GI:27871728
KEYWORDS    JP 2002191384-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dietmaier,W.
  TITLE     Method for melting curve analysis of repetitive PCR products
  JOURNAL   Patent: JP 2002191384-A 4 09-JUL-2002;
            F HOFFMANN LA ROCHE AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191384-A/4
            PD   09-JUL-2002
            PF   13-NOV-2001 JP 2001348017
            PR   15-NOV-2000 EP   00124897.0
            PI   WOLFGANG DIETMAIER
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Method for melting curve analysis of repetitive PCR products
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   82.8%;  Pred. No. 7.9e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAAAAA 2804
              | || ||   ||||||||||||||||||
Db          4 GGTAAAAAAAAAAAAAAAAAAAAAAAAAA 32


RESULT 235
AR014684
LOCUS       AR014684                32 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 7 from patent US 5773696.
ACCESSION   AR014684
VERSION     AR014684.1  GI:3972138
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
  TITLE     Antifungal polypeptide and methods for controlling plant pathogenic
            fungi
  JOURNAL   Patent: US 5773696-A 7 30-JUN-1998;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||
Db         12 TCCTTTTTTTTTTTTTTTTT 32


RESULT 236
AR341692
LOCUS       AR341692                32 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 16 from patent US 6573361.
ACCESSION   AR341692
VERSION     AR341692.1  GI:33734520
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Bunkers,G.J., Liang,J., Mittanck,C.A., Seale,J.W. and Wu,Y.S.
  TITLE     Antifungal proteins and methods for their use
  JOURNAL   Patent: US 6573361-A 16 03-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||
Db         12 TCCTTTTTTTTTTTTTTTTT 32


RESULT 237
AR366811
LOCUS       AR366811                32 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 8 from patent US 6329504.
ACCESSION   AR366811
VERSION     AR366811.1  GI:34599783
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Liang,J., Shah,D.M., Wu,Y.S., Rosenberger,C.A. and Hakimi,S.
  TITLE     Antifungal polypeptide and methods for controlling plant pathogenic
            fungi
  JOURNAL   Patent: US 6329504-A 8 11-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 7.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||
Db         12 TCCTTTTTTTTTTTTTTTTT 32


RESULT 238
AR432384
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Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
                ||  |||||||  | ||||||||||||||
Db         29 TTTTTTTTTTAACGTTTTTTTTTTTTTT 1


RESULT 229
AX351706/c
LOCUS       AX351706                  30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 2 from Patent WO0193902.
ACCESSION   AX351706
VERSION     AX351706.1  GI:18616989
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 2 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     DNA/RNA oligonucleotide~Synthetic DNA/RNA oligonucleotide"

  Query Match             0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 6.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
                ||  |||||||  | ||||||||||||||
Db         29 TTTTTTTTTTAACGTTTTTTTTTTTTTT 1


RESULT 230
AX351707/c
LOCUS       AX351707                  30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 3 from Patent WO0193902.
ACCESSION   AX351707
VERSION     AX351707.1  GI:18616990
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 3 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     DNA/RNA oligonucleotide~Synthetic DNA/RNA oligonucleotide"

  Query Match             0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 6.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
                ||  |||||||  | ||||||||||||||
Db         29 TTTTTTTTTTAACGTTTTTTTTTTTTTT 1


RESULT 231
AX351708/c
LOCUS       AX351708                  30 bp    RNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 4 from Patent WO0193902.
ACCESSION   AX351708
VERSION     AX351708.1  GI:18616991
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 4 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     oligonucleotide"

  Query Match             0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 6.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
                ||  |||||||  | ||||||||||||||
Db         29 TTTTTTTTTTAACGTTTTTTTTTTTTTT 1


RESULT 232
AX351715/c
LOCUS       AX351715                  30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 11 from Patent WO0193902.
ACCESSION   AX351715
VERSION     AX351715.1  GI:18616998
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 11 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"

  Query Match             0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 6.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
                ||  |||||||   |||||||||||||||
Db         29 TTTTTTTTTTTAAGCTTTTTTTTTTTTTT 1


RESULT 233
AX430213
LOCUS       AX430213                  32 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 4 from Patent EP1207210.
ACCESSION   AX430213
VERSION     AX430213.1  GI:21655578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dietmaier,W.
  TITLE     Method for melting curve analysis of repetitive pcr products
```

```
          FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 21;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 225
AX492939
LOCUS       AX492939                 27 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 16 from Patent EP1227150.
ACCESSION   AX492939
VERSION     AX492939.1  GI:23338609
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tai-Jay,C.
  TITLE     Androgen receptor complex-associated protein
  JOURNAL   Patent: EP 1227150-A 16 31-JUL-2002;
            Veterans General Hospital (TW)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetically generated primer"

  Query Match              0.7%;  Score 21;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 226
BD175131
LOCUS       BD175131                 27 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Androgen receptor complex-associated protein.
ACCESSION   BD175131
VERSION     BD175131.1  GI:29120825
KEYWORDS    JP 2002262871-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Chan,T.Z.
  TITLE     Androgen receptor complex-associated protein
  JOURNAL   Patent: JP 2002262871-A 12 17-SEP-2002;
            VETERANS GENERAL HOSPITAL
COMMENT     OS   Artificial Sequence
            PN   JP 2002262871-A/12
            PD   17-SEP-2002
            PF   28-FEB-2001 JP 2001055192
            PI   TAI ZHAI CHAN
            PC   C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
            ,C12P21/02,C12Q1/68,
            PC   G01N33/15,G01N33/50,G01N33/566,C12N15/00,C12N5/00 CC   n =
            A,T,C or G
            CC   synthetically generated primer
            FH   Key             Location/Qualifiers
          FT   misc_feature    (1). .(27).
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 21;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 227
A79651/c
LOCUS       A79651                   30 bp    DNA     linear   PAT 20-OCT-1999
DEFINITION  Sequence 2 from Patent EP0780479.
ACCESSION   A79651
VERSION     A79651.1  GI:6092605
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Fritton,H.D. and Hinzpeter,M.D.
  TITLE     METHOD FOR QUANTITATIVE DETERMINATION OF SPECIFIC NUCLEIC ACID
            SEQUENCES
  JOURNAL   Patent: EP 0780479-A 2 25-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 6.7e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||||
Db         22 TGAAAAAAAAAAAAAAAAAAA 2


RESULT 228
AX351705/c
LOCUS       AX351705                 30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 1 from Patent WO0193902.
ACCESSION   AX351705
VERSION     AX351705.1  GI:18616988
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 1 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"

  Query Match              0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 6.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 220
I79495
LOCUS       I79495                    26 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 2 from patent US 5707807.
ACCESSION   I79495
VERSION     I79495.1  GI:3207785
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 2 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 221
AR279358
LOCUS       AR279358                  26 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 2 from patent US 6514699.
ACCESSION   AR279358
VERSION     AR279358.1  GI:29714110
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   O'Neill,R.A., Chen,J.-K., Chiesa,C. and Fry,G.
  TITLE     Multiplex polynucleotide capture methods and compositions
  JOURNAL   Patent: US 6514699-A 2 04-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 222
AR374074
LOCUS       AR374074                  26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 39 from patent US 6605272.
ACCESSION   AR374074
VERSION     AR374074.1  GI:40076646
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Methods of using zalphal1 ligand
  JOURNAL   Patent: US 6605272-A 39 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 223
AR404597
LOCUS       AR404597                  26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6627748.
ACCESSION   AR404597
VERSION     AR404597.1  GI:40153233
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Ju,J., Li,Z., Tong,A. and Russo,J.J.
  TITLE     Combinatorial fluorescence energy transfer tags and their
            applications for multiplex genetic analyses
  JOURNAL   Patent: US 6627748-A 1 30-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 224
BD007174
LOCUS       BD007174                  26 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Method and composition for capturing multiple polynucleotide.
ACCESSION   BD007174
VERSION     BD007174.1  GI:18635545
KEYWORDS    JP 2001503973-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   OGneill,R.A., Chen,J.C., Chiesa,C. and Fry,G.
  TITLE     Method and composition for capturing multiple polynucleotide
  JOURNAL   Patent: JP 2001503973-A 2 27-MAR-2001;
            THE PERKIN ELMAR CORP
COMMENT     OS   Unidentified
            PN   JP 2001503973-A/2
            PD   27-MAR-2001
            PF   02-OCT-1997 JP 1998516839
            PR   04-OCT-1996 US    60/027832,12-JUN-1997 US    08/873437 PI
            ROGER A O'NEILL,JAR CAIN CHEN,CLAUDIA CHIESA,GEORGE FRY PC
            C12Q1/68,C12N15/09,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .26
```

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  JOURNAL    Patent: JP 2003014773-A 4 15-JAN-2003;
             CANON INC
COMMENT      OS   Artificial Sequence
             PN   JP 2003014773-A/4
             PD   15-JAN-2003
             PF   28-MAR-2002 JP 2002093024
             PI   nobuyuki okamura,tadashi okamoto,makoto kameyama CC   Designed
             oligonucleotide used as a probe to be stabilized CC   on a surface
             of a
             CC   carrier
             FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 217
BD204988
LOCUS       BD204988                  25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein array enabling site specification.
ACCESSION   BD204988
VERSION     BD204988.1  GI:33014758
KEYWORDS    JP 2002510505-A/23.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Protein array enabling site specification
  JOURNAL   Patent: JP 2002510505-A 23 09-APR-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002510505-A/23
            PD   09-APR-2002
            PF   31-MAR-1999 JP 2000542484
            PR   03-APR-1998 US    60/080686
            PI   ROBERT G KUIMELIS,RICHARD WAGNER
            PC   C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
              G01N33/68,
            PC   C12N15/00
            CC   Capture probe sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 218
AR174582
LOCUS       AR174582                  26 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 39 from patent US 6307024.
ACCESSION   AR174582
VERSION     AR174582.1  GI:17914902
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 39 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 219
BD248975
LOCUS       BD248975                  26 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel cytokine ZALPHA11 ligand.
ACCESSION   BD248975
VERSION     BD248975.1  GI:33058745
KEYWORDS    JP 2002537839-A/36.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Novel cytokine ZALPHA11 ligand
  JOURNAL   Patent: JP 2002537839-A 36 12-NOV-2002;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002537839-A/36
            PD   12-NOV-2002
            PF   09-MAR-2000 JP 2000603382
            PR   09-MAR-1999 US    09/264908,11-MAR-1999 US    09/265992 PR
            01-JUL-1999 US    60/142013
            PI   JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C  PI
            FOSTER,
            PI   RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
            PI   STACEY R DILLON,ANGELA K HAMMOND
            PC   C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
            PC   C07K14/53,
            PC   C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
             A61K37/02
            CC   Oligonucleotide primer ZC7764b
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          2 TTTTTTTTTTTTTTTTTTTT 22


RESULT 212
I58009
LOCUS       I58009                    25 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 2 from patent US 5610287.
ACCESSION   I58009
VERSION     I58009.1  GI:2483073
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Nikiforov,T. and Knapp,M.R.
  TITLE     Method for immobilizing nucleic acid molecules
  JOURNAL   Patent: US 5610287-A 2 11-MAR-1997;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 213
I96072
LOCUS       I96072                    25 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 2 from patent US 5734020.
ACCESSION   I96072
VERSION     I96072.1  GI:3940542
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Wong,Y.N.
  TITLE     Production and use of magnetic porous inorganic materials
  JOURNAL   Patent: US 5734020-A 2 31-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 214
AR288252
LOCUS       AR288252                  25 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 23 from patent US 6537749.
ACCESSION   AR288252
VERSION     AR288252.1  GI:31675536
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Addressable protein arrays
  JOURNAL   Patent: US 6537749-A 23 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 215
BD187513/c
LOCUS       BD187513                  25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Probe carrier, Method and Apparatus for producing Probe carrier.
ACCESSION   BD187513
VERSION     BD187513.1  GI:32997252
KEYWORDS    JP 2003014773-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Okamura,N., Okamoto,T. and Kameyama,M.
  TITLE     Probe carrier, Method and Apparatus for producing Probe carrier
  JOURNAL   Patent: JP 2003014773-A 3 15-JAN-2003;
            CANON INC
COMMENT     OS   Artificial Sequence
            PN   JP 2003014773-A/3
            PD   15-JAN-2003
            PF   28-MAR-2002 JP 2002093024
            PI   nobuyuki okamura,tadashi okamoto,makoto kameyama CC   Designed
            oligonucleotide to be hybridized with the designed CC
            oligonucleotide
            CC   'ttttttttttttttttttttttttt'
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         25 TTTTTTTTTTTTTTTTTTTT 5


RESULT 216
BD187514
LOCUS       BD187514                  25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Probe carrier, Method and Apparatus for producing Probe carrier.
ACCESSION   BD187514
VERSION     BD187514.1  GI:32997253
KEYWORDS    JP 2003014773-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Okamura,N., Okamoto,T. and Kameyama,M.
  TITLE     Probe carrier, Method and Apparatus for producing Probe carrier
```

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     modified_base   8. .24
                     /note="t at positions 8-24 may be present or absent"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 208
AX838369/c
LOCUS       AX838369                 24 bp    DNA     linear   PAT 15-DEC-2003
DEFINITION  Sequence 8 from Patent WO02068627.
ACCESSION   AX838369
VERSION     AX838369.1  GI:39922050
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   .
  TITLE     Vector constructs
  JOURNAL   Patent: WO 02068627-A 8 06-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Viral vector sequence"
     misc_feature    1. .24
                     /note="Fig. 1C. SV40 early Poly(A) site"
     polyA_site      3. .24

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 209
BD136714/c
LOCUS       BD136714                 24 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Quantitative assay of nucleic acid amplification product.
ACCESSION   BD136714
VERSION     BD136714.1  GI:23231659
KEYWORDS    JP 2002504350-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Patel,R. and Kurn,N.
  TITLE     Quantitative assay of nucleic acid amplification product
  JOURNAL   Patent: JP 2002504350-A 4 12-FEB-2002;
            DADE BEHRING INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002504350-A/4
            PD   12-FEB-2002
            PF   17-FEB-1999 JP 2000532556
            PR   18-FEB-1998 US    09/025639
            PI   RAJESH PATEL,NURITH KURN
            PC   C12Q1/68,C12N15/09,C12N15/00
            CC   Synthetic DNA Probe
            FH   Key             Location/Qualifiers
            FT   misc_binding    (1). .(24).
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 210
AR105982
LOCUS       AR105982                 25 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 5 from patent US 6103474.
ACCESSION   AR105982
VERSION     AR105982.1  GI:12820047
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
  TITLE     Hybridization assay signal enhancement
  JOURNAL   Patent: US 6103474-A 5 15-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 211
BD234336
LOCUS       BD234336                 25 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234336
VERSION     BD234336.1  GI:33044106
KEYWORDS    JP 2002532085-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 9 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/9
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .25
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
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ACCESSION   AX547823
VERSION     AX547823.1  GI:25812967
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 962 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 204
AX684290
LOCUS       AX684290                 24 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 13 from Patent WO02059609.
ACCESSION   AX684290
VERSION     AX684290.1  GI:29371160
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mack,D.H., Gish,K.C. and Wilson,K.E.
  TITLE     Methods of diagnosing colorectal cancer and/or breast cancer,
            compositions, and methods of screening for colorectal cancer and/or
            breast cancer modulators
  JOURNAL   Patent: WO 02059609-A 13 01-AUG-2002;
            EOS Biotechnology, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="T7-(dT)-24 primer"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 205
AX750585
LOCUS       AX750585                 24 bp    DNA     linear   PAT 20-JUN-2003
DEFINITION  Sequence 11 from Patent WO0221134.
ACCESSION   AX750585
VERSION     AX750585.1  GI:32133003
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mack,D. and Gish,K.C.
  TITLE     Methods of diagnosing breast cancer and screening for modulators
  JOURNAL   Patent: WO 0221134-A 11 14-MAR-2002;
            EOS Biotechnology, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="T7-(dT)-24 primer"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 206
AX817782/c
LOCUS       AX817782                 24 bp    DNA     linear   PAT 10-DEC-2003
DEFINITION  Sequence 18 from Patent WO02067861.
ACCESSION   AX817782
VERSION     AX817782.1  GI:39722977
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   .
  TITLE     Oncolytic adenoviral vectors
  JOURNAL   Patent: WO 02067861-A 18 06-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Viral vector sequence"
     misc_feature    1. .24
                     /note="Fig. 1C. SV40 early Poly(A) site"
     polyA_site      3. .24

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 207
AX829247
LOCUS       AX829247                 24 bp    DNA     linear   PAT 12-DEC-2003
DEFINITION  Sequence 140 from Patent WO02059377.
ACCESSION   AX829247
VERSION     AX829247.1  GI:39838972
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mack,D.H., Gish,K.C. and Afar,D.
  TITLE     Methods of diagnosis of breast cancer, compositions and methods of
            screening for modulators of breast cancer
  JOURNAL   Patent: WO 02059377-A 140 01-AUG-2002;
            EOS Biotechnology, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence:T7-T24 oligo"
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            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 199
AX427163
LOCUS       AX427163                  24 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 12 from Patent WO0210374.
ACCESSION   AX427163
VERSION     AX427163.1  GI:21530544
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lin,S.L., Chuong,C.M. and Widelitz,R.B.
  TITLE     Gene silencing using mrna-cdna hybrids
  JOURNAL   Patent: WO 0210374-A 12 07-FEB-2002;
            UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Poly(dT)24 primer"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 200
AX428574/c
LOCUS       AX428574                  24 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 1 from Patent WO0184157.
ACCESSION   AX428574
VERSION     AX428574.1  GI:21538485
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Pease,J.S., Cromer,R., Patel,R., Kurn,N. and de Keczer,S.
  TITLE     Compositions for detection of multiple analytes
  JOURNAL   Patent: WO 0184157-A 1 08-NOV-2001;
            Dade Behring Marburg GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthesized"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 201
AX547294
LOCUS       AX547294                  24 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 433 from Patent WO02053141.
ACCESSION   AX547294
VERSION     AX547294.1  GI:25812438
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 433 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 202
AX547822
LOCUS       AX547822                  24 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 961 from Patent WO02053141.
ACCESSION   AX547822
VERSION     AX547822.1  GI:25812966
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 961 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 203
AX547823/c
LOCUS       AX547823                  24 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 962 from Patent WO02053141.
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  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 194
AX104241
LOCUS       AX104241                  24 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 433 from Patent WO0122972.
ACCESSION   AX104241
VERSION     AX104241.1  GI:13920438
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 433 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 195
AX104769
LOCUS       AX104769                  24 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 961 from Patent WO0122972.
ACCESSION   AX104769
VERSION     AX104769.1  GI:13920966
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 961 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 196
AX104770/c
LOCUS       AX104770                  24 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 962 from Patent WO0122972.
ACCESSION   AX104770
VERSION     AX104770.1  GI:13920967
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 962 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 197
AX354553/c
LOCUS       AX354553                  24 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 11 from Patent WO0173129.
ACCESSION   AX354553
VERSION     AX354553.1  GI:18619355
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Pollner,R.B.
  TITLE     Real time monitoring of PCR using loci
  JOURNAL   Patent: WO 0173129-A 11 04-OCT-2001;
            DADE BEHRING INC. (US)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide attached to beads"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 198
AX355813
LOCUS       AX355813                  24 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 841 from Patent WO0197843.
ACCESSION   AX355813
VERSION     AX355813.1  GI:18620481
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 841 27-DEC-2001;
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                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 189
AR213697/c
LOCUS       AR213697                  24 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 4 from patent US 6406667.
ACCESSION   AR213697
VERSION     AR213697.1  GI:23310978
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Singh,S. and Ullman,E.F.
  TITLE     Chemiluminescent compositions for use in detection of multiple
            analytes
  JOURNAL   Patent: US 6406667-A 4 18-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 190
AR232949/c
LOCUS       AR232949                  24 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6457426.
ACCESSION   AR232949
VERSION     AR232949.1  GI:27275296
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Cruson,I.
  TITLE     Front tube furrow opener attachment
  JOURNAL   Patent: US 6457426-A 1 01-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 191
AR241846
LOCUS       AR241846                  24 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 134 from patent US 6472154.
ACCESSION   AR241846
VERSION     AR241846.1  GI:27287658
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 134 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 192
AR340571/c
LOCUS       AR340571                  24 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 4 from patent US 6573054.
ACCESSION   AR340571
VERSION     AR340571.1  GI:33732217
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Patel,R. and Kurn,N.
  TITLE     Quantitative determination of nucleic acid amplification products
  JOURNAL   Patent: US 6573054-A 4 03-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 193
AR345020/c
LOCUS       AR345020                  24 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6582938.
ACCESSION   AR345020
VERSION     AR345020.1  GI:33741140
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Su,X., Dong,H. and Ryder,T.B.
  TITLE     Amplification of nucleic acids
  JOURNAL   Patent: US 6582938-A 1 24-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
```

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                    ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 184
AR107972/c
LOCUS       AR107972                  24 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 1 from patent US 6110682.
ACCESSION   AR107972
VERSION     AR107972.1  GI:12823459
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dellinger,D.J., Dahm,S.C. and Troll,M.A.
  TITLE     Signal enhancement method and kit
  JOURNAL   Patent: US 6110682-A 1 29-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
                ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 185
BD234330
LOCUS       BD234330                  24 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234330
VERSION     BD234330.1  GI:33044100
KEYWORDS    JP 2002532085-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 3 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/3
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
                ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 186
I24762/c
LOCUS       I24762                    24 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 25 from patent US 5545551.
ACCESSION   I24762
VERSION     I24762.1  GI:1604632
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Johnson,E.M. and Bergmann,A.D.
  TITLE     Cloning and expression of pur protein
  JOURNAL   Patent: US 5545551-A 25 13-AUG-1996;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
                ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 187
AR184443/c
LOCUS       AR184443                  24 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 11 from patent US 6346384.
ACCESSION   AR184443
VERSION     AR184443.1  GI:20230408
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Pollner,R.B.
  TITLE     Real-time monitoring of PCR using LOCI
  JOURNAL   Patent: US 6346384-A 11 12-FEB-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
                ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 188
AR202876/c
LOCUS       AR202876                  24 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 4 from patent US 6365346.
ACCESSION   AR202876
VERSION     AR202876.1  GI:21499117
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Patel,R. and Kurn,N.
  TITLE     Quantitative determination of nucleic acid amplification products
  JOURNAL   Patent: US 6365346-A 4 02-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .24
```

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ACCESSION   BD244857
VERSION     BD244857.1  GI:33054627
KEYWORDS    JP 2002532063-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Pelletier,J. and Das,M.
  TITLE     Oligonucleotide primer capable of making the non-specific double
            strand formation unstable
  JOURNAL   Patent: JP 2002532063-A 2 02-OCT-2002;
            MCGILL UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002532063-A/2
            PD   02-OCT-2002
            PF   06-OCT-1999 JP 2000574722
            PR   07-OCT-1998 CA      2246623
            PI   JERRY PELLETIER,MANJULA DAS
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 180
AR010037/c
LOCUS       AR010037                 24 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 50 from patent US 5756684.
ACCESSION   AR010037
VERSION     AR010037.1  GI:3968842
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Johnson,E.M. and Bergemann,A.D.
  TITLE     Cloning and expression of PUR protein
  JOURNAL   Patent: US 5756684-A 50 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 181
AR034772/c
LOCUS       AR034772                 24 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 50 from patent US 5869622.
ACCESSION   AR034772
VERSION     AR034772.1  GI:5950377
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Johnson,E.M. and Bergemann,A.D.
  TITLE     Monoclonal antibodies to the pur protein
  JOURNAL   Patent: US 5869622-A 50 09-FEB-1999;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 182
AR068465/c
LOCUS       AR068465                 24 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5853993.
ACCESSION   AR068465
VERSION     AR068465.1  GI:6000672
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dellinger,D.J., Dahm,S.C. and Troll,M.A.
  TITLE     Signal enhancement method and kit
  JOURNAL   Patent: US 5853993-A 1 29-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 183
AR105984/c
LOCUS       AR105984                 24 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 7 from patent US 6103474.
ACCESSION   AR105984
VERSION     AR105984.1  GI:12820049
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dellinger,D.J., Dahm,S.C., Ilsley,D.D., Ach,R.A. and Troll,M.A.
  TITLE     Hybridization assay signal enhancement
  JOURNAL   Patent: US 6103474-A 7 15-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
```

```
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 175
BD224108
LOCUS       BD224108                 21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Mammaglobin, breast cancer secretory protein specific to mamma.
ACCESSION   BD224108
VERSION     BD224108.1  GI:33033878
KEYWORDS    JP 2002525098-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Mammaglobin, breast cancer secretory protein specific to mamma
  JOURNAL   Patent: JP 2002525098-A 10 13-AUG-2002;
            WASHINGTON UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002525098-A/10
            PD   13-AUG-2002
            PF   29-SEP-1999 JP 2000572241
            PR   29-SEP-1998 US    09/162622
            PI   MARK A WATSON,TIMOTHY P FLEMING
            PC
            C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/577//G01N33/574, PC
             C12N15/00
            CC   Description of Artificial Sequence:Synthetic
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 176
AR164336/c
LOCUS       AR164336                 22 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 19 from patent US 6271369.
ACCESSION   AR164336
VERSION     AR164336.1  GI:16235464
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P.F., Silverman,R.H., Maitra,R.K. and Lesiak,K.
  TITLE     Chimeric molecules targeted to viral RNAs
  JOURNAL   Patent: US 6271369-A 19 07-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 21;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         22 TTTTTTTTTTTTTTTTTTTT 2


RESULT 177
I31828/c
LOCUS       I31828                   22 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 19 from patent US 5583032.
ACCESSION   I31828
VERSION     I31828.1  GI:1822619
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA
  JOURNAL   Patent: US 5583032-A 19 10-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 21;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         22 TTTTTTTTTTTTTTTTTTTT 2


RESULT 178
I69425/c
LOCUS       I69425                   22 bp    DNA     linear   PAT 04-FEB-1998
DEFINITION  Sequence 19 from patent US 5677289.
ACCESSION   I69425
VERSION     I69425.1  GI:2831547
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
  TITLE     Method of cleaving specific strands of RNA and medical treatments
            thereby
  JOURNAL   Patent: US 5677289-A 19 14-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.7%;  Score 21;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         22 TTTTTTTTTTTTTTTTTTTT 2


RESULT 179
BD244857
LOCUS       BD244857                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Oligonucleotide primer capable of making the non-specific double
            strand formation unstable.
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  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||||
Db         21 TGAAAAAAAAAAAAAAAAAAA 1


RESULT 172
AX825163
LOCUS       AX825163                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 61 from Patent WO03072818.
ACCESSION   AX825163
VERSION     AX825163.1  GI:39750892
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 61 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTA 21


RESULT 173
AX825166
LOCUS       AX825166                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 64 from Patent WO03072818.
ACCESSION   AX825166
VERSION     AX825166.1  GI:39750895
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 64 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 174
BD080832
LOCUS       BD080832                 21 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Mammaglobin, a secreted mammary specific breast cancer protein.
ACCESSION   BD080832
VERSION     BD080832.1  GI:22626435
KEYWORDS    JP 2001516569-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Mammaglobin, a secreted mammary specific breast cancer protein
  JOURNAL   Patent: JP 2001516569-A 10 02-OCT-2001;
            WASHINGTON UNIVERSITY
COMMENT     OS   Unidentified
            PN   JP 2001516569-A/10
            PD   02-OCT-2001
            PF   18-SEP-1998 JP 2000511779
            PR   18-SEP-1997 US    08/933149
            PI   MARK A WATSON,TIMOTHY P FLEMING
            PC   C12N15/09,A61K35/26,A61K39/00,A61K39/00,A61K39/395,A61K39/395,
            PC   A61P35/00,
            PC   C07K14/47,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Mammaglobin, a secreted mammary specific breast cancer protein
            FH   Key             Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .21
```

```
RESULT 169
AX825135/c
LOCUS       AX825135                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 33 from Patent WO03072818.
ACCESSION   AX825135
VERSION     AX825135.1  GI:39750864
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 33 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              |||||||||||||||||||||
Db         21 TTGAAAAAAAAAAAAAAAAAA 1


RESULT 170
AX825151
LOCUS       AX825151                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 49 from Patent WO03072818.
ACCESSION   AX825151
VERSION     AX825151.1  GI:39750880
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 49 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTAA 21


RESULT 171
AX825159/c
LOCUS       AX825159                21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 57 from Patent WO03072818.
ACCESSION   AX825159
VERSION     AX825159.1  GI:39750888
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 57 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
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AX104720
LOCUS       AX104720                 21 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 912 from Patent WO0122972.
ACCESSION   AX104720
VERSION     AX104720.1  GI:13920917
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 912 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 166
AX355812
LOCUS       AX355812                 21 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 840 from Patent WO0197843.
ACCESSION   AX355812
VERSION     AX355812.1  GI:18620480
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 840 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 167
AX547773
LOCUS       AX547773                 21 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 912 from Patent WO02053141.
ACCESSION   AX547773
VERSION     AX547773.1  GI:25812917
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 912 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 168
AX825105
LOCUS       AX825105                 21 bp    DNA     linear   PAT 11-DEC-2003
DEFINITION  Sequence 3 from Patent WO03072818.
ACCESSION   AX825105
VERSION     AX825105.1  GI:39750834
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
  TITLE     Method for sorting single-stranded nucleic acids
  JOURNAL   Patent: WO 03072818-A 3 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen
                     Sequenz:Capture-Oligonukleotid"
     misc_binding    1
                     /bound_moiety="Biotin"
     modified_base   3
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   6
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   9
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   12
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   15
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER
     modified_base   18
                     /note="LNA-T (Locked Nucleic Acid)"
                     /mod_base=OTHER

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAAC 21
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RESULT 160
AR084524
LOCUS       AR084524                 21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 13 from patent US 5981185.
ACCESSION   AR084524
VERSION     AR084524.1  GI:10011295
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 13 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 161
AR093143
LOCUS       AR093143                 21 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 12 from patent US 5998596.
ACCESSION   AR093143
VERSION     AR093143.1  GI:10019895
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Bergan,R. and Neckers,L.
  TITLE     Inhibition of protein kinase activity by aptameric action of
            oligonucleotides
  JOURNAL   Patent: US 5998596-A 12 07-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 162
AR095412
LOCUS       AR095412                 21 bp    DNA     linear   PAT 08-SEP-2000
DEFINITION  Sequence 13 from patent US 6004756.
ACCESSION   AR095412
VERSION     AR095412.1  GI:10023262
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Method for detecting the presence of breast cancer by detecting an
            increase in mammaglobin mRNA expression
  JOURNAL   Patent: US 6004756-A 13 21-DEC-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 163
I65744
LOCUS       I65744                   21 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 13 from patent US 5668267.
ACCESSION   I65744
VERSION     I65744.1  GI:2482314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Polynucleotides encoding mammaglobin, a mammary-specific breast
            cancer protein
  JOURNAL   Patent: US 5668267-A 13 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 164
AR322245
LOCUS       AR322245                 21 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 13 from patent US 6566072.
ACCESSION   AR322245
VERSION     AR322245.1  GI:33707814
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Mammaglobin, a secreted mammary-specific breast cancer protein
  JOURNAL   Patent: US 6566072-A 13 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 165
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LOCUS       S64862S3                  27 bp    DNA     linear   PRI 17-DEC-1993
DEFINITION  alpha 1-theta 1 globin intergenic region (3' alpha 1-Alu 1 repeat)
            [Hylobates sp.=gibbons, Genomic, 27 nt, segment 3 of 5].
ACCESSION   S64864
VERSION     S64864.1  GI:415419
KEYWORDS    .
SEGMENT     3 of 5
SOURCE      Hylobates sp. (gibbon)
  ORGANISM  Hylobates sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Bailey,A.D. and Shen,C.K.
  TITLE     Sequential insertion of Alu family repeats into specific genomic
            sites of higher primates
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7205-7209 (1993)
  MEDLINE   93348242
   PUBMED   8394013
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 136653] from the original journal article.
            This sequence comes from Fig. 2A.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Hylobates sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9581"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 27;
  Best Local Similarity   88.5%;  Pred. No. 4.5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTT 2179
              |||||||| |  ||||||||||||||
Db         26 ATTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 156
I29892
LOCUS       I29892                    32 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 5 from patent US 5578468.
ACCESSION   I29892
VERSION     I29892.1  GI:1820683
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Pickup,D.J., Patel,D. and Antczak,J.B.
  TITLE     Site-specific RNA cleavage
  JOURNAL   Patent: US 5578468-A 5 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 32;
  Best Local Similarity   88.5%;  Pred. No. 7.4e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              ||| || | ||||||||||||||||||
Db          7 AGATTTTATAAAAAAAAAAAAAAAAA 32


RESULT 157
AR222454/c
LOCUS       AR222454                  32 bp    RNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 14 from patent US 6429300.
ACCESSION   AR222454
VERSION     AR222454.1  GI:23329985
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
  TITLE     Peptide acceptor ligation methods
  JOURNAL   Patent: US 6429300-A 14 06-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 32;
  Best Local Similarity   88.5%;  Pred. No. 7.4e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||||||  | |
Db         32 TTTTTTTTTTTTTTTTTTTTTGCAT 7


RESULT 158
AR080294
LOCUS       AR080294                  21 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 13 from patent US 5968754.
ACCESSION   AR080294
VERSION     AR080294.1  GI:10007029
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Watson,M.A. and Fleming,T.P.
  TITLE     Mammaglobin, a mammary-specific breast cancer protein
  JOURNAL   Patent: US 5968754-A 13 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 159
AR084521/c
LOCUS       AR084521                  21 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 10 from patent US 5981185.
ACCESSION   AR084521
VERSION     AR084521.1  GI:10011292
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
  TITLE     Oligonucleotide repeat arrays
  JOURNAL   Patent: US 5981185-A 10 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         21 TTTTTTTTTTTTTTTTTTTT 1
```

```
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Conklin,D.C. and Blumberg,H.
  TITLE     A human 2-19 protein homologue, Z219A
  JOURNAL   Patent: JP 2001507946-A 4 19-JUN-2001;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001507946-A/4
            PD   19-JUN-2001
            PF   06-OCT-1998 JP 1999522287
            PR   06-OCT-1997 US    60/061712
            PI   DARRELL C CONKLIN,HAL BLUMBERG
            PC   C12N15/12,C12N15/62,C12N5/10,C07K14/47,C07K16/18,C12Q1/68, PC
             A01K67/027
            CC   Oligonucleotide primer ZC7231
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 4.1e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 152
BD192375
LOCUS       BD192375                 26 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Reagents and methods useful for detecting diseases of the breast.
ACCESSION   BD192375
VERSION     BD192375.1  GI:33002114
KEYWORDS    JP 2002516576-A/14.
SOURCE      Mus sp.
  ORGANISM  Mus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
            Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D.,
            Russell,J.C., Scheffel,C.P., Stroupe,S.D. and Yu,H.
  TITLE     Reagents and methods useful for detecting diseases of the breast
  JOURNAL   Patent: JP 2002516576-A 14 04-JUN-2002;
            ABBOTT LABORATORIES
COMMENT     PN   JP 2002516576-A/14
            PD   04-JUN-2002
            PF   19-JUN-1998 JP 1999504891
            PR   20-JUN-1997 US    08/879354
            PI   PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA

            PI   N FRIEDMAN,
            PI   JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R  PI
             KLASS,
            PI   JON D KRATOCHVIL,JOHN C RUSSELL,CHRISTI P SCHEFFEL,STEPHEN D
            PI   STROUPE,
            PI   HONG YU
            PC   C12N15/12,C07K14/47,C12Q1/68,C12N15/85,C12N5/10,C07K16/18, PC
             G01N33/574
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="Mus sp."
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10095"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 4.1e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||||||||  ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTG 26


RESULT 153
AX327980
LOCUS       AX327980                 27 bp    DNA     linear   PAT 07-JAN-2002
DEFINITION  Sequence 37 from Patent WO0190747.
ACCESSION   AX327980
VERSION     AX327980.1  GI:18098134
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Rhode,P., Wittman,V., Weidanz,J.A., Burkhardt,M., Card,K.F.,
            Tal,R., Acevedo,J. and Wong,H.C.
  TITLE     Modulation of t-cell receptor interactions
  JOURNAL   Patent: WO 0190747-A 37 29-NOV-2001;
            Sunol Molecular Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 27;
  Best Local Similarity   95.5%;  Pred. No. 4.5e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTD 26


RESULT 154
AX513052
LOCUS       AX513052                 27 bp    DNA     linear   PAT 03-OCT-2002
DEFINITION  Sequence 42 from Patent WO02062135.
ACCESSION   AX513052
VERSION     AX513052.1  GI:23504143
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Egelrud,T. and Hansson,L.
  TITLE     Scce modified transgenic mammals and their use as models of human
            disease
  JOURNAL   Patent: WO 02062135-A 42 15-AUG-2002;
            Egelrud, Torbjorn (SE) ; Hansson, Lennart (SE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="5 -RACE cDNA synthesis primer."

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 27;
  Best Local Similarity   95.5%;  Pred. No. 4.5e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 155
S64862S3/c
```

```
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 147
AX338547/c
LOCUS       AX338547                 26 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3 from Patent WO0188192.
ACCESSION   AX338547
VERSION     AX338547.1  GI:18128947
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Nicolaides,N.C., Sass,P.M., Grasso,L., Vogelstein,B. and
            Kinzler,K.W.
  TITLE     A method for generating hypermutable organisms
  JOURNAL   Patent: WO 0188192-A 3 22-NOV-2001;
            The Johns Hopkins UNiversity School of Medicine (US) ; Morphotek
            Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Sass, Philip, M. (US) ;
            Grasso, Luigi (US) ; Vogelstein, Bert (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Recombinant DNA"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 4.1e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||||||  | |
Db         26 TTTTTTTTTTTTTTTTTTTTGCCAT 1


RESULT 148
AX427154
LOCUS       AX427154                 26 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 3 from Patent WO0210374.
ACCESSION   AX427154
VERSION     AX427154.1  GI:21530535
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Lin,S.L., Chuong,C.M. and Widelitz,R.B.
  TITLE     Gene silencing using mrna-cdna hybrids
  JOURNAL   Patent: WO 0210374-A 3 07-FEB-2002;
            UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Poly(dT)-26mer primer"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 4.1e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTT 2180
              |||||||  |  ||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTT 26


RESULT 149
AX528804
LOCUS       AX528804                 26 bp    DNA     linear   PAT 21-NOV-2002
DEFINITION  Sequence 53 from Patent WO02059357.
ACCESSION   AX528804
VERSION     AX528804.1  GI:25172859
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Pedersen,M.L.
  TITLE     Assay and kit for analyzing gene expression
  JOURNAL   Patent: WO 02059357-A 53 01-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic construct"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 4.1e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTT 2180
              |||||||  |  ||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTT 26


RESULT 150
AX814950
LOCUS       AX814950                 26 bp    DNA     linear   PAT 05-DEC-2003
DEFINITION  Sequence 36 from Patent WO03064691.
ACCESSION   AX814950
VERSION     AX814950.1  GI:39104088
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
            Montelius,A.
  TITLE     Methods and means for manipulating nucleic acid
  JOURNAL   Patent: WO 03064691-A 36 07-AUG-2003;
            Global Genomics AB (SE)
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: Primer"
     misc_feature    26
                     /note="v is a, c or g"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 4.1e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 151
BD062456
LOCUS       BD062456                 26 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A human 2-19 protein homologue, Z219A.
ACCESSION   BD062456
VERSION     BD062456.1  GI:22608059
KEYWORDS    JP 2001507946-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
```

```
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.
  TITLE     Method for generating full-length cDNA library from single cells
  JOURNAL   Patent: US 6197554-A 5 06-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 4.1e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTT 2180
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTT 26


RESULT 143
BD237566
LOCUS       BD237566                 26 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Genes and proteins predicting and treating fit, hypertension,
            diabetes and obesity.
ACCESSION   BD237566
VERSION     BD237566.1  GI:33047336
KEYWORDS    JP 2002525115-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Shimkets,R.A.
  TITLE     Genes and proteins predicting and treating fit, hypertension,
            diabetes and obesity
  JOURNAL   Patent: JP 2002525115-A 1 13-AUG-2002;
            CURAGEN CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002525115-A/1
            PD   13-AUG-2002
            PF   28-SEP-1999 JP 2000572365
            PR   28-SEP-1998 US    09/161939
            PI   RICHARD A SHIMKETS
            PC   C12N15/09,A01K67/027,A61K31/7088,A61K38/00,A61K39/395,A61K39/
            PC   395,
            PC   A61K39/395,A61K48/00,A61P3/04,A61P3/06,A61P9/10,A61P9/12, PC
            A61P43/00,
            PC   C07K14/47,C07K16/18,C12N9/10,C12N9/88,C12Q1/25,C12Q1/52 PC
            ,C12Q1/68,G01N33/15,
            PC   G01N33/50,C12N15/00,A61K37/02
            CC   Description of Artificial Sequence: oligo(dT)<25>V FH   Key
                 Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 4.1e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 144
I79496
LOCUS       I79496                   26 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 3 from patent US 5707807.
ACCESSION   I79496
VERSION     I79496.1  GI:3207786
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 3 13-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 4.1e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||||||||    ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTG 26


RESULT 145
AR257336
LOCUS       AR257336                 26 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 43 from patent US 6486299.
ACCESSION   AR257336
VERSION     AR257336.1  GI:27307233
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Shimkets,R.A.
  TITLE     Genes and proteins predictive and therapeutic for stroke,
            hypertension, diabetes and obesity
  JOURNAL   Patent: US 6486299-A 43 26-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 4.1e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 146
AR263647
LOCUS       AR263647                 26 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 6 from patent US 6331413.
ACCESSION   AR263647
VERSION     AR263647.1  GI:28075580
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Adler,D.A. and Sheppard,P.O.
  TITLE     Secreted salivary ZSIG63 Polypeptide
  JOURNAL   Patent: US 6331413-A 6 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 4.1e+02;
```

```
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 28;
  Best Local Similarity   95.7%;  Pred. No. 4.7e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              | ||||||||||||||||||||
Db         24 CATTTTTTTTTTTTTTTTTTTT 2


RESULT 138
AR268128/c
LOCUS       AR268128                  29 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 5 from patent US 6498025.
ACCESSION   AR268128
VERSION     AR268128.1  GI:29698371
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Miller,J.E.
  TITLE     Methods and compositions for cDNA synthesis
  JOURNAL   Patent: US 6498025-A 5 24-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 29;
  Best Local Similarity   95.7%;  Pred. No. 5.2e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTT 2185
              | ||||||||||||||||||||
Db         23 TTCTTTTTTTTTTTTTTTTTTT 1


RESULT 139
AX394623/c
LOCUS       AX394623                  31 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 21 from Patent EP1186673.
ACCESSION   AX394623
VERSION     AX394623.1  GI:21065736
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 21 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 31;
  Best Local Similarity   80.6%;  Pred. No. 6.2e+02;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              |||||||      ||||||||||||||||||
Db         31 TTTTTTTGGGAGATTTTTTTTTTTTTTTTT 1


RESULT 140
AX394625/c
LOCUS       AX394625                  32 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 23 from Patent EP1186673.
ACCESSION   AX394625
VERSION     AX394625.1  GI:21065738
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wobler,P.K. and Delenstarr,G.C.
  TITLE     Calibration of molecular array data
  JOURNAL   Patent: EP 1186673-A 23 13-MAR-2002;
            Agilent Technologies Inc (US)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="probes to target sequences"

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 32;
  Best Local Similarity   80.6%;  Pred. No. 6.8e+02;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              |||||||      ||||||||||||||||||
Db         31 TTTTTTTGGGAGATTTTTTTTTTTTTTTTT 1


RESULT 141
AX391871
LOCUS       AX391871                  24 bp    DNA     linear   PAT 23-MAR-2002
DEFINITION  Sequence 21 from Patent WO0216618.
ACCESSION   AX391871
VERSION     AX391871.1  GI:19700451
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Basten,D., Dekker,P.J., Schuurhuizen,P.W., Schaap,P.J. and
            Visser,J.
  TITLE     Aminopeptidase
  JOURNAL   Patent: WO 0216618-A 21 28-FEB-2002;
            DSM N.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="RT reaction primer"

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 24;
  Best Local Similarity   95.5%;  Pred. No. 3.2e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||:
Db          3 TTTTTTTTTTTTTTTTTTTTV 24


RESULT 142
AR137712
LOCUS       AR137712                  26 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 5 from patent US 6197554.
ACCESSION   AR137712
VERSION     AR137712.1  GI:14479221
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
```

```
  Query Match             0.8%;  Score 21.4;  DB 1;  Length 25;
  Best Local Similarity   95.7%;  Pred. No. 3.3e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
              | ||||||||||||||||||||||
Db          1 CATTTTTTTTTTTTTTTTTTTTT 23


RESULT 134
AX711956
LOCUS       AX711956                  27 bp    DNA     linear   PAT 12-MAY-2003
DEFINITION  Sequence 35 from Patent WO02103060.
ACCESSION   AX711956
VERSION     AX711956.1  GI:29787747
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tuvemo,H.T., Frisk,G.E. and Yin,H.
  TITLE     Enterovirus nucleic acids
  JOURNAL   Patent: WO 02103060-A 35 27-DEC-2002;
            Innoventus Project AB (SE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 27;
  Best Local Similarity   85.2%;  Pred. No. 4.2e+02;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTTA 2187
              | |  |||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTV 27


RESULT 135
BD097128
LOCUS       BD097128                  27 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Support for immobilizing nucleotide and process for producing the
            same.
ACCESSION   BD097128
VERSION     BD097128.1  GI:22642702
KEYWORDS    WO 0155365-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
  TITLE     Support for immobilizing nucleotide and process for producing the
  JOURNAL   Patent: WO 0155365-A 2 02-AUG-2001;
            TOYO KOHAN CO LTD,MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,
            KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   WO 0155365-A/2
            PD   02-AUG-2001
            PF   24-JAN-2001 WO 2001JP000443
            PR   27-JAN-2000 JP 00P   019301
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KENICHI TAKAGI,KOJIRO  PI
            TAKAHASHI
            PC   C12N15/10,C07H21/04//G01N33/50,C12Q1/68
            CC   Support for immobilizing nucleotide and process for producing
            CC           the same
            FH   Key             Location/Qualifiers
            FT   source          1. .27
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 27;
  Best Local Similarity   95.7%;  Pred. No. 4.2e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2803
              |||| ||||||||||||||||||
Db          1 AATTCAAAAAAAAAAAAAAAAAA 23


RESULT 136
BD161932
LOCUS       BD161932                  27 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate.
ACCESSION   BD161932
VERSION     BD161932.1  GI:27867690
KEYWORDS    JP 2002191369-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
  TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized
            substrate
  JOURNAL   Patent: JP 2002191369-A 9 09-JUL-2002;
            TOYO KOHAN CO LTD,KOJIRO TAKAHASHI
COMMENT     OS   Artificial Sequence
            PN   JP 2002191369-A/9
            PD   09-JUL-2002
            PF   27-DEC-2000 JP 2000399573
            PI   MICHIFUMI TANGA,HIROSHI OKAMURA,KOJIRO TAKAHASHI PC
            C12N15/09,C12N15/09,C12Q1/68,C12N15/00,C12N15/00 CC   Method for
            carrying out thermal cycle of PCR using DNA- CC
            immobilized
            CC   substrate
            FH   Key             Location/Qualifiers
            FT   source          1. .24
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 27;
  Best Local Similarity   95.7%;  Pred. No. 4.2e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAA 2803
              |||| ||||||||||||||||||
Db          1 AATTCAAAAAAAAAAAAAAAAAA 23


RESULT 137
AX427136/c
LOCUS       AX427136                  28 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 36 from Patent WO0196559.
ACCESSION   AX427136
VERSION     AX427136.1  GI:21530519
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ellington,A.D., Hesselberth,J., Marshall,K., Robertson,M.,
            Sooter,L., Davidson,E., Cox,J.C. and Reidel,T.
  TITLE     Regulatable, catalytically active nucleic acids
  JOURNAL   Patent: WO 0196559-A 36 20-DEC-2001;
            Board of Regents, The University of Texas System (US)
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| | ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 131
BD166030
LOCUS       BD166030                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166030
VERSION     BD166030.1  GI:27871842
KEYWORDS    JP 2002191372-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 10 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/10
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| || ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 132
BD166031
LOCUS       BD166031                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166031
VERSION     BD166031.1  GI:27871843
KEYWORDS    JP 2002191372-A/11.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 11 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/11
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match              0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| | ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 133
AX116188
LOCUS       AX116188                  25 bp    DNA     linear   PAT 11-MAY-2001
DEFINITION  Sequence 1311 from Patent WO0129262.
ACCESSION   AX116188
VERSION     AX116188.1  GI:14033130
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Picoult-Newburg,L. and Pohl,M.
  TITLE     Genotyping reagents, kits and methods of use thereof
  JOURNAL   Patent: WO 0129262-A 1311 26-APR-2001;
            Orchid BioSciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
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DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107499
VERSION     BD107499.1  GI:23202317
KEYWORDS    JP 2002000275-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 8 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/8
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| | ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 129
BD145030
LOCUS       BD145030                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145030
VERSION     BD145030.1  GI:27850788
KEYWORDS    JP 2002119291-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 11 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/11
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                 hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| || ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 130
BD145031
LOCUS       BD145031                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145031
VERSION     BD145031.1  GI:27850789
KEYWORDS    JP 2002119291-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 12 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/12
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                 hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
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COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/9
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| || ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 126
BD072872
LOCUS       BD072872                 30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072872
VERSION     BD072872.1  GI:22618475
KEYWORDS    JP 2001286300-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 10 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/10
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                 examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| || ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 127
BD107498
LOCUS       BD107498                 30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107498
VERSION     BD107498.1  GI:23202316
KEYWORDS    JP 2002000275-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 7 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/7
            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| || ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 128
BD107499
LOCUS       BD107499                 30 bp    DNA     linear   PAT 18-SEP-2002
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  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||||||||||    | ||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTGTG 3


RESULT 121
AR127791/c
LOCUS       AR127791                  30 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 12 from patent US 6180777.
ACCESSION   AR127791
VERSION     AR127791.1  GI:14114386
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Horn,T.
  TITLE     Synthesis of branched nucleic acids
  JOURNAL   Patent: US 6180777-A 12 30-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||||||||||    | ||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTGTG 3


RESULT 122
I28373/c
LOCUS       I28373                    30 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 12 from patent US 5571677.
ACCESSION   I28373
VERSION     I28373.1  GI:1819149
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromomolecular structures
  JOURNAL   Patent: US 5571677-A 12 05-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||||||||||    | ||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTGTG 3


RESULT 123
AR264926
LOCUS       AR264926                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 10 from patent US 6492121.
ACCESSION   AR264926
VERSION     AR264926.1  GI:29693313
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 10 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| || ||||||||||||
Db          3 ATATATTTTTTTTCTTTTTTTTTTTTT 30


RESULT 124
AR264927
LOCUS       AR264927                  30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 11 from patent US 6492121.
ACCESSION   AR264927
VERSION     AR264927.1  GI:29693314
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 11 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| | ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 125
BD072871
LOCUS       BD072871                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072871
VERSION     BD072871.1  GI:22618474
KEYWORDS    JP 2001286300-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 9 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 29 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/29
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .32
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .32
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 32;
  Best Local Similarity   92.0%;  Pred. No. 5.8e+02;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||||||||||||||||
Db          5 CTAGTTTTTTTTTTTTTTTTTTTT 29


RESULT 117
AX556148/c
LOCUS       AX556148                 35 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 79 from Patent WO0246472.
ACCESSION   AX556148
VERSION     AX556148.1  GI:25899530
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 79 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .35
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="random synthetic sequence"

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 35;
  Best Local Similarity   78.8%;  Pred. No. 7.4e+02;
  Matches   26;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
              |||||||||||||||||||  |||    || | |
Db         34 TTTTTTTTTTTTTTTTTTTTATAAGAAGGATATT 2


RESULT 118
AR098648
LOCUS       AR098648                 29 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 6 from patent US 6077668.
ACCESSION   AR098648
VERSION     AR098648.1  GI:12808414
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kool,E.T.
  TITLE     Highly sensitive multimeric nucleic acid probes
  JOURNAL   Patent: US 6077668-A 6 20-JUN-2000;
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 29;
  Best Local Similarity   85.7%;  Pred. No. 4.7e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||| |  |||||||| ||||||||||
Db          1 TTTGTTTTTTTTTTTGTTTTTTTTTT 28


RESULT 119
AR204722
LOCUS       AR204722                 29 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 6 from patent US 6368802.
ACCESSION   AR204722
VERSION     AR204722.1  GI:21502121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kool,E.T.
  TITLE     Circular DNA vectors for synthesis of RNA and DNA
  JOURNAL   Patent: US 6368802-A 6 09-APR-2002;
FEATURES              Location/Qualifiers
     source           1. .29
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 29;
  Best Local Similarity   85.7%;  Pred. No. 4.7e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||| |  |||||||| ||||||||||
Db          1 TTTGTTTTTTTTTTTGTTTTTTTTTT 28


RESULT 120
AR051244/c
LOCUS       AR051244                 30 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 12 from patent US 5830658.
ACCESSION   AR051244
VERSION     AR051244.1  GI:5974608
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Gryaznov,S.M.
  TITLE     Convergent synthesis of branched and multiply connected
            macromolecular structures
  JOURNAL   Patent: US 5830658-A 12 03-NOV-1998;
FEATURES              Location/Qualifiers
     source           1. .30
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
```

```
DEFINITION  Sequence 2 from Patent WO03076654.
ACCESSION   AX838502
VERSION     AX838502.1  GI:39922105
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Palecek,E. and Kosak,H.
  TITLE     Method for identifying, quantifying and/or characterizing an
            analyte
  JOURNAL   Patent: WO 03076654-A 2 18-SEP-2003;
            November Aktiengesellschaft Gesellschaft fuer Molekulare Medizin
            (DE)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kuenstlichen Sequenz:
                     Willkuerliche Sequenz"

  Query Match             0.8%;  Score 22;  DB 1;  Length 32;
  Best Local Similarity   83.3%;  Pred. No. 5.4e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              |||||||||||||||||||| |    ||||
Db         32 TTTTTTTTTTTTTTTTTTTTGAGAAGGAAA 3


RESULT 113
AR214918
LOCUS       AR214918                  27 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 18 from patent US 6410235.
ACCESSION   AR214918
VERSION     AR214918.1  GI:23312859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Weindel,K. and Brand,J.
  TITLE     DNA detection by means of a strand reassociation complex
  JOURNAL   Patent: US 6410235-A 18 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 27;
  Best Local Similarity   85.2%;  Pred. No. 3.5e+02;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  |||||||||||||:|
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTYT 27


RESULT 114
AX009609
LOCUS       AX009609                  27 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 18 from Patent EP0962536.
ACCESSION   AX009609
VERSION     AX009609.1  GI:9996841
KEYWORDS    .
SOURCE      Mycobacterium tuberculosis
  ORGANISM  Mycobacterium tuberculosis
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            tuberculosis complex.
REFERENCE   1
  AUTHORS   Brand,J. and Weindel,K.D.
  TITLE     Dna detection by a strand reassociation complex
  JOURNAL   Patent: EP 0962536-A 18 08-DEC-1999;
            ROCHE DIAGNOSTICS GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Mycobacterium tuberculosis"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:1773"
     misc_signal     1
                     /note="Phosphate linked to biotin via Aminolinker"
     misc_signal     27
                     /note="Y means incorporation of
                     Aminolinker-phosphoramidite subsequently estered with 3-O
                     carboxymethyl digoxigenin"

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 27;
  Best Local Similarity   85.2%;  Pred. No. 3.5e+02;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  |||||||||||||:|
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTYT 27


RESULT 115
BD234335
LOCUS       BD234335                  28 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234335
VERSION     BD234335.1  GI:33044105
KEYWORDS    JP 2002532085-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 8 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/8
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
            FH   Key             Location/Qualifiers
            FT   source          1. .28
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 28;
  Best Local Similarity   92.0%;  Pred. No. 3.9e+02;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||||||||||||||||
Db          1 CTAGTTTTTTTTTTTTTTTTTTTT 25


RESULT 116
BD234356
LOCUS       BD234356                  32 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234356
VERSION     BD234356.1  GI:33044126
KEYWORDS    JP 2002532085-A/29.
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            PD   08-JAN-2002
            PF   27-JUN-2000 JP 2000193133
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU
            PC   C12N15/09,C12M1/00,C12M1/34,C12Q1/68,C12N15/00 CC   The base
            sequence was prepared synthetically on the aim of  CC
            examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 4.5e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || ||||| | ||||||||||||||||
Db          1 ATATATATTTTTTTCTTTTTTTTTTTTTT 30


RESULT 110
BD145029
LOCUS       BD145029                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD145029
VERSION     BD145029.1  GI:27850787
KEYWORDS    JP 2002119291-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2002119291-A 10 23-APR-2002;
            JAPAN BIOINDUSTRY ASSOCIATION, NATIONAL INSTITUTE OF ADVANCED
            INDUSTRIAL SCIENCE AND TECHNOLOGY, KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002119291-A/10
            PD   23-APR-2002
            PF   27-APR-2001 JP 2001133529
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N1/28,G01N1/28,G01N33/ PC
             53,
            PC   G01N33/566,G01N33/58,G01N37/00,G06F17/10,C12N15/00,C12N15/00,
            PC   G01N1/28,
            PC   G01N1/28
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of
            CC   a nucleic acid probe labeled with BODIBY FL/C6 upon the  CC
                   hybridization of
            CC   the probe with a target nucleic acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 4.5e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || ||||| | ||||||||||||||||
Db          1 ATATATATTTTTTTCTTTTTTTTTTTTTT 30


RESULT 111
BD166029
LOCUS       BD166029                  30 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method.
ACCESSION   BD166029
VERSION     BD166029.1  GI:27871841
KEYWORDS    JP 2002191372-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Torimura,M., Kurata,S.,
            Yamada,K. and Yokomaku,T.
  TITLE     Novel nucleic acid probes, method for determining concentrations of
            nucleic acid by using the probes, and method for analyzing data
            obtained by the method
  JOURNAL   Patent: JP 2002191372-A 9 09-JUL-2002;
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY,
            KANKYO ENGINEERING CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002191372-A/9
            PD   09-JUL-2002
            PF   26-SEP-2001 JP 2001295145
            PI   RYUICHIRO KURANE,TAKAHIRO KANAGAWA,YOICHI KAMAGATA,MASAKI  PI
             TORIMURA,
            PI   SHINYA KURATA,KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU PC
            C12N15/09,C12M1/00,C12Q1/68,G01N33/58//G01N33/53,G01N33/566, PC
            C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                   examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                   labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC            nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 4.5e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || ||||| | ||||||||||||||||
Db          1 ATATATATTTTTTTCTTTTTTTTTTTTTT 30


RESULT 112
AX838502/c
LOCUS       AX838502                  32 bp    DNA     linear   PAT 15-DEC-2003
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  Query Match             0.8%;  Score 22;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTTA 26


RESULT 106
AR264925
LOCUS       AR264925                 30 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 9 from patent US 6492121.
ACCESSION   AR264925
VERSION     AR264925.1  GI:29693312
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanagawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for determining a concentration of target nucleic acid
            molecules, nucleic acid probes for the method, and method for
            analyzing data obtained by the method
  JOURNAL   Patent: US 6492121-A 9 10-DEC-2002;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 4.5e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || |||||  | ||||||||||||||
Db          1 ATATATATTTTTTTTCTTTTTTTTTTTTTT 30


RESULT 107
AX079108/c
LOCUS       AX079108                 30 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 6 from Patent WO0106226.
ACCESSION   AX079108
VERSION     AX079108.1  GI:13158682
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mueller,O.
  TITLE     Methods for determining the proliferation activity of cells
  JOURNAL   Patent: WO 0106226-A 6 25-JAN-2001;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||||
Db         30 CTTTTTTTTTTTTTTTTTTTTT 9


RESULT 108
BD072870
LOCUS       BD072870                 30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method.
ACCESSION   BD072870
VERSION     BD072870.1  GI:22618473
KEYWORDS    JP 2001286300-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K.,
            Yokomaku,T., Koyama,O. and Furusho,K.
  TITLE     Method for assaying nucleic acid, nucleic acid probe used therefor,
            and method for analyzing data obtained by that method
  JOURNAL   Patent: JP 2001286300-A 8 16-OCT-2001;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, DIRECTOR GENERAL OF
            NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MINISTRY OF
            AGRICULTURE FORESTRY AND FISHERIES, TECHNOLOGY
COMMENT     OS   Artificial Sequence
            PN   JP 2001286300-A/8
            PD   16-OCT-2001
            PF   20-APR-2000 JP 2000120097
            PI   RYUICHIRO KURANE,TAKAHIRO KANEKAWA,YOICHI KAMAGATA,SHINYA  PI
             KURATA,
            PI   KAZUTAKA YAMADA,TOYOKAZU YOKOMAKU,OSAMU KOYAMA,KENTA FURUSHO
            PC   C12Q1/68,C12M1/00,C12N15/09,G01N31/22,G01N33/53,G01N33/542, PC
              G01N33/566,
            PC   C12N15/00
            CC   The base sequence was prepared synthetically on the aim of  CC
                      examining the
            CC   decrease in fluorescence emission of a nucleic acid probe  CC
                 labeled with
            CC   BODIBY FL/C6 upon the hybridization of the
            probe with a target
            CC             nucleic
            CC   acid.
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 4.5e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || |||||  | ||||||||||||||
Db          1 ATATATATTTTTTTTCTTTTTTTTTTTTTT 30


RESULT 109
BD107497
LOCUS       BD107497                 30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Novel quantitative polymorphism analysis method.
ACCESSION   BD107497
VERSION     BD107497.1  GI:23202315
KEYWORDS    JP 2002000275-A/6.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Kurane,R., Kanekawa,T., Kamagata,Y., Kurata,S., Yamada,K. and
            Yokomaku,T.
  TITLE     Novel quantitative polymorphism analysis method
  JOURNAL   Patent: JP 2002000275-A 6 08-JAN-2002;
            JAPAN BIO INDUSTRY ASSOCIATION,KANKYO ENG KK, AGENCY OF IND SCIENCE
            & TECHNOL
COMMENT     OS   Artificial Sequence
            PN   JP 2002000275-A/6
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  TITLE     Novel cytokine ZALPHA11 ligand
  JOURNAL   Patent: JP 2002537839-A 35 12-NOV-2002;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002537839-A/35
            PD   12-NOV-2002
            PF   09-MAR-2000 JP 2000603382
            PR   09-MAR-1999 US    09/264908,11-MAR-1999 US    09/265992 PR
            01-JUL-1999 US    60/142013
            PI   JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C  PI
            FOSTER,
            PI   RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
            PI   STACEY R DILLON,ANGELA K HAMMOND
            PC   C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
            PC   C07K14/53,
            PC   C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
             A61K37/02
            CC   Oligonucleotide primer ZC7764a
            FH   Key             Location/Qualifiers
            FT   source          1. .26
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match             0.8%;  Score 22;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTTA 26


RESULT 102
I79494
LOCUS       I79494                  26 bp    DNA     linear   PAT 10-JUN-1998
DEFINITION  Sequence 1 from patent US 5707807.
ACCESSION   I79494
VERSION     I79494.1  GI:3207784
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Kato,K.
  TITLE     Molecular indexing for expressed gene analysis
  JOURNAL   Patent: US 5707807-A 1 13-JAN-1998;
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="unknown"
                      /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 22;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTTA 26


RESULT 103
AR263648
LOCUS       AR263648                26 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 7 from patent US 6331413.
ACCESSION   AR263648
VERSION     AR263648.1  GI:28075581
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Adler,D.A. and Sheppard,P.O.
  TITLE     Secreted salivary ZSIG63 Polypeptide
  JOURNAL   Patent: US 6331413-A 7 18-DEC-2001;
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTTA 26


RESULT 104
AR374073
LOCUS       AR374073                26 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 38 from patent US 6605272.
ACCESSION   AR374073
VERSION     AR374073.1  GI:40076645
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Methods of using zalpha11 ligand
  JOURNAL   Patent: US 6605272-A 38 12-AUG-2003;
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTTA 26


RESULT 105
AX106717
LOCUS       AX106717                26 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 9 from Patent WO0125444.
ACCESSION   AX106717
VERSION     AX106717.1  GI:13922378
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Presnell,S.R., Novak,J.E. and Gao,Z.
  TITLE     Human phosphodiesterase zcytor13
  JOURNAL   Patent: WO 0125444-A 9 12-APR-2001;
            ZymoGenetics, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .26
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Oligonucleotide primer ZC7764b"
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                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTA 22


RESULT 97
AR431310
LOCUS       AR431310                  24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 4 from patent US 6651008.
ACCESSION   AR431310
VERSION     AR431310.1  GI:40193278
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 4 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db          1 CTTTTTTTTTTTTTTTTTTTT 22


RESULT 98
AX394507/c
LOCUS       AX394507                  25 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 52 from Patent WO0218638.
ACCESSION   AX394507
VERSION     AX394507.1  GI:21065645
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
  TITLE     Detection of cyp2d6 polymorphisms
  JOURNAL   Patent: WO 0218638-A 52 07-MAR-2002;
            Gemini Genomics PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"

  Query Match             0.8%;  Score 22;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db         25 CTTTTTTTTTTTTTTTTTTTT 4


RESULT 99
AX394514
LOCUS       AX394514                  25 bp    DNA     linear   PAT 18-MAY-2002
DEFINITION  Sequence 59 from Patent WO0218638.
ACCESSION   AX394514
VERSION     AX394514.1  GI:21065652
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Risinger,C., Andersson,M.K., Lewander,T. and Oliasson,E.
  TITLE     Detection of cyp2d6 polymorphisms
  JOURNAL   Patent: WO 0218638-A 59 07-MAR-2002;
            Gemini Genomics PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide"

  Query Match             0.8%;  Score 22;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db          1 CTTTTTTTTTTTTTTTTTTTT 22


RESULT 100
AR174581
LOCUS       AR174581                  26 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 38 from patent US 6307024.
ACCESSION   AR174581
VERSION     AR174581.1  GI:17914901
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 38 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .26
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 22;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTA 26


RESULT 101
BD248974
LOCUS       BD248974                  26 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel cytokine ZALPHA11 ligand.
ACCESSION   BD248974
VERSION     BD248974.1  GI:33058744
KEYWORDS    JP 2002537839-A/35.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
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Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTT 27


RESULT 92
AX355814
LOCUS       AX355814                  27 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 842 from Patent WO0197843.
ACCESSION   AX355814
VERSION     AX355814.1  GI:18620482
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 842 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide-phosphorothioate
                     backbone"

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTT 27


RESULT 93
AX547772
LOCUS       AX547772                  27 bp    DNA     linear   PAT 01-MAR-2003
DEFINITION  Sequence 911 from Patent WO02053141.
ACCESSION   AX547772
VERSION     AX547772.1  GI:25812916
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bratzler,R.L.
  TITLE     Inhibition of angiogenesis by nucleic acids
  JOURNAL   Patent: WO 02053141-A 911 11-JUL-2002;
            Coley Pharmaceutical Group, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTT 27


RESULT 94
I32124
LOCUS       I32124                    32 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 14 from patent US 5585242.
ACCESSION   I32124
VERSION     I32124.1  GI:1822915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Bouma,S.R., Khalil,O.S. and Pabich,E.K.
  TITLE     Method for detection of nucleic acid using total internal
            reflectance
  JOURNAL   Patent: US 5585242-A 14 17-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 32;
  Best Local Similarity   88.9%;  Pred. No. 4.9e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTT 2185
              | ||  ||||||||||||||||||||
Db          6 TGTCCGCTTTTTTTTTTTTTTTTTT 32


RESULT 95
AR365237/c
LOCUS       AR365237                  33 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 1 from patent US 5478746.
ACCESSION   AR365237
VERSION     AR365237.1  GI:34428753
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Cohen,J.I., Purcell,R.H., Feinstone,S.M. and Ticehurst,J.R.
  TITLE     cDNA encoding attenuated cell culture adapted hepatitis A virus
            genome
  JOURNAL   Patent: US 5478746-A 1 26-DEC-1995;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 33;
  Best Local Similarity   88.9%;  Pred. No. 5.4e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTA 2187
              | |  ||||||||||||||||||||||
Db         28 TTTTTTTTTTTTTTTTTTTTTTTTA 2


RESULT 96
AR431307
LOCUS       AR431307                  24 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 1 from patent US 6651008.
ACCESSION   AR431307
VERSION     AR431307.1  GI:40193275
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
  TITLE     Database system including computer code for predictive cellular
            bioinformatics
  JOURNAL   Patent: US 6651008-A 1 18-NOV-2003;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 15 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 33;
  Best Local Similarity   95.8%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2803
              ||| ||||||||||||||||||||
Db          8 GAACTGAAAAAAAAAAAAAAAAAAA 31


RESULT 88
AR098680
LOCUS       AR098680                34 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 38 from patent US 6077668.
ACCESSION   AR098680
VERSION     AR098680.1  GI:12808446
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Kool,E.T.
  TITLE     Highly sensitive multimeric nucleic acid probes
  JOURNAL   Patent: US 6077668-A 38 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 34;
  Best Local Similarity   81.2%;  Pred. No. 5.4e+02;
  Matches   26;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              || |||||||  | |||| ||| |||||||||
Db          2 TTCTTTTCTCGATCTTTTCTTTCTTTTTTTT 33


RESULT 89
AR204754
LOCUS       AR204754                34 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 38 from patent US 6368802.
ACCESSION   AR204754
VERSION     AR204754.1  GI:21502161
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Kool,E.T.
  TITLE     Circular DNA vectors for synthesis of RNA and DNA
  JOURNAL   Patent: US 6368802-A 38 09-APR-2002;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 34;
  Best Local Similarity   81.2%;  Pred. No. 5.4e+02;
  Matches   26;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              || |||||||  | |||| ||| |||||||||
Db          2 TTCTTTTCTCGATCTTTTCTTTCTTTTTTTT 33


RESULT 90
E04985/c
LOCUS       E04985                  27 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence of 3'terminal fragment of ITR.
ACCESSION   E04985
VERSION     E04985.1  GI:2173180
KEYWORDS    JP 1993103673-A/79.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Sengu,K.Y. and Ito,S.
  TITLE     REPLICATION OF DNA
  JOURNAL   Patent: JP 1993103673-A 79 27-APR-1993;
            ARIZONA BOARD OF REGENTS
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1993103673-A/79
            PD   27-APR-1993
            PF   26-AUG-1991 JP 1991240525
            PI   SENGU KUU YUU, ITO SUMIYOSHI
            PC   C12N15/10,C12N15/11//C12Q1/68;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   misc_feature    1. .27
            FT                   /note='3'terminal fragment of ITR'.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db         27 TTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 91
AX104719
LOCUS       AX104719                27 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 911 from Patent WO0122972.
ACCESSION   AX104719
VERSION     AX104719.1  GI:13920916
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 911 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
VERSION     AX351711.1  GI:18616994
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mond,J.J., Flora,M. and Klinman,D.M.
  TITLE     Immunostimulatory rna/dna hybrid molecules
  JOURNAL   Patent: WO 0193902-A 7 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Combined DNA/RNA Molecule: Synthetic
                     DNA/RNA oligonucleotide~Synthetic DNA/RNA oligonucleotide"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 30;
  Best Local Similarity   86.2%;  Pred. No. 3.5e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  ||||||| || ||||||||||||||
Db         29 TTTTTTTTTTTTTCGTTTTTTTTTTTTT 1


RESULT 84
BD056964
LOCUS       BD056964                  25 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Sets of labeled energy transfer fluorescent primers and their use
            in multi component analysis.
ACCESSION   BD056964
VERSION     BD056964.1  GI:22602570
KEYWORDS    JP 2001509271-A/1.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Ju,J.
  TITLE     Sets of labeled energy transfer fluorescent primers and their use
            in multi component analysis
  JOURNAL   Patent: JP 2001509271-A 1 10-JUL-2001;
            INCYTE PHARMACEUTICALS INC
COMMENT     PN   JP 2001509271-A/1
            PD   10-JUL-2001
            PF   12-DEC-1997 JP 1998534358
            PR   15-JAN-1997 US    08/784162
            PI   JINGYUE JU
            PC   G01N21/78,C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3702"

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 25;
  Best Local Similarity   95.8%;  Pred. No. 2.2e+02;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAAC 2189
              |||||||||||||||||||| ||
Db          2 TTTTTTTTTTTTTTTTTTTTTAC 25


RESULT 85
I30206
LOCUS       I30206                    30 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 2 from patent US 5580731.
ACCESSION   I30206
VERSION     I30206.1  GI:1820997
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Chang,C.-A., Urdea,M.S. and Horn,T.
  TITLE     N-4 modified pyrimidine deoxynucleotides and oligonucleotide probes
            synthesized therewith
  JOURNAL   Patent: US 5580731-A 2 03-DEC-1996;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 30;
  Best Local Similarity   79.3%;  Pred. No. 3.8e+02;
  Matches   23;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTT 2183
              ||||||| |      ||||||||||||||
Db          2 TTTTTTTTNNNNNTTTTTTTTTTTTTT 30


RESULT 86
BD238394
LOCUS       BD238394                  33 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238394
VERSION     BD238394.1  GI:33048164
KEYWORDS    JP 2002536025-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 12 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/12
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US    09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
            FT   source          1. .33
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 33;
  Best Local Similarity   95.8%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2803
              ||| ||||||||||||||||||||||
Db          8 GAACTGAAAAAAAAAAAAAAAAAAA 31


RESULT 87
AR279820
LOCUS       AR279820                  33 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 15 from patent US 6518018.
ACCESSION   AR279820
VERSION     AR279820.1  GI:29714965
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RESULT 79
AX052994/c
LOCUS       AX052994                 29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 10 from Patent WO0071749.
ACCESSION   AX052994
VERSION     AX052994.1  GI:12227096
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 10 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Puromycin-Linker"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 80
AX353685/c
LOCUS       AX353685                 29 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 5 from Patent WO0204656.
ACCESSION   AX353685
VERSION     AX353685.1  GI:18618749
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Wagner,P. and Polakowski,T.
  TITLE     Bio-probes and use thereof
  JOURNAL   Patent: WO 0204656-A 5 17-JAN-2002;
            Xzillion GmbH & CO.KG (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Linker mit Puromycin am 3'-Ende"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 81
AX662302/c
LOCUS       AX662302                 29 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 41 from Patent WO02059293.
ACCESSION   AX662302
VERSION     AX662302.1  GI:29163186
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Forster,A.C. and Blacklow,S.C.
  TITLE     Process and compositions for peptide, protein and peptidomimetic
            synthesis
  JOURNAL   Patent: WO 02059293-A 41 01-AUG-2002;
            Forster, Anthony C. (US) ; Blacklow, Stephen C. (US)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="FROM SYNTHETIC DNA"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 82
BD204968/c
LOCUS       BD204968                 29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Protein array enabling site specification.
ACCESSION   BD204968
VERSION     BD204968.1  GI:33014738
KEYWORDS    JP 2002510505-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Protein array enabling site specification
  JOURNAL   Patent: JP 2002510505-A 3 09-APR-2002;
            PHYLOS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002510505-A/3
            PD   09-APR-2002
            PF   31-MAR-1999 JP 2000542484
            PR   03-APR-1998 US    60/080686
            PI   ROBERT G KUIMELIS,RICHARD WAGNER
            PC   C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
              G01N33/68,
            PC   C12N15/00
            CC   Oligonucleotide used for attaching puromycin
            FH   Key             Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 83
AX351711/c
LOCUS       AX351711                 30 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 7 from Patent WO0193902.
ACCESSION   AX351711
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DEFINITION  Sequence 13 from patent US 5668295.
ACCESSION   I65795
VERSION     I65795.1  GI:2482365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Wahab,S.Z. and Malik,V.S.
  TITLE     Protein involved in nicotine synthesis, DNA encoding, and use of
            sense and antisense DNAs corresponding thereto to affect nicotine
            content in transgenic tobacco cells and plants
  JOURNAL   Patent: US 5668295-A 13 16-SEP-1997;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
                ||| | ||||||||||||||||||||
Db          1 TTTGAATTCTTTTTTTTTTTTTTTTTT 29


RESULT 75
AR279813/c
LOCUS       AR279813                  29 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 8 from patent US 6518018.
ACCESSION   AR279813
VERSION     AR279813.1  GI:29714958
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 8 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 76
AR288232/c
LOCUS       AR288232                  29 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6537749.
ACCESSION   AR288232
VERSION     AR288232.1  GI:31675516
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Kuimelis,R.G. and Wagner,R.
  TITLE     Addressable protein arrays
  JOURNAL   Patent: US 6537749-A 3 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 77
AX048408
LOCUS       AX048408                  29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 7 from Patent WO0071747.
ACCESSION   AX048408
VERSION     AX048408.1  GI:12225572
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 7 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Region A"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                | ||||||| |  ||||||||||||||||
Db          1 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 29


RESULT 78
AX048409/c
LOCUS       AX048409                  29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 8 from Patent WO0071747.
ACCESSION   AX048409
VERSION     AX048409.1  GI:12225573
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
  TITLE     Detection system for separating constituents of a sample and
            production and use of the same
  JOURNAL   Patent: WO 0071747-A 8 30-NOV-2000;
            Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Linker"

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1
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     source          1. .35
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.8%;  Score 22.8;  DB 1;  Length 35;
  Best Local Similarity   79.4%;  Pred. No. 5e+02;
  Matches   27;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
              ||  ||| | ||||||||| |||| ||||||| ||
Db          1 TTAGTTTTTACTTTTTTTGTTTTGTTTTTTTAAA 34


RESULT 70
AX556148
LOCUS       AX556148                 35 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 79 from Patent WO0246472.
ACCESSION   AX556148
VERSION     AX556148.1  GI:25899530
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 79 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.8%;  Score 22.8;  DB 1;  Length 35;
  Best Local Similarity   79.4%;  Pred. No. 5e+02;
  Matches   27;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2767 AGTATTCTTGTTAGAATTGAAAAAAAAAAAAAAA 2800
              | ||| ||| ||| ||   ||||||||||||||||
Db          2 AATATCCTTCTTATAAAAAAAAAAAAAAAAAAAAA 35


RESULT 71
AR162080/c
LOCUS       AR162080                 29 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6258558.
ACCESSION   AR162080
VERSION     AR162080.1  GI:16229144
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Method for selection of proteins using RNA-protein fusions
  JOURNAL   Patent: US 6258558-A 8 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 72
AR166605/c
LOCUS       AR166605                 29 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6281344.
ACCESSION   AR166605
VERSION     AR166605.1  GI:16241997
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Nucleic acid-protein fusion molecules and libraries
  JOURNAL   Patent: US 6281344-A 8 28-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 73
BD238387/c
LOCUS       BD238387                 29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238387
VERSION     BD238387.1  GI:33048157
KEYWORDS    JP 2002536025-A/5.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 5 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/5
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US    09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.1e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 74
I65795
LOCUS       I65795                   29 bp    DNA     linear   PAT 07-OCT-1997
```

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Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              |||||| |  ||  ||||||||||||||||
Db          1 TTTTTTTTAATTAATTTTTTTTTTTTTTTT 31


RESULT 65
AX080522
LOCUS       AX080522                 32 bp    DNA     linear   PAT 26-FEB-2001
DEFINITION  Sequence 10 from Patent WO0109291.
ACCESSION   AX080522
VERSION     AX080522.1  GI:13162176
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Brownlee,G.G., Fodor,E.S. and Poon,L.S.
  TITLE     Attenuated influenza virus useful as vaccine
  JOURNAL   Patent: WO 0109291-A 10 08-FEB-2001;
            ISIS INNOVATION LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="PRIMER"

  Query Match             0.8%;  Score 23;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||||||||||||
Db         10 TCCTTTTTTTTTTTTTTTTTTTT 32


RESULT 66
A63566
LOCUS       A63566                   35 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 7 from Patent WO9720924.
ACCESSION   A63566
VERSION     A63566.1  GI:3717221
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
            AGENTS
  JOURNAL   Patent: WO 9720924-A 7 12-JUN-1997;
            SAICOM S R L (IT)
COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.8%;  Score 23;  DB 1;  Length 35;
  Best Local Similarity   83.9%;  Pred. No. 4.6e+02;
  Matches   26;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  |||| ||||||| |||||||
Db          3 TTTTTTGTTTTTTGTTTTTTGTTTTTT 33


RESULT 67
AR241865
LOCUS       AR241865                 27 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 153 from patent US 6472154.
ACCESSION   AR241865
VERSION     AR241865.1  GI:27287677
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
  TITLE     Polymorphic repeats in human genes
  JOURNAL   Patent: US 6472154-A 153 29-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.8%;  Score 22.8;  DB 1;  Length 27;
  Best Local Similarity   92.3%;  Pred. No. 2.3e+02;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||||||||||||| | ||
Db          2 TTTTTTTTTTTTTTTTTTTTTATTT 27


RESULT 68
AX052989/c
LOCUS       AX052989                 29 bp    DNA     linear   PAT 12-JAN-2001
DEFINITION  Sequence 5 from Patent WO0071749.
ACCESSION   AX052989
VERSION     AX052989.1  GI:12227091
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Boekenkamp,D., Hoppe,H.U., Burgstaller,P., Konz,D., Woelk,U. and
            Pignot,M.
  TITLE     Detection system for analyzing molecular interactions, production
            and utilization thereof
  JOURNAL   Patent: WO 0071749-A 5 30-NOV-2000;
            Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Beschreibung der kunstlichen
                     Sequenz:Puromycin-Linker"

  Query Match             0.8%;  Score 22.8;  DB 1;  Length 29;
  Best Local Similarity   88.9%;  Pred. No. 2.9e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTT 2182
              |||||| |  ||||||||||||||||||
Db         27 TTTTTTTTNTTTTTTTTTTTTTTTTT 1


RESULT 69
I35032
LOCUS       I35032                   35 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 118 from patent US 5599704.
ACCESSION   I35032
VERSION     I35032.1  GI:2088000
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Thompson,J.D. and Draper,K.G.
  TITLE     ErbB2/neu targeted ribozymes
  JOURNAL   Patent: US 5599704-A 118 04-FEB-1997;
FEATURES             Location/Qualifiers
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            FH   Key             Location/Qualifiers
            FT   source          1. .28
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .28
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 23;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||||
Db          3 CCTTTTTTTTTTTTTTTTTTTTT 25


RESULT 61
HSA241944
LOCUS       HSA241944                29 bp    DNA     linear   PRI 24-FEB-2000
DEFINITION  Homo sapiens gp130 gene, partial, intron 14 splice acceptor site.
ACCESSION   AJ241944
VERSION     AJ241944.1  GI:7105900
KEYWORDS    gp130 gene; splice acceptor site.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Szalai,C., Toth,S. and Falus,A.
  TITLE     Exon-intron organization of the human gp130 gene
  JOURNAL   Gene 243 (1-2), 161-166 (2000)
  MEDLINE   20156380
   PUBMED   10675624
REFERENCE   2  (bases 1 to 29)
  AUTHORS   Szalai,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-APR-1999) Szalai C., Heim Pal Pediatric Hospital
            Budapest, Budapest POBOX 66, H-1958 Hungary
COMMENT     Related sequence M57230.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /map="5q11"
     gene            1. .29
                     /gene="gp130"
     intron          1. .24
                     /gene="gp130"
                     /note="splice acceptor site"
                     /number=14
     exon            25. .29
                     /gene="gp130"
                     /number=15

  Query Match             0.8%;  Score 23;  DB 1;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTAA 23


RESULT 62
AR051291
LOCUS       AR051291                 32 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 8 from patent US 5830662.
ACCESSION   AR051291
VERSION     AR051291.1  GI:5974655
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Soares,M.B. and Efstratiadis,A.
  TITLE     Method for construction of normalized cDNA libraries
  JOURNAL   Patent: US 5830662-A 8 03-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 23;  DB 1;  Length 32;
  Best Local Similarity   83.9%;  Pred. No. 3.6e+02;
  Matches   26;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||  |  ||  |||||||||||||||||
Db          1 TTTTTTTTAATTAATTTTTTTTTTTTTTTT 31


RESULT 63
I16939
LOCUS       I16939                   32 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 8 from patent US 5482845.
ACCESSION   I16939
VERSION     I16939.1  GI:1251847
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Soares,M.B. and Efstratiadis,A.
  TITLE     Method for construction of normalized cDNA libraries
  JOURNAL   Patent: US 5482845-A 8 09-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 23;  DB 1;  Length 32;
  Best Local Similarity   83.9%;  Pred. No. 3.6e+02;
  Matches   26;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||  |  ||  |||||||||||||||||
Db          1 TTTTTTTTAATTAATTTTTTTTTTTTTTTT 31


RESULT 64
I45733
LOCUS       I45733                   32 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 8 from patent US 5637685.
ACCESSION   I45733
VERSION     I45733.1  GI:2469835
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Soares,M.B. and Efstratiadis,A.
  TITLE     Normalized cDNA libraries
  JOURNAL   Patent: US 5637685-A 8 10-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.8%;  Score 23;  DB 1;  Length 32;
  Best Local Similarity   83.9%;  Pred. No. 3.6e+02;
  Matches   26;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;
```

```
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 11 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/11
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US    09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
            FT   source          1. .36
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .36
                      /organism="synthetic construct"
                      /mol_type="genomic RNA"
                      /db_xref="taxon:32630"

  Query Match             0.8%;  Score 23.2;  DB 1;  Length 36;
  Best Local Similarity   89.3%;  Pred. No. 4.6e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||||||||| | || |
Db         34 TTTTTTTTTTTTTTTTTTTTTCAGTTCG 7


RESULT 57
AR279819/c
LOCUS       AR279819                  36 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 14 from patent US 6518018.
ACCESSION   AR279819
VERSION     AR279819.1  GI:29714964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 14 11-FEB-2003;
FEATURES              Location/Qualifiers
     source           1. .36
                      /organism="unknown"
                      /mol_type="unassigned RNA"

  Query Match             0.8%;  Score 23.2;  DB 1;  Length 36;
  Best Local Similarity   89.3%;  Pred. No. 4.6e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||||||||||| | || |
Db         34 TTTTTTTTTTTTTTTTTTTTTCAGTTCG 7


RESULT 58
AR261539/c
LOCUS       AR261539                  24 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 6 from patent US 6322971.
ACCESSION   AR261539
VERSION     AR261539.1  GI:28072607
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Chetverin,A.B. and Kramer,F.R.
  TITLE     Oligonucleotide arrays and their use for sorting, isolating,
            sequencing, and manipulating nucleic acids
  JOURNAL   Patent: US 6322971-A 6 27-NOV-2001;
FEATURES              Location/Qualifiers
     source           1. .24
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match             0.8%;  Score 23;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTTTAA 2


RESULT 59
AX454028
LOCUS       AX454028                  25 bp    DNA     linear   PAT 06-JUL-2002
DEFINITION  Sequence 4 from Patent WO0198539.
ACCESSION   AX454028
VERSION     AX454028.1  GI:21713668
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mitsuhashi,M., Kambara,H., Matsunaga,H. and Kawamura,M.
  TITLE     Gene markers for lung cancer
  JOURNAL   Patent: WO 0198539-A 4 27-DEC-2001;
            Hitachi Chemical Co., Ltd. (JP) ; HITACHI CHEMICAL RESEARCH CENTER,
            INC. (US) ; Hitachi, Ltd. (JP)
FEATURES              Location/Qualifiers
     source           1. .25
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="anchor primer P4."

  Query Match             0.8%;  Score 23;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||||
Db          1 TCTCCTTTTTTTTTTTTTTTTT 23


RESULT 60
BD234339
LOCUS       BD234339                  28 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234339
VERSION     BD234339.1  GI:33044109
KEYWORDS    JP 2002532085-A/12.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 28)
  AUTHORS   Romantchikov,Y.
  TITLE     Improved method for inserting nucleic acid into cyclic vector
  JOURNAL   Patent: JP 2002532085-A 12 02-OCT-2002;
            YURI ROMANTCHIKOV
COMMENT     OS   Artificial Sequence
            PN   JP 2002532085-A/12
            PD   02-OCT-2002
            PF   17-DEC-1999 JP 2000588337
            PR   17-DEC-1998 US    09/213834
            PI   YURI ROMANTCHIKOV
            PC   C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/
            PC   00
            CC   Cloning Vector
```

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DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238393
VERSION     BD238393.1  GI:33048163
KEYWORDS    JP 2002536025-A/11.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Szostak,J.W., Roberts,R.W. and Liu,R.
  TITLE     Sorting of proteins using RNA-protein fused body
  JOURNAL   Patent: JP 2002536025-A 11 29-OCT-2002;
            THE GENERAL HOSPITAL CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002536025-A/11
            PD   29-OCT-2002
            PF   01-FEB-2000 JP 2000598669
            PR   09-FEB-1999 US    09/247190
            PI   JACK W SZOSTAK,RICHARD W ROBERTS,RIHE LIU
            PC   C12N15/09,C07K7/00,C07K14/00,C12Q1/68,C12N15/00 CC
            Translation template
            FH   Key             Location/Qualifiers
            FT   source          1. .36
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             0.8%;  Score 23.4;  DB 1;  Length 36;
  Best Local Similarity   96.0%;  Pred. No. 4.3e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              ||| ||||||||||||||||||||||
Db          8 GAACTGAAAAAAAAAAAAAAAAAAA 32


RESULT 53
AR279819
LOCUS       AR279819                36 bp    RNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 14 from patent US 6518018.
ACCESSION   AR279819
VERSION     AR279819.1  GI:29714964
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Szostak,J.W. and Roberts,R.W.
  TITLE     RNA-antibody fusions and their selection
  JOURNAL   Patent: US 6518018-A 14 11-FEB-2003;
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="unknown"
                     /mol_type="unassigned RNA"

  Query Match             0.8%;  Score 23.4;  DB 1;  Length 36;
  Best Local Similarity   96.0%;  Pred. No. 4.3e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              ||| ||||||||||||||||||||||
Db          8 GAACTGAAAAAAAAAAAAAAAAAAA 32


RESULT 54
AX430216/c
LOCUS       AX430216                29 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 7 from Patent EP1207210.
ACCESSION   AX430216
VERSION     AX430216.1  GI:21655581
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dietmaier,W.
  TITLE     Method for melting curve analysis of repetitive pcr products
  JOURNAL   Patent: EP 1207210-A 7 22-MAY-2002;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.8%;  Score 23.2;  DB 1;  Length 29;
  Best Local Similarity   89.3%;  Pred. No. 2.4e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTTTTTTTTTTT 2179
              |||||||||| |  |||||||||||||
Db         29 TGATTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 55
BD165919/c
LOCUS       BD165919                29 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for melting curve analysis of repetitive PCR products.
ACCESSION   BD165919
VERSION     BD165919.1  GI:27871731
KEYWORDS    JP 2002191384-A/7.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Dietmaier,W.
  TITLE     Method for melting curve analysis of repetitive PCR products
  JOURNAL   Patent: JP 2002191384-A 7 09-JUL-2002;
            F HOFFMANN LA ROCHE AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191384-A/7
            PD   09-JUL-2002
            PF   13-NOV-2001 JP 2001348017
            PR   15-NOV-2000 EP   00124897.0
            PI   WOLFGANG DIETMAIER
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Method for melting curve analysis of repetitive PCR products
            FH   Key             Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"

  Query Match             0.8%;  Score 23.2;  DB 1;  Length 29;
  Best Local Similarity   89.3%;  Pred. No. 2.4e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTTTTTTTTTTT 2179
              |||||||||| |  |||||||||||||
Db         29 TGATTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 56
BD238393/c
LOCUS       BD238393                36 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Sorting of proteins using RNA-protein fused body.
ACCESSION   BD238393
VERSION     BD238393.1  GI:33048163
KEYWORDS    JP 2002536025-A/11.
SOURCE      synthetic construct
```

```
                    /db_xref="taxon:32644"

  Query Match              0.8%;  Score 23.6;  DB 1;  Length 32;
  Best Local Similarity   86.7%;  Pred. No. 2.8e+02;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTAACT 2190
              | |  |||||||||||||||||||||| ||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTACCT 3


RESULT 48
AX196237/c
LOCUS       AX196237                 30 bp    DNA     linear   PAT 28-AUG-2001
DEFINITION  Sequence 68 from Patent WO0151665.
ACCESSION   AX196237
VERSION     AX196237.1  GI:15386440
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0151665-A 68 19-JUL-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.8%;  Score 23.4;  DB 1;  Length 30;
  Best Local Similarity   96.0%;  Pred. No. 2.5e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||| ||||||||||||||||||||
Db         25 TCTGCTTTTTTTTTTTTTTTTTTT 1


RESULT 49
AX440138/c
LOCUS       AX440138                 30 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 68 from Patent WO0173123.
ACCESSION   AX440138
VERSION     AX440138.1  GI:21664949
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0173123-A 68 04-OCT-2001;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.8%;  Score 23.4;  DB 1;  Length 30;
  Best Local Similarity   96.0%;  Pred. No. 2.5e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||| ||||||||||||||||||||
Db         25 TCTGCTTTTTTTTTTTTTTTTTTT 1


RESULT 50
AX465324/c
LOCUS       AX465324                 30 bp    DNA     linear   PAT 16-JUL-2002
DEFINITION  Sequence 68 from Patent WO0218643.
ACCESSION   AX465324
VERSION     AX465324.1  GI:21899687
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0218643-A 68 07-MAR-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.8%;  Score 23.4;  DB 1;  Length 30;
  Best Local Similarity   96.0%;  Pred. No. 2.5e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||| ||||||||||||||||||||
Db         25 TCTGCTTTTTTTTTTTTTTTTTTT 1


RESULT 51
AX556137/c
LOCUS       AX556137                 30 bp    DNA     linear   PAT 27-NOV-2002
DEFINITION  Sequence 68 from Patent WO0246472.
ACCESSION   AX556137
VERSION     AX556137.1  GI:25899519
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
            Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
  TITLE     Nanoparticles having oligonucleotides attached thereto and uses
            therefor
  JOURNAL   Patent: WO 0246472-A 68 13-JUN-2002;
            Nanosphere, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="random synthetic sequence"

  Query Match              0.8%;  Score 23.4;  DB 1;  Length 30;
  Best Local Similarity   96.0%;  Pred. No. 2.5e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||| ||||||||||||||||||||
Db         25 TCTGCTTTTTTTTTTTTTTTTTTT 1


RESULT 52
BD238393
LOCUS       BD238393                 36 bp    RNA     linear   PAT 17-JUL-2003
```

```
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Methods of using zalpha11 ligand
  JOURNAL   Patent: US 6605272-A 27 12-AUG-2003;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             0.9%;  Score 24;  DB 1;  Length 34;
  Best Local Similarity   84.4%;  Pred. No. 2.8e+02;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||     ||||||||||||||||
Db          1 TTTTTTTCTCGAGACTTTTTTTTTTTTTTTT 32


RESULT 44
AX179588
LOCUS       AX179588                 34 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 11 from Patent WO0146422.
ACCESSION   AX179588
VERSION     AX179588.1  GI:15132019
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Presnell,S.R. and Kindsvogel,W.
  TITLE     Cytokine zcyto18
  JOURNAL   Patent: WO 0146422-A 11 28-JUN-2001;
            ZymoGenetics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide primer ZC18698"

  Query Match             0.9%;  Score 24;  DB 1;  Length 34;
  Best Local Similarity   84.4%;  Pred. No. 2.8e+02;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||     ||||||||||||||||
Db          1 TTTTTTTCTCGAGACTTTTTTTTTTTTTTTT 32


RESULT 45
A08914/c
LOCUS       A08914                   31 bp    DNA     linear   PAT 02-SEP-1993
DEFINITION  H.sapiens (haplotype 3, allele MS32, isolate Mormon, serial number
            2) minisatellite sequence.
ACCESSION   A08914
VERSION     A08914.1  GI:411836
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Jeffreys,A.J.
  TITLE     Extended nucleotide sequences
  JOURNAL   Patent: EP 0370719-A 97 30-MAY-1990;
            IMPERIAL CHEMICAL INDUSTRIES PLC
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.8%;  Score 23.6;  DB 1;  Length 31;
  Best Local Similarity   86.7%;  Pred. No. 2.5e+02;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              || ||||| |  ||||||||||||||||||
Db         31 ATATTTTTTTTTTTTTTTTTTTTTTTTTT 2


RESULT 46
AX430213/c
LOCUS       AX430213                 32 bp    DNA     linear   PAT 28-JUN-2002
DEFINITION  Sequence 4 from Patent EP1207210.
ACCESSION   AX430213
VERSION     AX430213.1  GI:21655578
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dietmaier,W.
  TITLE     Method for melting curve analysis of repetitive pcr products
  JOURNAL   Patent: EP 1207210-A 4 22-MAY-2002;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.8%;  Score 23.6;  DB 1;  Length 32;
  Best Local Similarity   86.7%;  Pred. No. 2.8e+02;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTTAACT 2190
              | |  |||||||||||||||||||||| ||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTACCT 3


RESULT 47
BD165916/c
LOCUS       BD165916                 32 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method for melting curve analysis of repetitive PCR products.
ACCESSION   BD165916
VERSION     BD165916.1  GI:27871728
KEYWORDS    JP 2002191384-A/4.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 32)
  AUTHORS   Dietmaier,W.
  TITLE     Method for melting curve analysis of repetitive PCR products
  JOURNAL   Patent: JP 2002191384-A 4 09-JUL-2002;
            F HOFFMANN LA ROCHE AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191384-A/4
            PD   09-JUL-2002
            PF   13-NOV-2001 JP 2001348017
            PR   15-NOV-2000 EP   00124897.0
            PI   WOLFGANG DIETMAIER
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Method for melting curve analysis of repetitive PCR products
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .32
                     /organism="unidentified"
                     /mol_type="genomic DNA"
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```
     source          1. .33
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.9%;  Score 24;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
             ||||||||||||||||||||||||
Db          6 TCCTTTTTTTTTTTTTTTTTTTTT 29


RESULT 40
BD173750
LOCUS       BD173750                 33 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Process for producing cytochrome c.
ACCESSION   BD173750
VERSION     BD173750.1  GI:28415083
KEYWORDS    WO 02059339-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Oku,T., Nishio,T. and Sato,T.
  TITLE     Process for producing cytochrome c
  JOURNAL   Patent: WO 02059339-A 2 01-AUG-2002;
            NIHON UNIVERSITY,TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
COMMENT     OS   Artificial Sequence
            PN   WO 02059339-A/2
            PD   01-AUG-2002
            PF   23-JAN-2002 WO 2002JP000467
            PR   23-JAN-2001 JP 01P   014510
            PI   TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
            PC   C12P21/02,C12N15/53,C12N15/63,C12N1/21//(C12P21/02,C12R1:91),
            PC   (C12N15/53,C12R1:01),(C12N1/21,C12R1:01)
            CC   Process for producing cytochrome c
            FH   Key             Location/Qualifiers
            FT   source          1. .33
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.9%;  Score 24;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
             ||||||||||||||||||||||||
Db          6 TCCTTTTTTTTTTTTTTTTTTTTT 29


RESULT 41
AR174572
LOCUS       AR174572                 34 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 27 from patent US 6307024.
ACCESSION   AR174572
VERSION     AR174572.1  GI:17914892
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Cytokine zalpha11 Ligand
  JOURNAL   Patent: US 6307024-A 27 23-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match              0.9%;  Score 24;  DB 1;  Length 34;
  Best Local Similarity   84.4%;  Pred. No. 2.8e+02;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
             |||||||||||     ||||||||||||||||
Db          1 TTTTTTTCTCGAGACTTTTTTTTTTTTTTTT 32


RESULT 42
BD248965
LOCUS       BD248965                 34 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Novel cytokine ZALPHA11 ligand.
ACCESSION   BD248965
VERSION     BD248965.1  GI:33058735
KEYWORDS    JP 2002537839-A/26.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 34)
  AUTHORS   Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
  TITLE     Novel cytokine ZALPHA11 ligand
  JOURNAL   Patent: JP 2002537839-A 26 12-NOV-2002;
            ZYMOGENETICS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002537839-A/26
            PD   12-NOV-2002
            PF   09-MAR-2000 JP 2000603382
            PR   09-MAR-1999 US    09/264908,11-MAR-1999 US    09/265992 PR
            01-JUL-1999 US    60/142013
            PI   JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C  PI
            FOSTER,
            PI   RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
            PI   STACEY R DILLON,ANGELA K HAMMOND
            PC   C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
            PC   C07K14/53,
            PC   C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
             C12N1/21,
            PC   C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
             A61K37/02
            CC   Oligonucleotide primer ZC18698
            FH   Key             Location/Qualifiers
            FT   source          1. .34
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match              0.9%;  Score 24;  DB 1;  Length 34;
  Best Local Similarity   84.4%;  Pred. No. 2.8e+02;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
             |||||||||||     ||||||||||||||||
Db          1 TTTTTTTCTCGAGACTTTTTTTTTTTTTTTT 32


RESULT 43
AR374064
LOCUS       AR374064                 34 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 27 from patent US 6605272.
ACCESSION   AR374064
VERSION     AR374064.1  GI:40076636
KEYWORDS    .
SOURCE      Unknown.
```

```
RESULT 36
BD274321
LOCUS       BD274321                  29 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION   BD274321
VERSION     BD274321.1  GI:33084089
KEYWORDS    JP 2002526030-A/288.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
  TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
  JOURNAL   Patent: JP 2002526030-A 288 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526030-A/288
            PD   20-AUG-2002
            PF   12-MAY-1999 JP 2000548510
            PR   12-MAY-1998 US    60/085092,12-MAY-1998 US    09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC   Description
            of Artificial Sequence: Novel Sequence FH   Key
            Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.9%;  Score 24.4;  DB 1;  Length 29;
  Best Local Similarity   96.2%;  Pred. No. 1.5e+02;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2803
              ||||| ||||||||||||||||||||
Db          4 TAGAACTGAAAAAAAAAAAAAAAAAAA 29


RESULT 37
BD274339
LOCUS       BD274339                  29 bp    RNA     linear   PAT 17-JUL-2003
DEFINITION  Identification of molecular interaction sites in RNA for novel drug
            discovery.
ACCESSION   BD274339
VERSION     BD274339.1  GI:33084107
KEYWORDS    JP 2002526030-A/306.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J.
  TITLE     Identification of molecular interaction sites in RNA for novel drug
            discovery
  JOURNAL   Patent: JP 2002526030-A 306 20-AUG-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002526030-A/306
            PD   20-AUG-2002
            PF   12-MAY-1999 JP 2000548510
            PR   12-MAY-1998 US    60/085092,12-MAY-1998 US    09/076440 PI
            DAVID J ECKER,RANGA SAMPATH,RICHARD GRIFFEY,JOHN MCNEIL PC
            C12Q1/68,A61K31/7105,A61K48/00,C12N15/09,C12N15/00 CC   Description
            of Artificial Sequence: Novel Sequence FH   Key
            Location/Qualifiers
            FT   source          1. .29
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             0.9%;  Score 24.4;  DB 1;  Length 29;
  Best Local Similarity   96.2%;  Pred. No. 1.5e+02;
  Matches   25;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2803
              ||||| ||||||||||||||||||||
Db          4 TAGAACTGAAAAAAAAAAAAAAAAAAA 29


RESULT 38
AX079109
LOCUS       AX079109                  30 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 7 from Patent WO0106226.
ACCESSION   AX079109
VERSION     AX079109.1  GI:13158683
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Mueller,O.
  TITLE     Methods for determining the proliferation activity of cells
  JOURNAL   Patent: WO 0106226-A 7 25-JAN-2001;
            Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonukleotid"

  Query Match             0.9%;  Score 24;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||||||
Db          3 TCCTTTTTTTTTTTTTTTTTTTT 26


RESULT 39
BD171339
LOCUS       BD171339                  33 bp    DNA     linear   PAT 18-FEB-2003
DEFINITION  Production method of cytochrome c.
ACCESSION   BD171339
VERSION     BD171339.1  GI:28412629
KEYWORDS    JP 2002218979-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Oku,T., Nishio,T. and Sato,T.
  TITLE     Production method of cytochrome c
  JOURNAL   Patent: JP 2002218979-A 2 06-AUG-2002;
            NIHON UNIVERSITY
COMMENT     OS   Artificial Sequence
            PN   JP 2002218979-A/2
            PD   06-AUG-2002
            PF   23-JAN-2001 JP 2001014510
            PI   TADATAKE OKU,TOSHIYUKI NISHIO,TADASHI SATO
            PC   C12N15/09,C12N1/21,C12P21/02//(C12N15/09,C12R1:91),(C12N1/21,
            PC   C12R1:01),
            PC   (C12P21/02,C12R1:01),C12N15/00,(C12N15/00,C12R1:91) CC
            Production method of cytochrome c
            FH   Key             Location/Qualifiers
            FT   source          1. .33
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
```

```
DEFINITION  Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION   BD181359
VERSION     BD181359.1  GI:30792277
KEYWORDS    JP 2002327130-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
  TITLE     Novel fluorescent colorant and method of assaying nucleic acid
  JOURNAL   Patent: JP 2002327130-A 2 15-NOV-2002;
            TOSOH CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002327130-A/2
            PD   15-NOV-2002
            PF   11-JAN-2002 JP 2002005267
            PI   TAKUMI TOKUNAGA,TAKAHIKO ISHIGURO,RYUICHI HORIE PC
            C09B23/00,C07D417/14,C07H21/04,C09K11/06,C12N15/09,C12Q1/68, PC
            G01N33/58,
            PC   C12N15/00
            CC   dA30mer
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 33
BD170449
LOCUS       BD170449                  40 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of detecting DNA polymorphism using mass spectrometry.
ACCESSION   BD170449
VERSION     BD170449.1  GI:27876261
KEYWORDS    WO 0250307-A/4.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Inoko,H., Tamiya,G., Nakajima,K., Kimura,N., Nagashima,R.,
            Morikawa,M. and Okamoto,K.
  TITLE     Method of detecting DNA polymorphism using mass spectrometry
  JOURNAL   Patent: WO 0250307-A 4 27-JUN-2002;
            CHUGAI PHARMACEUTICAL CO LTD,HIDETOSHI INOKO,GEN TAMIYA, KENJI
            NAKAJIMA, NAOKI KIMURA,RENPEI NAGASHIMA,MINORU MORIKAWA,KOICHI
            OKAMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250307-A/4
            PD   27-JUN-2002
            PF   12-DEC-2001 WO 2001JP010892
            PR   12-DEC-2000 JP 00P   378091
            PI   HIDETOSHI INOKO,GEN TAMIYA,KENJI NAKAJIMA,NAOKI KIMURA,RENPEI
            PI   NAGASHIMA,
            PI   MINORU MORIKAWA,KOICHI OKAMOTO
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N27/62,G01N33/566,C12M1/00 CC
             Description of Artificial Sequence:an artificially synthesized CC
             DNA sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .40
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.9%;  Score 24.8;  DB 1;  Length 40;
  Best Local Similarity   80.6%;  Pred. No. 3.3e+02;
  Matches   29;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2769 TATTCTTGTTAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | || || ||| ||   ||||||||||||||||||||
Db          1 TTTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAA 36


RESULT 34
AR029830
LOCUS       AR029830                  35 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 19 from patent US 5861244.
ACCESSION   AR029830
VERSION     AR029830.1  GI:5943044
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 35)
  AUTHORS   Wang,C.-G. and Hepburn,A.G.
  TITLE     Genetic sequence assay using DNA triple strand formation
  JOURNAL   Patent: US 5861244-A 19 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .35
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.9%;  Score 24.6;  DB 1;  Length 35;
  Best Local Similarity   87.1%;  Pred. No. 2.4e+02;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              |||| | | |||||| ||||||||||||||||
Db          1 TTTTCTATTCTTTTTCTTTTTTTTTTTTTT 31


RESULT 35
AX495372/c
LOCUS       AX495372                  36 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 1137 from Patent WO02059256.
ACCESSION   AX495372
VERSION     AX495372.1  GI:23340982
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or virus resistance and their use as
            medicines
  JOURNAL   Patent: WO 02059256-A 1137 01-AUG-2002;
            MOLECULAR ENGINES LAB (FR)
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"

  Query Match             0.9%;  Score 24.6;  DB 1;  Length 36;
  Best Local Similarity   84.4%;  Pred. No. 2.6e+02;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              | |  |||||||||||||||||||||| || |
Db         34 TTTANTTTTTTTTTTTTTTTTTTTACCTGT 3
```

```
  TITLE     Oligonucleotides for labeling oligonucleotide probes and proteins
  JCURNAL   Patent: WO 0222874-A 115 21-MAR-2002;
            VENTANA MEDICAL SYSTEMS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="oligonucleotide probe"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 29
BD105776/c
LOCUS       BD105776                  30 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Conjugates of biologically stable polymers and polynucleotides for
            treating systemic lupus erythematosus.
ACCESSION   BD105776
VERSION     BD105776.1  GI:22651350
KEYWORDS    JP 2001354569-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Conrad,M.J. and Coutts,S.
  TITLE     Conjugates of biologically stable polymers and polynucleotides for
            treating systemic lupus erythematosus
  JOURNAL   Patent: JP 2001354569-A 1 25-DEC-2001;
            LA JOLLA PHARMACEUTICAL CO
COMMENT     OS   Artificial Sequence
            PN   JP 2001354569-A/1
            PD   25-DEC-2001
            PF   04-APR-2001 JP 2001106534
            PR   16-JAN-1990 US       466138,13-MAR-1990 US       494118 PI
            MICHAEL J CONRAD,STEPHEN COUTTS
            PC   A61K31/7088,A61K47/48,A61P37/02,C07K14/00,C12N15/00,C12N15/00
            CC   Synthetic Construct
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 30
BD132851
LOCUS       BD132851                  30 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Methods of nucleic acid detection.
ACCESSION   BD132851
VERSION     BD132851.1  GI:23227796
KEYWORDS    JP 2002509443-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
  TITLE     Methods of nucleic acid detection
  JOURNAL   Patent: JP 2002509443-A 2 26-MAR-2002;
            GEN PROBE INC
COMMENT     OS   Artificial Sequence
            PN   JP 2002509443-A/2
            PD   26-MAR-2002
            PF   30-OCT-1998 JP 1999526687
            PR   31-OCT-1997 US    60/063969
            PI   WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
            C12Q1/68
            CC   Description of Artificial Sequence: synthetic oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 31
BD181358
LOCUS       BD181358                  30 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Novel fluorescent colorant and method of assaying nucleic acid.
ACCESSION   BD181358
VERSION     BD181358.1  GI:30792276
KEYWORDS    JP 2002327130-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
  TITLE     Novel fluorescent colorant and method of assaying nucleic acid
  JOURNAL   Patent: JP 2002327130-A 1 15-NOV-2002;
            TOSOH CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002327130-A/1
            PD   15-NOV-2002
            PF   11-JAN-2002 JP 2002005267
            PI   TAKUMI TOKUNAGA,TAKAHIKO ISHIGURO,RYUICHI HORIE PC
            C09B23/00,C07D417/14,C07H21/04,C09K11/06,C12N15/09,C12Q1/68, PC
            G01N33/58,
            PC   C12N15/00
            CC   dT30mer
            FH   Key             Location/Qualifiers
            FT   source          1. .30
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 32
BD181359/c
LOCUS       BD181359                  30 bp    DNA     linear   PAT 15-MAY-2003
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```
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 24
AX104902
LOCUS       AX104902                  30 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1094 from Patent WO0122972.
ACCESSION   AX104902
VERSION     AX104902.1  GI:13921099
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1094 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 25
AX104903/c
LOCUS       AX104903                  30 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 1095 from Patent WO0122972.
ACCESSION   AX104903
VERSION     AX104903.1  GI:13921100
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Krieg,A.M., Schetter,C. and Vollmer,J.C.
  TITLE     Immunostimulatory nucleic acids
  JOURNAL   Patent: WO 0122972-A 1095 05-APR-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
            GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 26
AX474673
LOCUS       AX474673                  30 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1 from Patent EP1223226.
ACCESSION   AX474673
VERSION     AX474673.1  GI:22214013
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
  TITLE     Novel fluorescent dye and method of measuring nucleic acid
  JOURNAL   Patent: EP 1223226-A 1 17-JUL-2002;
            Tosoh Corporation (JP)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificial"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 27
AX474674/c
LOCUS       AX474674                  30 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 2 from Patent EP1223226.
ACCESSION   AX474674
VERSION     AX474674.1  GI:22214014
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tokunaga,T., Ishiguro,T. and Horie,R.
  TITLE     Novel fluorescent dye and method of measuring nucleic acid
  JOURNAL   Patent: EP 1223226-A 2 17-JUL-2002;
            Tosoh Corporation (JP)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificial"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 28
AX521609
LOCUS       AX521609                  30 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 115 from Patent WO0222874.
ACCESSION   AX521609
VERSION     AX521609.1  GI:23572654
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Utermohlen,J.G. and Connaughton,J.
```

```
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  JOURNAL   Patent: WO 9720068-A 7 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 20
AR179066
LOCUS       AR179066                30 bp    DNA     linear   PAT 16-MAY-2002
DEFINITION  Sequence 3 from patent US 6326143.
ACCESSION   AR179066
VERSION     AR179066.1  GI:20220621
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Orum,H. and Seeger,C.
  TITLE     Method for generating multiple double stranded nucleic acids
  JOURNAL   Patent: US 6326143-A 3 04-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 21
AR179070/c
LOCUS       AR179070                30 bp    DNA     linear   PAT 16-MAY-2002
DEFINITION  Sequence 7 from patent US 6326143.
ACCESSION   AR179070
VERSION     AR179070.1  GI:20220625
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Orum,H. and Seeger,C.
  TITLE     Method for generating multiple double stranded nucleic acids
  JOURNAL   Patent: US 6326143-A 7 04-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 22
E04638
LOCUS       E04638                  30 bp    RNA     linear   PAT 29-SEP-1997
DEFINITION  Synthesized Oligoribonucleotides of more than 20 mers.
ACCESSION   E04638
VERSION     E04638.1  GI:5708508
KEYWORDS    JP 1992330093-A/2.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Tanimura,H. and Imada,M.
  TITLE     PRODUCTION OF OLIGORIBONUCLEOTIDE
  JOURNAL   Patent: JP 1992330093-A 2 18-NOV-1992;
            TAKEDA CHEM IND LTD
COMMENT     OS   Artificial gene
            OC   Artificial sequence; Genes.
            PN   JP 1992330093-A/2
            PD   18-NOV-1992
            PF   07-JUN-1991 JP 1991136086
            PR   20-JUL-1990 JP 90P   190762
            PI   TANIMURA HIROSHI, IMADA MICHI
            PC   C07H21/02;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   misc_feature    1. .30
            FT                   /note='suitably selected protection of RNA  FT
                                 units
            FT                   facilitates 20 or more-mer oligonucleotides'.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="synthetic construct"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32630"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 23
I84450/c
LOCUS       I84450                  30 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 9 from patent US 5695936.
ACCESSION   I84450
VERSION     I84450.1  GI:3021970
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Mandrand,B., Cros,P., Delair,T., Charles,M.-H., Erout,M.-N. and
            Pichot,C.
  TITLE     Reagent and method for the detection of a nucleotide sequence with
            signal amplification
  JOURNAL   Patent: US 5695936-A 9 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
```

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COMMENT     Other publication IT MI952539 19970604
            Other publication AU 1175497 19970627.
FEATURES             Location/Qualifiers
     source          1. .34
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.9%;  Score 26;  DB 1;  Length 34;
  Best Local Similarity   85.3%;  Pred. No. 1.2e+02;
  Matches   29;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              || ||||||| |  |||||||||||||||||| |
Db          1 TGTTTTTTTTTTTTTTTTTTTTTTTTTTTTGT 34


RESULT 15
AR099615
LOCUS       AR099615                33 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 26 from patent US 6077934.
ACCESSION   AR099615
VERSION     AR099615.1  GI:12809381
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
            Grilley,M., Watkins,M. and Hillyard,D.R.
  TITLE     Contryphan peptides
  JOURNAL   Patent: US 6077934-A 26 20-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.9%;  Score 25.6;  DB 1;  Length 33;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+02;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              | ||||||| |  |||||||||||||||||
Db          2 GCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 33


RESULT 16
AR120128
LOCUS       AR120128                33 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 26 from patent US 6153738.
ACCESSION   AR120128
VERSION     AR120128.1  GI:14102827
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Jacobsen,R., Jimenez,E., Cruz,L.J., Olivera,B.M., Gray,W.R.,
            Grilley,M., Watkins,M. and Hillyard,D.R.
  TITLE     Contryphan peptides
  JOURNAL   Patent: US 6153738-A 26 28-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             0.9%;  Score 25.6;  DB 1;  Length 33;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+02;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              | ||||||| |  |||||||||||||||||
Db          2 GCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 33


RESULT 17
A43784/c
LOCUS       A43784                  30 bp    DNA     linear   PAT 06-MAR-1997
DEFINITION  Sequence 9 from Patent WO9508000.
ACCESSION   A43784
VERSION     A43784.1  GI:2298962
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Mandrand,B., Cros,P., Delair,T., Charles,M., Erout,M. and Pichot,C.
  TITLE     REAGENT AND METHOD FOR THE DETECTION OF A NUCLEOTIDE SEQUENCE WITH
            SIGNAL AMPLIFICATION
  JOURNAL   Patent: WO 9508000-A 9 23-MAR-1995;
            BIO MERIEUX (FR)
COMMENT     Other publication CA 2149315 950323
            Other publication FR 2710075 950324.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 18
A62991
LOCUS       A62991                  30 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 3 from Patent WO9720068.
ACCESSION   A62991
VERSION     A62991.1  GI:3716863
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Oerum,H. and Seeger,C.
  TITLE     METHOD FOR GENERATING MULTIPLE DOUBLE STRANDED NUCLEIC ACIDS
  JOURNAL   Patent: WO 9720068-A 3 05-JUN-1997;
            BOEHRINGER MANNHEIM GMBH (DE)
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.2e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 19
A62995/c
LOCUS       A62995                  30 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 7 from Patent WO9720068.
ACCESSION   A62995
VERSION     A62995.1  GI:3716867
KEYWORDS    .
SOURCE      unidentified
```

```
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Inoko,H., Tamiya,G., Nakajima,K., Kimura,N., Nagashima,R.,
            Morikawa,M. and Okamoto,K.
  TITLE     Method of detecting DNA polymorphism using mass spectrometry
  JOURNAL   Patent: WO 0250307-A 4 27-JUN-2002;
            CHUGAI PHARMACEUTICAL CO LTD,HIDETOSHI INOKO,GEN TAMIYA, KENJI
            NAKAJIMA, NAOKI KIMURA,RENPEI NAGASHIMA,MINORU MORIKAWA,KOICHI
            OKAMOTO
COMMENT     OS   Artificial Sequence
            PN   WO 0250307-A/4
            PD   27-JUN-2002
            PF   12-DEC-2001 WO 2001JP010892
            PR   12-DEC-2000 JP 00P   378091
            PI   HIDETOSHI INOKO,GEN TAMIYA,KENJI NAKAJIMA,NAOKI KIMURA,RENPEI
            PI   NAGASHIMA,
            PI   MINORU MORIKAWA,KOICHI OKAMOTO
            PC   C12Q1/68,C12N15/09,G01N33/53,G01N27/62,G01N33/566,C12M1/00 CC
             Description of Artificial Sequence:an artificially synthesized CC
             DNA sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .40
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .40
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"

  Query Match              1.0%;  Score 27.2;  DB 1;  Length 40;
  Best Local Similarity   90.6%;  Pred. No. 1.2e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
              ||||| |  ||||||||||||||||||||||
Db         40 TTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 9


RESULT 11
AR309630
LOCUS       AR309630                  41 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9 from patent US 6555657.
ACCESSION   AR309630
VERSION     AR309630.1  GI:31701680
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Christensen,T.
  TITLE     Isolated transcription factor for an alpha-amylase promoter in
            filamentous fungi
  JOURNAL   Patent: US 6555657-A 9 29-APR-2003;
FEATURES              Location/Qualifiers
     source           1. .41
                      /organism="unknown"
                      /mol_type="genomic DNA"

  Query Match              1.0%;  Score 26.8;  DB 1;  Length 41;
  Best Local Similarity   81.6%;  Pred. No. 1.5e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||   | |||||||  |  ||||||||||||||||||
Db          4 TGTAAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 41


RESULT 12
AX516913
LOCUS       AX516913                  41 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 3111 from Patent WO02052044.
ACCESSION   AX516913
VERSION     AX516913.1  GI:23565110
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  TITLE     Detection of genetic polymorphisms
  JOURNAL   Patent: WO 02052044-A 3111 04-JUL-2002;
            Riken (JP)
FEATURES              Location/Qualifiers
     source           1. .41
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match              1.0%;  Score 26.8;  DB 1;  Length 41;
  Best Local Similarity   87.5%;  Pred. No. 1.5e+02;
  Matches   28;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||| |||||  ||:|||||||||||||||||
Db          8 TTTATTTCTGTTTKTTTTTTTTTTTTTTTT 39


RESULT 13
AX519424
LOCUS       AX519424                  41 bp    DNA     linear   PAT 05-OCT-2002
DEFINITION  Sequence 5622 from Patent WO02052044.
ACCESSION   AX519424
VERSION     AX519424.1  GI:23569690
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
  TITLE     Detection of genetic polymorphisms
  JOURNAL   Patent: WO 02052044-A 5622 04-JUL-2002;
            Riken (JP)
FEATURES              Location/Qualifiers
     source           1. .41
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"

  Query Match              1.0%;  Score 26.8;  DB 1;  Length 41;
  Best Local Similarity   87.5%;  Pred. No. 1.5e+02;
  Matches   28;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||| |||||  ||:|||||||||||||||||
Db          8 TTTATTTCTGTTTKTTTTTTTTTTTTTTTT 39


RESULT 14
A63578
LOCUS       A63578                    34 bp    DNA     linear   PAT 12-MAR-1998
DEFINITION  Sequence 19 from Patent WO9720924.
ACCESSION   A63578
VERSION     A63578.1  GI:3717233
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Scaggiante,B. and Quadrifoglio,F.
  TITLE     A CLASS OF OLIGONUCLEOTIDES, THERAPEUTICALLY USEFUL AS ANTITUMOURAL
            AGENTS
  JOURNAL   Patent: WO 9720924-A 19 12-JUN-1997;
            SAICOM S R L (IT)
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REFERENCE   1  (bases 1 to 37)
  AUTHORS   Pickup,D.J., Patel,D. and Antczak,J.B.
  TITLE     Site-specific RNA cleavage
  JOURNAL   Patent: US 5578468-A 44 26-NOV-1996;
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="unknown"
                     /mol_type="unassigned DNA"

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 67;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db         37 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 7
AX106972
LOCUS       AX106972                37 bp    DNA     linear   PAT 30-APR-2001
DEFINITION  Sequence 25 from Patent WO0125442.
ACCESSION   AX106972
VERSION     AX106972.1  GI:13922521
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
  TITLE     Dna polymerase lambda and uses thereof
  JOURNAL   Patent: WO 0125442-A 25 12-APR-2001;
            CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES             Location/Qualifiers
     source          1. .37
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="poly dT"

  Query Match             1.0%;  Score 28;  DB 1;  Length 37;
  Best Local Similarity   86.1%;  Pred. No. 67;
  Matches   31;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 36

RESULT 8
E50766
LOCUS       E50766                  38 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Vector expressing full-length gene of RNA virus and utilization
            thereof.
ACCESSION   E50766
VERSION     E50766.1  GI:18628191
KEYWORDS    JP 2000152793-A/19.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Obara,M., Obara,K., Tabira,K., Matsuzaki,J. and Om,H.
  TITLE     Vector expressing full-length gene of RNA virus and utilization
  JOURNAL   Patent: JP 2000152793-A 19 06-JUN-2000;
            TOKYO METROPOLITAN ORGANIZATION FOR MEDICAL RESEARCH, CHUGAI
            PHARMACEUT CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2000152793-A/19
            PD   06-JUN-2000
            PF   24-JUN-1999 JP 1999178347
            PR
            PI   MICHINORI OBARA,KYOKO OBARA,KAZUNARI TABIRA,JUNICHI MATSUZAKI,
            PI   HIROSHI OMORI
            PC   C12N15/09,A01K67/027,C12N5/10,C12Q1/70,C12N15/00,C12N5/00 CC

            FH   Key             Location/Qualifiers
            FT   source          1. .38
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             1.0%;  Score 27.4;  DB 1;  Length 38;
  Best Local Similarity   83.8%;  Pred. No. 94;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | |  ||||||| |  ||||||||||||||||||||
Db          2 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38

RESULT 9
BD011883
LOCUS       BD011883                33 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  Detection kit for SRSV.
ACCESSION   BD011883
VERSION     BD011883.1  GI:22092072
KEYWORDS    WO 0079280-A/13.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Takeda,N., Natori,K., Miyamura,T., Kunio, Kamata, Sato,T. and
            Sato,S.
  TITLE     Detection kit for SRSV
  JOURNAL   Patent: WO 0079280-A 13 28-DEC-2000;
            JAPAN AS REPRESENTED BY DIRECTOR GE YOSHIHIKO HIROSE,MITSUAKI
            MORIGUCHI,KIMIYASU ISOBE DISEASES, DENKA SEIKEN CO LTD,NAOKAZU
            TAKEDA,KATSURO NATORI,TATSUO MIYAMURA, KUNIO KAMATA,TOSHINORI
            SATO,SEIYA SATO
COMMENT     OS   Artificial Sequence
            PN   WO 0079280-A/13
            PD   28-DEC-2000
            PF   22-JUN-2000 WO 2000JP004095
            PR   22-JUN-1999 JP 99P   175928
            PI   NAOKAZU TAKEDA,KATSURO NATORI,TATSUO MIYAMURA,KUNIO PI
            KAMATA,TOSHINORI  SATO,
            PI   SEIYA SATO
            PC   G01N33/569,C12N15/40
            CC
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 33;
  Best Local Similarity   90.6%;  Pred. No. 66;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              |||||||  |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 10
BD170449/c
LOCUS       BD170449                40 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Method of detecting DNA polymorphism using mass spectrometry.
ACCESSION   BD170449
VERSION     BD170449.1  GI:27876261
KEYWORDS    WO 0250307-A/4.
SOURCE      synthetic construct
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     source          1. .45
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"

  Query Match             1.1%;  Score 30;  DB 1;  Length 45;
  Best Local Similarity   86.8%;  Pred. No. 52;
  Matches   33;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  |||||||||||||||||||| || ||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41


RESULT 2
AX287575
LOCUS       AX287575                 45 bp    DNA     linear   PAT 21-NOV-2001
DEFINITION  Sequence 18 from Patent WO0177390.
ACCESSION   AX287575
VERSION     AX287575.1  GI:17049341
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   abarz A,P.
  TITLE     Process for allele discrimation utilizing primer extension
  JOURNAL   Patent: WO 0177390-A 18 18-OCT-2001;
            Molecular Staging, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="P1 primer for use in allele discrimination"

  Query Match             1.1%;  Score 30;  DB 1;  Length 45;
  Best Local Similarity   86.8%;  Pred. No. 52;
  Matches   33;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  |||||||||||||||||||| || ||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41


RESULT 3
AX225198
LOCUS       AX225198                 43 bp    DNA     linear   PAT 10-SEP-2001
DEFINITION  Sequence 7 from Patent WO0161033.
ACCESSION   AX225198
VERSION     AX225198.1  GI:15555219
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Schouten,J.P.
  TITLE     Multiplex ligatable probe amplification
  JOURNAL   Patent: WO 0161033-A 7 23-AUG-2001;
            Schouten, Johannes Petrus (NL)
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic DNA"

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 43;
  Best Local Similarity   81.0%;  Pred. No. 64;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||  ||||||| |  |||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 4
A48799/c
LOCUS       A48799                   40 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 6 from Patent WO9603528.
ACCESSION   A48799
VERSION     A48799.1  GI:2302466
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Petrik,J., Allain,J. and Pearson,G.J.
  TITLE     OLIGONUCLEOTIDES AND THEIR USE
  JOURNAL   Patent: WO 9603528-A 6 08-FEB-1996;
            LYNXVALE LTD (GB)
COMMENT     Other publication AU 3118395 960222.
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 72;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  |||||||||||||||||||   |||
Db         40 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 5
AR232955/c
LOCUS       AR232955                 40 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 7 from patent US 6457426.
ACCESSION   AR232955
VERSION     AR232955.1  GI:27275302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 40)
  AUTHORS   Cruson,I.
  TITLE     Front tube furrow opener attachment
  JOURNAL   Patent: US 6457426-A 7 01-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .40
                     /organism="unknown"
                     /mol_type="genomic DNA"

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 72;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  |||||||||||||||||||   |||
Db         40 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 6
I29931/c
LOCUS       I29931                   37 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 44 from patent US 5578468.
ACCESSION   I29931
VERSION     I29931.1  GI:1820722
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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4487	12.6	0.4	20	1	BD065818	ACCESSION:BD065818
c4488	12.6	0.4	20	1	BD144137	ACCESSION:BD144137
4489	12.6	0.4	20	1	AX149168	ACCESSION:AX149168
4490	12.6	0.4	20	1	AX149224	ACCESSION:AX149224
c4491	12.6	0.4	21	1	AR236360	ACCESSION:AR236360
4492	12.6	0.4	21	1	AX183997	ACCESSION:AX183997
c4493	12.6	0.4	22	1	AR003288	ACCESSION:AR003288
c4494	12.6	0.4	22	1	I30199	ACCESSION:I30199
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ALIGNMENTS

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DEFINITION Sequence 14 from Patent WO0177390.
ACCESSION AX287571
VERSION AX287571.1 GI:17049337
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS abarz A,P.
TITLE Process for allele discrimation utilizing primer extension
JOURNAL Patent: WO 0177390-A 14 18-OCT-2001;
Molecular Staging, Inc. (US)
FEATURES Location/Qualifiers

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c4215	13.2	0.5	20	1	I31143	ACCESSION:I31143
c4216	13.2	0.5	20	1	I31432	ACCESSION:I31432
c4217	13.2	0.5	20	1	I31478	ACCESSION:I31478
c4218	13.2	0.5	20	1	I36563	ACCESSION:I36563
c4219	13.2	0.5	20	1	I36567	ACCESSION:I36567
c4220	13.2	0.5	20	1	I69263	ACCESSION:I69263
c4221	13.2	0.5	20	1	I72481	ACCESSION:I72481
c4222	13.2	0.5	20	1	I79665	ACCESSION:I79665
4223	13.2	0.5	20	1	I86619	ACCESSION:I86619
c4224	13.2	0.5	20	1	I88643	ACCESSION:I88643
4225	13.2	0.5	20	1	AR182757	ACCESSION:AR182757
c4226	13.2	0.5	20	1	AR202004	ACCESSION:AR202004
4227	13.2	0.5	20	1	AR210682	ACCESSION:AR210682
c4228	13.2	0.5	20	1	AR210772	ACCESSION:AR210772
c4229	13.2	0.5	20	1	AR211143	ACCESSION:AR211143
c4230	13.2	0.5	20	1	AR224714	ACCESSION:AR224714
c4231	13.2	0.5	20	1	AR224726	ACCESSION:AR224726
4232	13.2	0.5	20	1	AR225136	ACCESSION:AR225136
c4233	13.2	0.5	20	1	AR228184	ACCESSION:AR228184
c4234	13.2	0.5	20	1	AR228185	ACCESSION:AR228185
4235	13.2	0.5	20	1	AR228758	ACCESSION:AR228758
c4236	13.2	0.5	20	1	AR230837	ACCESSION:AR230837
4237	13.2	0.5	20	1	AR231037	ACCESSION:AR231037
c4238	13.2	0.5	20	1	AR232228	ACCESSION:AR232228
c4239	13.2	0.5	20	1	AR232233	ACCESSION:AR232233
4240	13.2	0.5	20	1	AR232385	ACCESSION:AR232385
c4241	13.2	0.5	20	1	AR243633	ACCESSION:AR243633
c4242	13.2	0.5	20	1	AR253861	ACCESSION:AR253861
c4243	13.2	0.5	20	1	AR264949	ACCESSION:AR264949
c4244	13.2	0.5	20	1	AR265965	ACCESSION:AR265965
c4245	13.2	0.5	20	1	AR266035	ACCESSION:AR266035
4246	13.2	0.5	20	1	AR279178	ACCESSION:AR279178
c4247	13.2	0.5	20	1	AR292352	ACCESSION:AR292352
c4248	13.2	0.5	20	1	AR292453	ACCESSION:AR292453
c4249	13.2	0.5	20	1	AR293260	ACCESSION:AR293260
4250	13.2	0.5	20	1	AR295417	ACCESSION:AR295417
c4251	13.2	0.5	20	1	AR298823	ACCESSION:AR298823
4252	13.2	0.5	20	1	AR300837	ACCESSION:AR300837
c4253	13.2	0.5	20	1	AR311291	ACCESSION:AR311291
4254	13.2	0.5	20	1	AR311500	ACCESSION:AR311500
4255	13.2	0.5	20	1	AR311776	ACCESSION:AR311776
c4256	13.2	0.5	20	1	AR311993	ACCESSION:AR311993
c4257	13.2	0.5	20	1	AR312044	ACCESSION:AR312044
4258	13.2	0.5	20	1	AR313482	ACCESSION:AR313482
c4259	13.2	0.5	20	1	AR314502	ACCESSION:AR314502
c4260	13.2	0.5	20	1	AR314593	ACCESSION:AR314593
4261	13.2	0.5	20	1	AR315581	ACCESSION:AR315581
4262	13.2	0.5	20	1	AR315755	ACCESSION:AR315755
c4263	13.2	0.5	20	1	AR316042	ACCESSION:AR316042
c4264	13.2	0.5	20	1	AR316220	ACCESSION:AR316220
c4265	13.2	0.5	20	1	AR337010	ACCESSION:AR337010
c4266	13.2	0.5	20	1	AR337070	ACCESSION:AR337070
4267	13.2	0.5	20	1	AR337073	ACCESSION:AR337073
c4268	13.2	0.5	20	1	AR337126	ACCESSION:AR337126
c4269	13.2	0.5	20	1	AR337644	ACCESSION:AR337644
4270	13.2	0.5	20	1	AR362210	ACCESSION:AR362210
4271	13.2	0.5	20	1	AR362212	ACCESSION:AR362212
c4272	13.2	0.5	20	1	AR362213	ACCESSION:AR362213
4273	13.2	0.5	20	1	AR362233	ACCESSION:AR362233
c4274	13.2	0.5	20	1	AR370243	ACCESSION:AR370243
4275	13.2	0.5	20	1	AR373462	ACCESSION:AR373462
4276	13.2	0.5	20	1	AR373710	ACCESSION:AR373710
c4277	13.2	0.5	20	1	AR373832	ACCESSION:AR373832
c4278	13.2	0.5	20	1	AR379352	ACCESSION:AR379352
c4279	13.2	0.5	20	1	AR404363	ACCESSION:AR404363
4280	13.2	0.5	20	1	AR428434	ACCESSION:AR428434
c4281	13.2	0.5	20	1	AR437017	ACCESSION:AR437017
4282	13.2	0.5	20	1	AX004337	ACCESSION:AX004337
c4283	13.2	0.5	20	1	AX008651	ACCESSION:AX008651
c4284	13.2	0.5	20	1	AX020523	ACCESSION:AX020523
4285	13.2	0.5	20	1	AX020603	ACCESSION:AX020603
4286	13.2	0.5	20	1	AX026102	ACCESSION:AX026102
4287	13.2	0.5	20	1	AX039285	ACCESSION:AX039285
4288	13.2	0.5	20	1	AX039577	ACCESSION:AX039577
c4289	13.2	0.5	20	1	AX054681	ACCESSION:AX054681
c4290	13.2	0.5	20	1	AX137266	ACCESSION:AX137266
c4291	13.2	0.5	20	1	AX148870	ACCESSION:AX148870
c4292	13.2	0.5	20	1	AX148871	ACCESSION:AX148871
4293	13.2	0.5	20	1	AX149070	ACCESSION:AX149070
4294	13.2	0.5	20	1	AX149130	ACCESSION:AX149130
c4295	13.2	0.5	20	1	AX149130	ACCESSION:AX149130
c4296	13.2	0.5	20	1	AX149168	ACCESSION:AX149168
c4297	13.2	0.5	20	1	AX149224	ACCESSION:AX149224
c4298	13.2	0.5	20	1	AX167874	ACCESSION:AX167874
c4299	13.2	0.5	20	1	AX167876	ACCESSION:AX167876
4300	13.2	0.5	20	1	AX167955	ACCESSION:AX167955
4301	13.2	0.5	20	1	AX174999	ACCESSION:AX174999
4302	13.2	0.5	20	1	AX183993	ACCESSION:AX183993
c4303	13.2	0.5	20	1	AX224880	ACCESSION:AX224880
c4304	13.2	0.5	20	1	AX224881	ACCESSION:AX224881
c4305	13.2	0.5	20	1	AX295243	ACCESSION:AX295243
c4306	13.2	0.5	20	1	AX295575	ACCESSION:AX295575
4307	13.2	0.5	20	1	AX295954	ACCESSION:AX295954
4308	13.2	0.5	20	1	AX296316	ACCESSION:AX296316
c4309	13.2	0.5	20	1	AX298759	ACCESSION:AX298759
c4310	13.2	0.5	20	1	AX317648	ACCESSION:AX317648
c4311	13.2	0.5	20	1	AX323446	ACCESSION:AX323446
4312	13.2	0.5	20	1	AX418707	ACCESSION:AX418707
c4313	13.2	0.5	20	1	AX418829	ACCESSION:AX418829
4314	13.2	0.5	20	1	AX477131	ACCESSION:AX477131
4315	13.2	0.5	20	1	AX482149	ACCESSION:AX482149
c4316	13.2	0.5	20	1	AX488382	ACCESSION:AX488382
4317	13.2	0.5	20	1	AX488423	ACCESSION:AX488423
4318	13.2	0.5	20	1	AX511388	ACCESSION:AX511388
4319	13.2	0.5	20	1	AX525194	ACCESSION:AX525194
4320	13.2	0.5	20	1	AX526507	ACCESSION:AX526507
c4321	13.2	0.5	20	1	AX530262	ACCESSION:AX530262
c4322	13.2	0.5	20	1	AX535424	ACCESSION:AX535424
c4323	13.2	0.5	20	1	AX546284	ACCESSION:AX546284
c4324	13.2	0.5	20	1	AX546374	ACCESSION:AX546374
c4325	13.2	0.5	20	1	AX555049	ACCESSION:AX555049
4326	13.2	0.5	20	1	AX587369	ACCESSION:AX587369
c4327	13.2	0.5	20	1	AX613368	ACCESSION:AX613368
4328	13.2	0.5	20	1	AX613661	ACCESSION:AX613661
4329	13.2	0.5	20	1	AX613683	ACCESSION:AX613683
4330	13.2	0.5	20	1	AX613762	ACCESSION:AX613762
4331	13.2	0.5	20	1	AX613782	ACCESSION:AX613782
4332	13.2	0.5	20	1	AX613806	ACCESSION:AX613806
c4333	13.2	0.5	20	1	AX662935	ACCESSION:AX662935
c4334	13.2	0.5	20	1	AX671164	ACCESSION:AX671164
c4335	13.2	0.5	20	1	AX696916	ACCESSION:AX696916
4336	13.2	0.5	20	1	AX700802	ACCESSION:AX700802
4337	13.2	0.5	20	1	AX721749	ACCESSION:AX721749
4338	13.2	0.5	20	1	AX756534	ACCESSION:AX756534
4339	13.2	0.5	20	1	AX797528	ACCESSION:AX797528
4340	13.2	0.5	20	1	AX803658	ACCESSION:AX803658

4049	13.2	0.5	19	1	AR211759	ACCESSION:AR211759
c4050	13.2	0.5	19	1	AR211760	ACCESSION:AR211760
4051	13.2	0.5	19	1	AR211895	ACCESSION:AR211895
c4052	13.2	0.5	19	1	AR211920	ACCESSION:AR211920
4053	13.2	0.5	19	1	AR217737	ACCESSION:AR217737
c4054	13.2	0.5	19	1	AR241724	ACCESSION:AR241724
4055	13.2	0.5	19	1	AR267613	ACCESSION:AR267613
c4056	13.2	0.5	19	1	AR267614	ACCESSION:AR267614
4057	13.2	0.5	19	1	AR282797	ACCESSION:AR282797
4058	13.2	0.5	19	1	AR292807	ACCESSION:AR292807
4059	13.2	0.5	19	1	AR295171	ACCESSION:AR295171
4060	13.2	0.5	19	1	AR298367	ACCESSION:AR298367
c4061	13.2	0.5	19	1	AR298519	ACCESSION:AR298519
4062	13.2	0.5	19	1	AR342579	ACCESSION:AR342579
4063	13.2	0.5	19	1	AR382095	ACCESSION:AR382095
c4064	13.2	0.5	19	1	AX081958	ACCESSION:AX081958
4065	13.2	0.5	19	1	AX081959	ACCESSION:AX081959
4066	13.2	0.5	19	1	AX128817	ACCESSION:AX128817
4067	13.2	0.5	19	1	AX129062	ACCESSION:AX129062
4068	13.2	0.5	19	1	AX130221	ACCESSION:AX130221
c4069	13.2	0.5	19	1	AX130260	ACCESSION:AX130260
4070	13.2	0.5	19	1	AX130438	ACCESSION:AX130438
4071	13.2	0.5	19	1	AX130439	ACCESSION:AX130439
4072	13.2	0.5	19	1	AX130672	ACCESSION:AX130672
c4073	13.2	0.5	19	1	AX130690	ACCESSION:AX130690
4074	13.2	0.5	19	1	AX131033	ACCESSION:AX131033
4075	13.2	0.5	19	1	AX131607	ACCESSION:AX131607
4076	13.2	0.5	19	1	AX131608	ACCESSION:AX131608
c4077	13.2	0.5	19	1	AX131849	ACCESSION:AX131849
4078	13.2	0.5	19	1	AX132037	ACCESSION:AX132037
c4079	13.2	0.5	19	1	AX132095	ACCESSION:AX132095
c4080	13.2	0.5	19	1	AX132835	ACCESSION:AX132835
c4081	13.2	0.5	19	1	AX148872	ACCESSION:AX148872
c4082	13.2	0.5	19	1	AX149169	ACCESSION:AX149169
c4083	13.2	0.5	19	1	AX224438	ACCESSION:AX224438
4084	13.2	0.5	19	1	AX252279	ACCESSION:AX252279
c4085	13.2	0.5	19	1	AX252279	ACCESSION:AX252279
c4086	13.2	0.5	19	1	AX348014	ACCESSION:AX348014
4087	13.2	0.5	19	1	AX352872	ACCESSION:AX352872
4088	13.2	0.5	19	1	AX352996	ACCESSION:AX352996
4089	13.2	0.5	19	1	AX362717	ACCESSION:AX362717
4090	13.2	0.5	19	1	AX362841	ACCESSION:AX362841
4091	13.2	0.5	19	1	AX443261	ACCESSION:AX443261
c4092	13.2	0.5	19	1	AX472056	ACCESSION:AX472056
4093	13.2	0.5	19	1	AX497021	ACCESSION:AX497021
c4094	13.2	0.5	19	1	AX505292	ACCESSION:AX505292
4095	13.2	0.5	19	1	AX553752	ACCESSION:AX553752
c4096	13.2	0.5	19	1	AX554343	ACCESSION:AX554343
c4097	13.2	0.5	19	1	AX643288	ACCESSION:AX643288
4098	13.2	0.5	19	1	AX643291	ACCESSION:AX643291
4099	13.2	0.5	19	1	AX643355	ACCESSION:AX643355
c4100	13.2	0.5	19	1	AX643358	ACCESSION:AX643358
4101	13.2	0.5	19	1	AX643402	ACCESSION:AX643402
c4102	13.2	0.5	19	1	AX643405	ACCESSION:AX643405
4103	13.2	0.5	19	1	AX645142	ACCESSION:AX645142
c4104	13.2	0.5	19	1	AX706788	ACCESSION:AX706788
4105	13.2	0.5	19	1	AX706789	ACCESSION:AX706789
c4106	13.2	0.5	19	1	AX707718	ACCESSION:AX707718
4107	13.2	0.5	19	1	AX707719	ACCESSION:AX707719
c4108	13.2	0.5	19	1	AX711905	ACCESSION:AX711905
c4109	13.2	0.5	19	1	AX769623	ACCESSION:AX769623
c4110	13.2	0.5	19	1	AX802655	ACCESSION:AX802655
4111	13.2	0.5	19	1	AX806450	ACCESSION:AX806450
c4112	13.2	0.5	19	1	AX923861	ACCESSION:AX923861
4113	13.2	0.5	19	1	BD016786	ACCESSION:BD016786
c4114	13.2	0.5	19	1	BD082742	ACCESSION:BD082742
4115	13.2	0.5	19	1	BD090877	ACCESSION:BD090877
4116	13.2	0.5	19	1	BD101884	ACCESSION:BD101884
c4117	13.2	0.5	19	1	BD132730	ACCESSION:BD132730
4118	13.2	0.5	19	1	BD181170	ACCESSION:BD181170
4119	13.2	0.5	19	1	BD195704	ACCESSION:BD195704
4120	13.2	0.5	19	1	BD196950	ACCESSION:BD196950
4121	13.2	0.5	19	1	BD221965	ACCESSION:BD221965
c4122	13.2	0.5	19	1	BD221990	ACCESSION:BD221990
4123	13.2	0.5	19	1	AJ587912	ACCESSION:AJ587912
c4124	13.2	0.5	20	1	E12411	ACCESSION:E12411
4125	13.2	0.5	20	1	AR360400	ACCESSION:AR360400
4126	13.2	0.5	20	1	AR360427	ACCESSION:AR360427
4127	13.2	0.5	20	1	AX441511	ACCESSION:AX441511
4128	13.2	0.5	20	1	A40126	ACCESSION:A40126
c4129	13.2	0.5	20	1	AR030970	ACCESSION:AR030970
c4130	13.2	0.5	20	1	AR108815	ACCESSION:AR108815
c4131	13.2	0.5	20	1	AR205764	ACCESSION:AR205764
c4132	13.2	0.5	20	1	DOGP26302	ACCESSION:L15677
c4133	13.2	0.5	20	1	A24900	ACCESSION:A24900
4134	13.2	0.5	20	1	A25840	ACCESSION:A25840
c4135	13.2	0.5	20	1	A28702	ACCESSION:A28702
c4136	13.2	0.5	20	1	A28704	ACCESSION:A28704
c4137	13.2	0.5	20	1	A88156	ACCESSION:A88156
c4138	13.2	0.5	20	1	A90123	ACCESSION:A90123
c4139	13.2	0.5	20	1	AR015993	ACCESSION:AR015993
4140	13.2	0.5	20	1	AR023457	ACCESSION:AR023457
c4141	13.2	0.5	20	1	AR032199	ACCESSION:AR032199
4142	13.2	0.5	20	1	AR043098	ACCESSION:AR043098
c4143	13.2	0.5	20	1	AR043098	ACCESSION:AR043098
c4144	13.2	0.5	20	1	AR059098	ACCESSION:AR059098
c4145	13.2	0.5	20	1	AR070920	ACCESSION:AR070920
c4146	13.2	0.5	20	1	AR072276	ACCESSION:AR072276
c4147	13.2	0.5	20	1	AR072355	ACCESSION:AR072355
4148	13.2	0.5	20	1	AR076700	ACCESSION:AR076700
c4149	13.2	0.5	20	1	AR082034	ACCESSION:AR082034
c4150	13.2	0.5	20	1	AR086254	ACCESSION:AR086254
4151	13.2	0.5	20	1	AR092388	ACCESSION:AR092388
c4152	13.2	0.5	20	1	AR092398	ACCESSION:AR092398
4153	13.2	0.5	20	1	AR100057	ACCESSION:AR100057
4154	13.2	0.5	20	1	AR100058	ACCESSION:AR100058
c4155	13.2	0.5	20	1	AR100067	ACCESSION:AR100067
4156	13.2	0.5	20	1	AR100323	ACCESSION:AR100323
c4157	13.2	0.5	20	1	AR107574	ACCESSION:AR107574
4158	13.2	0.5	20	1	AR107608	ACCESSION:AR107608
4159	13.2	0.5	20	1	AR107609	ACCESSION:AR107609
c4160	13.2	0.5	20	1	AR107637	ACCESSION:AR107637
c4161	13.2	0.5	20	1	AR112528	ACCESSION:AR112528
c4162	13.2	0.5	20	1	AR112680	ACCESSION:AR112680
c4163	13.2	0.5	20	1	AR117618	ACCESSION:AR117618
c4164	13.2	0.5	20	1	AR117748	ACCESSION:AR117748
c4165	13.2	0.5	20	1	AR118903	ACCESSION:AR118903
c4166	13.2	0.5	20	1	AR124508	ACCESSION:AR124508
4167	13.2	0.5	20	1	AR125583	ACCESSION:AR125583
c4168	13.2	0.5	20	1	AR130116	ACCESSION:AR130116
4169	13.2	0.5	20	1	AR137244	ACCESSION:AR137244
4170	13.2	0.5	20	1	AR149978	ACCESSION:AR149978
c4171	13.2	0.5	20	1	AR150282	ACCESSION:AR150282
c4172	13.2	0.5	20	1	AR150299	ACCESSION:AR150299
4173	13.2	0.5	20	1	AR153557	ACCESSION:AR153557
4174	13.2	0.5	20	1	AR158938	ACCESSION:AR158938
c4175	13.2	0.5	20	1	AR162414	ACCESSION:AR162414
4176	13.2	0.5	20	1	AR162752	ACCESSION:AR162752
c4177	13.2	0.5	20	1	AR163069	ACCESSION:AR163069
c4178	13.2	0.5	20	1	AR163737	ACCESSION:AR163737
c4179	13.2	0.5	20	1	AR163800	ACCESSION:AR163800
4180	13.2	0.5	20	1	AR163845	ACCESSION:AR163845
4181	13.2	0.5	20	1	AR167027	ACCESSION:AR167027
c4182	13.2	0.5	20	1	AR174359	ACCESSION:AR174359
4183	13.2	0.5	20	1	AR174400	ACCESSION:AR174400
c4184	13.2	0.5	20	1	AR176820	ACCESSION:AR176820
4185	13.2	0.5	20	1	BD227851	ACCESSION:BD227851
c4186	13.2	0.5	20	1	BD228155	ACCESSION:BD228155
c4187	13.2	0.5	20	1	BD228172	ACCESSION:BD228172
c4188	13.2	0.5	20	1	BD230714	ACCESSION:BD230714
4189	13.2	0.5	20	1	BD237728	ACCESSION:BD237728
c4190	13.2	0.5	20	1	BD241885	ACCESSION:BD241885
c4191	13.2	0.5	20	1	BD244903	ACCESSION:BD244903
4192	13.2	0.5	20	1	BD262872	ACCESSION:BD262872
4193	13.2	0.5	20	1	BD276137	ACCESSION:BD276137
c4194	13.2	0.5	20	1	E11007	ACCESSION:E11007

c3903	13.2	0.5	14	1	A52265	ACCESSION:A52265
3904	13.2	0.5	14	1	E13665	ACCESSION:E13665
c3905	13.2	0.5	14	1	E13665	ACCESSION:E13665
3906	13.2	0.5	14	1	E13670	ACCESSION:E13670
c3907	13.2	0.5	14	1	E13670	ACCESSION:E13670
3908	13.2	0.5	14	1	AR266627	ACCESSION:AR266627
c3909	13.2	0.5	14	1	AR266627	ACCESSION:AR266627
3910	13.2	0.5	16	1	AR084213	ACCESSION:AR084213
c3911	13.2	0.5	18	1	AR264960	ACCESSION:AR264960
c3912	13.2	0.5	18	1	AR008470	ACCESSION:AR008470
3913	13.2	0.5	18	1	AR008471	ACCESSION:AR008471
c3914	13.2	0.5	18	1	AR009718	ACCESSION:AR009718
3915	13.2	0.5	18	1	AR009719	ACCESSION:AR009719
3916	13.2	0.5	18	1	AR063241	ACCESSION:AR063241
c3917	13.2	0.5	18	1	AR063243	ACCESSION:AR063243
3918	13.2	0.5	18	1	AX662307	ACCESSION:AX662307
c3919	13.2	0.5	18	1	A63086	ACCESSION:A63086
c3920	13.2	0.5	18	1	A87862	ACCESSION:A87862
c3921	13.2	0.5	18	1	A87864	ACCESSION:A87864
3922	13.2	0.5	18	1	A87993	ACCESSION:A87993
c3923	13.2	0.5	18	1	A89829	ACCESSION:A89829
c3924	13.2	0.5	18	1	A89831	ACCESSION:A89831
3925	13.2	0.5	18	1	A89960	ACCESSION:A89960
c3926	13.2	0.5	18	1	AR019212	ACCESSION:AR019212
c3927	13.2	0.5	18	1	AR019245	ACCESSION:AR019245
c3928	13.2	0.5	18	1	AR042299	ACCESSION:AR042299
c3929	13.2	0.5	18	1	AR055425	ACCESSION:AR055425
c3930	13.2	0.5	18	1	AR076325	ACCESSION:AR076325
c3931	13.2	0.5	18	1	AR092808	ACCESSION:AR092808
3932	13.2	0.5	18	1	AR092813	ACCESSION:AR092813
3933	13.2	0.5	18	1	AR098789	ACCESSION:AR098789
c3934	13.2	0.5	18	1	AR098791	ACCESSION:AR098791
3935	13.2	0.5	18	1	AR101834	ACCESSION:AR101834
c3936	13.2	0.5	18	1	AR101834	ACCESSION:AR101834
3937	13.2	0.5	18	1	AR144877	ACCESSION:AR144877
c3938	13.2	0.5	18	1	AR160886	ACCESSION:AR160886
c3939	13.2	0.5	18	1	BD234557	ACCESSION:BD234557
c3940	13.2	0.5	18	1	BD250635	ACCESSION:BD250635
c3941	13.2	0.5	18	1	I12014	ACCESSION:I12014
3942	13.2	0.5	18	1	I83492	ACCESSION:I83492
c3943	13.2	0.5	18	1	AR196142	ACCESSION:AR196142
c3944	13.2	0.5	18	1	AR196694	ACCESSION:AR196694
3945	13.2	0.5	18	1	AR211267	ACCESSION:AR211267
3946	13.2	0.5	18	1	AR264964	ACCESSION:AR264964
c3947	13.2	0.5	18	1	AR268663	ACCESSION:AR268663
c3948	13.2	0.5	18	1	AR294187	ACCESSION:AR294187
3949	13.2	0.5	18	1	AR295456	ACCESSION:AR295456
3950	13.2	0.5	18	1	AR305637	ACCESSION:AR305637
c3951	13.2	0.5	18	1	AR305637	ACCESSION:AR305637
3952	13.2	0.5	18	1	AR351522	ACCESSION:AR351522
3953	13.2	0.5	18	1	AR351534	ACCESSION:AR351534
3954	13.2	0.5	18	1	AR410329	ACCESSION:AR410329
3955	13.2	0.5	18	1	AR437532	ACCESSION:AR437532
c3956	13.2	0.5	18	1	AX098985	ACCESSION:AX098985
c3957	13.2	0.5	18	1	AX137004	ACCESSION:AX137004
3958	13.2	0.5	18	1	AX191970	ACCESSION:AX191970
c3959	13.2	0.5	18	1	AX469443	ACCESSION:AX469443
3960	13.2	0.5	18	1	AX473186	ACCESSION:AX473186
3961	13.2	0.5	18	1	AX572835	ACCESSION:AX572835
3962	13.2	0.5	18	1	AX599553	ACCESSION:AX599553
3963	13.2	0.5	18	1	AX599628	ACCESSION:AX599628
c3964	13.2	0.5	18	1	AX600742	ACCESSION:AX600742
c3965	13.2	0.5	18	1	AX637756	ACCESSION:AX637756
3966	13.2	0.5	18	1	AX705457	ACCESSION:AX705457
c3967	13.2	0.5	18	1	AX705459	ACCESSION:AX705459
3968	13.2	0.5	18	1	AX708192	ACCESSION:AX708192
3969	13.2	0.5	18	1	AX767877	ACCESSION:AX767877
3970	13.2	0.5	18	1	AX796513	ACCESSION:AX796513
3971	13.2	0.5	18	1	AX796532	ACCESSION:AX796532
3972	13.2	0.5	18	1	AX822178	ACCESSION:AX822178
3973	13.2	0.5	18	1	AX822998	ACCESSION:AX822998
3974	13.2	0.5	18	1	AX823077	ACCESSION:AX823077
3975	13.2	0.5	18	1	AX825818	ACCESSION:AX825818
3976	13.2	0.5	18	1	AX826638	ACCESSION:AX826638
3977	13.2	0.5	18	1	AX826717	ACCESSION:AX826717
c3978	13.2	0.5	18	1	BD065375	ACCESSION:BD065375
c3979	13.2	0.5	18	1	BD065377	ACCESSION:BD065377
3980	13.2	0.5	18	1	BD065506	ACCESSION:BD065506
c3981	13.2	0.5	18	1	BD072905	ACCESSION:BD072905
3982	13.2	0.5	18	1	BD081036	ACCESSION:BD081036
c3983	13.2	0.5	18	1	BD089313	ACCESSION:BD089313
c3984	13.2	0.5	18	1	BD089762	ACCESSION:BD089762
3985	13.2	0.5	18	1	BD104961	ACCESSION:BD104961
c3986	13.2	0.5	18	1	BD107532	ACCESSION:BD107532
c3987	13.2	0.5	18	1	BD145064	ACCESSION:BD145064
c3988	13.2	0.5	18	1	BD166064	ACCESSION:BD166064
3989	13.2	0.5	18	1	BD225045	ACCESSION:BD225045
3990	13.2	0.5	18	1	AJ589110	ACCESSION:AJ589110
c3991	13.2	0.5	19	1	AR030969	ACCESSION:AR030969
c3992	13.2	0.5	19	1	AR030972	ACCESSION:AR030972
c3993	13.2	0.5	19	1	AR030974	ACCESSION:AR030974
c3994	13.2	0.5	19	1	AR030975	ACCESSION:AR030975
c3995	13.2	0.5	19	1	AR030976	ACCESSION:AR030976
c3996	13.2	0.5	19	1	AR030977	ACCESSION:AR030977
c3997	13.2	0.5	19	1	AR030978	ACCESSION:AR030978
c3998	13.2	0.5	19	1	AR030981	ACCESSION:AR030981
c3999	13.2	0.5	19	1	AR030982	ACCESSION:AR030982
c4000	13.2	0.5	19	1	AR030983	ACCESSION:AR030983
c4001	13.2	0.5	19	1	AR030984	ACCESSION:AR030984
c4002	13.2	0.5	19	1	AR108814	ACCESSION:AR108814
c4003	13.2	0.5	19	1	AR108817	ACCESSION:AR108817
c4004	13.2	0.5	19	1	AR108819	ACCESSION:AR108819
c4005	13.2	0.5	19	1	AR108820	ACCESSION:AR108820
c4006	13.2	0.5	19	1	AR108821	ACCESSION:AR108821
c4007	13.2	0.5	19	1	AR108822	ACCESSION:AR108822
c4008	13.2	0.5	19	1	AR108823	ACCESSION:AR108823
c4009	13.2	0.5	19	1	AR108826	ACCESSION:AR108826
c4010	13.2	0.5	19	1	AR108827	ACCESSION:AR108827
c4011	13.2	0.5	19	1	AR108828	ACCESSION:AR108828
c4012	13.2	0.5	19	1	AR108829	ACCESSION:AR108829
c4013	13.2	0.5	19	1	I62823	ACCESSION:I62823
c4014	13.2	0.5	19	1	AR205763	ACCESSION:AR205763
c4015	13.2	0.5	19	1	AR205766	ACCESSION:AR205766
c4016	13.2	0.5	19	1	AR205768	ACCESSION:AR205768
c4017	13.2	0.5	19	1	AR205769	ACCESSION:AR205769
c4018	13.2	0.5	19	1	AR205770	ACCESSION:AR205770
c4019	13.2	0.5	19	1	AR205771	ACCESSION:AR205771
c4020	13.2	0.5	19	1	AR205772	ACCESSION:AR205772
c4021	13.2	0.5	19	1	AR205775	ACCESSION:AR205775
c4022	13.2	0.5	19	1	AR205776	ACCESSION:AR205776
c4023	13.2	0.5	19	1	AR205777	ACCESSION:AR205777
c4024	13.2	0.5	19	1	AR205778	ACCESSION:AR205778
c4025	13.2	0.5	19	1	A37094	ACCESSION:A37094
4026	13.2	0.5	19	1	A39742	ACCESSION:A39742
c4027	13.2	0.5	19	1	A41231	ACCESSION:A41231
c4028	13.2	0.5	19	1	A91188	ACCESSION:A91188
c4029	13.2	0.5	19	1	AR002990	ACCESSION:AR002990
4030	13.2	0.5	19	1	AR007260	ACCESSION:AR007260
c4031	13.2	0.5	19	1	AR007261	ACCESSION:AR007261
c4032	13.2	0.5	19	1	AR019659	ACCESSION:AR019659
4033	13.2	0.5	19	1	AR067985	ACCESSION:AR067985
c4034	13.2	0.5	19	1	AR067986	ACCESSION:AR067986
4035	13.2	0.5	19	1	AR069633	ACCESSION:AR069633
c4036	13.2	0.5	19	1	AR074187	ACCESSION:AR074187
4037	13.2	0.5	19	1	AR082444	ACCESSION:AR082444
4038	13.2	0.5	19	1	AR084247	ACCESSION:AR084247
c4039	13.2	0.5	19	1	AR084248	ACCESSION:AR084248
4040	13.2	0.5	19	1	AR097619	ACCESSION:AR097619
c4041	13.2	0.5	19	1	AR097620	ACCESSION:AR097620
4042	13.2	0.5	19	1	AR110289	ACCESSION:AR110289
4043	13.2	0.5	19	1	AR139000	ACCESSION:AR139000
c4044	13.2	0.5	19	1	AR162033	ACCESSION:AR162033
4045	13.2	0.5	19	1	BD252160	ACCESSION:BD252160
4046	13.2	0.5	19	1	BD262907	ACCESSION:BD262907
4047	13.2	0.5	19	1	I73729	ACCESSION:I73729
c4048	13.2	0.5	19	1	AR209033	ACCESSION:AR209033

3757	13.4	0.5	18	1	AR229573	ACCESSION:AR229573
c3758	13.4	0.5	18	1	AR292914	ACCESSION:AR292914
3759	13.4	0.5	18	1	AR295535	ACCESSION:AR295535
c3760	13.4	0.5	18	1	AR324012	ACCESSION:AR324012
3761	13.4	0.5	18	1	AR324101	ACCESSION:AR324101
c3762	13.4	0.5	18	1	AR431658	ACCESSION:AR431658
c3763	13.4	0.5	18	1	AX078831	ACCESSION:AX078831
c3764	13.4	0.5	18	1	AX078842	ACCESSION:AX078842
c3765	13.4	0.5	18	1	AX078848	ACCESSION:AX078848
c3766	13.4	0.5	18	1	AX078859	ACCESSION:AX078859
c3767	13.4	0.5	18	1	AX268173	ACCESSION:AX268173
3768	13.4	0.5	18	1	AX557193	ACCESSION:AX557193
c3769	13.4	0.5	18	1	AX599315	ACCESSION:AX599315
c3770	13.4	0.5	18	1	AX599746	ACCESSION:AX599746
c3771	13.4	0.5	18	1	AX601190	ACCESSION:AX601190
c3772	13.4	0.5	18	1	AX685128	ACCESSION:AX685128
c3773	13.4	0.5	18	1	AX767735	ACCESSION:AX767735
c3774	13.4	0.5	18	1	AX796171	ACCESSION:AX796171
3775	13.4	0.5	18	1	AX822843	ACCESSION:AX822843
3776	13.4	0.5	18	1	AX826483	ACCESSION:AX826483
3777	13.4	0.5	18	1	AX837788	ACCESSION:AX837788
3778	13.4	0.5	18	1	BD065376	ACCESSION:BD065376
c3779	13.4	0.5	18	1	BD065659	ACCESSION:BD065659
3780	13.4	0.5	18	1	BD089867	ACCESSION:BD089867
c3781	13.4	0.5	18	1	BD103917	ACCESSION:BD103917
c3782	13.4	0.5	18	1	BD104957	ACCESSION:BD104957
c3783	13.4	0.5	18	1	BD217399	ACCESSION:BD217399
3784	13.4	0.5	18	1	AB068476	ACCESSION:AB068476
c3785	13.4	0.5	19	1	A51090	ACCESSION:A51090
3786	13.4	0.5	19	1	AR029157	ACCESSION:AR029157
c3787	13.4	0.5	19	1	AR029157	ACCESSION:AR029157
3788	13.4	0.5	19	1	AR036541	ACCESSION:AR036541
c3789	13.4	0.5	19	1	AR036541	ACCESSION:AR036541
3790	13.4	0.5	19	1	AR096074	ACCESSION:AR096074
c3791	13.4	0.5	19	1	AR096074	ACCESSION:AR096074
3792	13.4	0.5	19	1	AR097400	ACCESSION:AR097400
3793	13.4	0.5	19	1	AR111930	ACCESSION:AR111930
c3794	13.4	0.5	19	1	AR111930	ACCESSION:AR111930
3795	13.4	0.5	19	1	AR124827	ACCESSION:AR124827
c3796	13.4	0.5	19	1	AR124827	ACCESSION:AR124827
3797	13.4	0.5	19	1	AR135275	ACCESSION:AR135275
c3798	13.4	0.5	19	1	AR135275	ACCESSION:AR135275
3799	13.4	0.5	19	1	AR137398	ACCESSION:AR137398
c3800	13.4	0.5	19	1	AR137402	ACCESSION:AR137402
3801	13.4	0.5	19	1	AR141345	ACCESSION:AR141345
c3802	13.4	0.5	19	1	AR141345	ACCESSION:AR141345
c3803	13.4	0.5	19	1	AR160892	ACCESSION:AR160892
3804	13.4	0.5	19	1	AR179524	ACCESSION:AR179524
c3805	13.4	0.5	19	1	AR179524	ACCESSION:AR179524
3806	13.4	0.5	19	1	I25705	ACCESSION:I25705
3807	13.4	0.5	19	1	AR212307	ACCESSION:AR212307
c3808	13.4	0.5	19	1	AR212307	ACCESSION:AR212307
3809	13.4	0.5	19	1	AR231437	ACCESSION:AR231437
c3810	13.4	0.5	19	1	AR231437	ACCESSION:AR231437
3811	13.4	0.5	19	1	AR412353	ACCESSION:AR412353
c3812	13.4	0.5	19	1	AR412353	ACCESSION:AR412353
c3813	13.4	0.5	19	1	AX115855	ACCESSION:AX115855
3814	13.4	0.5	19	1	AX132036	ACCESSION:AX132036
3815	13.4	0.5	19	1	AX192337	ACCESSION:AX192337
c3816	13.4	0.5	19	1	AX412083	ACCESSION:AX412083
c3817	13.4	0.5	19	1	AX535777	ACCESSION:AX535777
c3818	13.4	0.5	19	1	AX539268	ACCESSION:AX539268
c3819	13.4	0.5	19	1	AX815849	ACCESSION:AX815849
c3820	13.4	0.5	19	1	AX923652	ACCESSION:AX923652
c3821	13.4	0.5	19	1	BD000756	ACCESSION:BD000756
3822	13.4	0.5	19	1	BD222586	ACCESSION:BD222586
c3823	13.4	0.5	19	1	BD222586	ACCESSION:BD222586
c3824	13.4	0.5	20	1	AX048445	ACCESSION:AX048445
c3825	13.4	0.5	20	1	A91597	ACCESSION:A91597
3826	13.4	0.5	20	1	AR051133	ACCESSION:AR051133
c3827	13.4	0.5	20	1	AR051133	ACCESSION:AR051133
c3828	13.4	0.5	20	1	AR058747	ACCESSION:AR058747
c3829	13.4	0.5	20	1	AR082336	ACCESSION:AR082336
c3830	13.4	0.5	20	1	AR100054	ACCESSION:AR100054
c3831	13.4	0.5	20	1	AR100185	ACCESSION:AR100185
3832	13.4	0.5	20	1	AR107217	ACCESSION:AR107217
c3833	13.4	0.5	20	1	AR112276	ACCESSION:AR112276
c3834	13.4	0.5	20	1	AR120878	ACCESSION:AR120878
c3835	13.4	0.5	20	1	AR121079	ACCESSION:AR121079
c3836	13.4	0.5	20	1	AR124966	ACCESSION:AR124966
3837	13.4	0.5	20	1	AR130110	ACCESSION:AR130110
c3838	13.4	0.5	20	1	AR137875	ACCESSION:AR137875
3839	13.4	0.5	20	1	AR143184	ACCESSION:AR143184
c3840	13.4	0.5	20	1	AR149869	ACCESSION:AR149869
c3841	13.4	0.5	20	1	AR150391	ACCESSION:AR150391
3842	13.4	0.5	20	1	AR153754	ACCESSION:AR153754
c3843	13.4	0.5	20	1	AR153754	ACCESSION:AR153754
3844	13.4	0.5	20	1	AR158931	ACCESSION:AR158931
3845	13.4	0.5	20	1	AR163732	ACCESSION:AR163732
c3846	13.4	0.5	20	1	BD228264	ACCESSION:BD228264
c3847	13.4	0.5	20	1	BD243056	ACCESSION:BD243056
3848	13.4	0.5	20	1	BD249359	ACCESSION:BD249359
c3849	13.4	0.5	20	1	BD272700	ACCESSION:BD272700
c3850	13.4	0.5	20	1	E11827	ACCESSION:E11827
3851	13.4	0.5	20	1	E11838	ACCESSION:E11838
3852	13.4	0.5	20	1	E35764	ACCESSION:E35764
3853	13.4	0.5	20	1	I51693	ACCESSION:I51693
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c3855	13.4	0.5	20	1	I77271	ACCESSION:I77271
c3856	13.4	0.5	20	1	I78382	ACCESSION:I78382
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3858	13.4	0.5	20	1	AR229050	ACCESSION:AR229050
c3859	13.4	0.5	20	1	AR234664	ACCESSION:AR234664
c3860	13.4	0.5	20	1	AR305210	ACCESSION:AR305210
c3861	13.4	0.5	20	1	AR309314	ACCESSION:AR309314
3862	13.4	0.5	20	1	AR311840	ACCESSION:AR311840
c3863	13.4	0.5	20	1	AR312330	ACCESSION:AR312330
3864	13.4	0.5	20	1	AR312943	ACCESSION:AR312943
3865	13.4	0.5	20	1	AR312983	ACCESSION:AR312983
c3866	13.4	0.5	20	1	AR313616	ACCESSION:AR313616
3867	13.4	0.5	20	1	AR314827	ACCESSION:AR314827
c3868	13.4	0.5	20	1	AR315171	ACCESSION:AR315171
c3869	13.4	0.5	20	1	AR315937	ACCESSION:AR315937
3870	13.4	0.5	20	1	AR373738	ACCESSION:AR373738
c3871	13.4	0.5	20	1	AR373818	ACCESSION:AR373818
3872	13.4	0.5	20	1	AR432278	ACCESSION:AR432278
3873	13.4	0.5	20	1	AX099164	ACCESSION:AX099164
3874	13.4	0.5	20	1	AX148814	ACCESSION:AX148814
3875	13.4	0.5	20	1	AX149017	ACCESSION:AX149017
3876	13.4	0.5	20	1	AX149191	ACCESSION:AX149191
c3877	13.4	0.5	20	1	AX201485	ACCESSION:AX201485
c3878	13.4	0.5	20	1	AX338230	ACCESSION:AX338230
3879	13.4	0.5	20	1	AX418735	ACCESSION:AX418735
c3880	13.4	0.5	20	1	AX418815	ACCESSION:AX418815
c3881	13.4	0.5	20	1	AX462751	ACCESSION:AX462751
3882	13.4	0.5	20	1	AX477137	ACCESSION:AX477137
3883	13.4	0.5	20	1	AX526513	ACCESSION:AX526513
3884	13.4	0.5	20	1	AX613548	ACCESSION:AX613548
c3885	13.4	0.5	20	1	AX697401	ACCESSION:AX697401
3886	13.4	0.5	20	1	AX753521	ACCESSION:AX753521
3887	13.4	0.5	20	1	AX753625	ACCESSION:AX753625
c3888	13.4	0.5	20	1	BD023379	ACCESSION:BD023379
c3889	13.4	0.5	20	1	BD088505	ACCESSION:BD088505
c3890	13.4	0.5	20	1	BD106121	ACCESSION:BD106121
3891	13.4	0.5	20	1	BD128192	ACCESSION:BD128192
c3892	13.4	0.5	20	1	BD134696	ACCESSION:BD134696
c3893	13.4	0.5	20	1	BD138288	ACCESSION:BD138288
3894	13.4	0.5	20	1	BD182266	ACCESSION:BD182266
c3895	13.4	0.5	20	1	AB069398	ACCESSION:AB069398
3896	13.4	0.5	21	1	AR138736	ACCESSION:AR138736
c3897	13.4	0.5	21	1	AX498248	ACCESSION:AX498248
3898	13.4	0.5	21	1	I24714	ACCESSION:I24714
c3899	13.4	0.5	24	1	AR364668	ACCESSION:AR364668
3900	13.4	0.5	25	1	AR434873	ACCESSION:AR434873
c3901	13.4	0.5	25	1	AX043060	ACCESSION:AX043060
3902	13.2	0.5	14	1	A52265	ACCESSION:A52265

3611	13.4	0.5	15	1	AR045206	ACCESSION:AR045206
3612	13.4	0.5	15	1	AR051237	ACCESSION:AR051237
3613	13.4	0.5	15	1	AR084519	ACCESSION:AR084519
3614	13.4	0.5	15	1	AR127784	ACCESSION:AR127784
3615	13.4	0.5	15	1	I16031	ACCESSION:I16031
3616	13.4	0.5	15	1	I28366	ACCESSION:I28366
3617	13.4	0.5	15	1	A15242	ACCESSION:A15242
3618	13.4	0.5	15	1	A16457	ACCESSION:A16457
3619	13.4	0.5	15	1	AR084518	ACCESSION:AR084518
c3620	13.4	0.5	15	1	AR084518	ACCESSION:AR084518
3621	13.4	0.5	15	1	AR084532	ACCESSION:AR084532
3622	13.4	0.5	15	1	BD244856	ACCESSION:BD244856
c3623	13.4	0.5	15	1	BD244856	ACCESSION:BD244856
c3624	13.4	0.5	15	1	I25868	ACCESSION:I25868
3625	13.4	0.5	15	1	AR241876	ACCESSION:AR241876
c3626	13.4	0.5	15	1	AR241876	ACCESSION:AR241876
3627	13.4	0.5	15	1	AR278935	ACCESSION:AR278935
c3628	13.4	0.5	15	1	BD208567	ACCESSION:BD208567
c3629	13.4	0.5	16	1	BD233092	ACCESSION:BD233092
c3630	13.4	0.5	16	1	E33197	ACCESSION:E33197
c3631	13.4	0.5	16	1	AR328462	ACCESSION:AR328462
c3632	13.4	0.5	16	1	AX007646	ACCESSION:AX007646
c3633	13.4	0.5	17	1	BD255422	ACCESSION:BD255422
c3634	13.4	0.5	17	1	BD255423	ACCESSION:BD255423
c3635	13.4	0.5	17	1	BD255424	ACCESSION:BD255424
c3636	13.4	0.5	17	1	AX738493	ACCESSION:AX738493
c3637	13.4	0.5	17	1	AX757892	ACCESSION:AX757892
c3638	13.4	0.5	17	1	A05414	ACCESSION:A05414
c3639	13.4	0.5	17	1	A09621	ACCESSION:A09621
c3640	13.4	0.5	17	1	AR046832	ACCESSION:AR046832
3641	13.4	0.5	17	1	AR047114	ACCESSION:AR047114
c3642	13.4	0.5	17	1	AR088824	ACCESSION:AR088824
3643	13.4	0.5	17	1	AR158488	ACCESSION:AR158488
3644	13.4	0.5	17	1	AR158489	ACCESSION:AR158489
3645	13.4	0.5	17	1	AR158490	ACCESSION:AR158490
c3646	13.4	0.5	17	1	AR164080	ACCESSION:AR164080
c3647	13.4	0.5	17	1	AR164081	ACCESSION:AR164081
3648	13.4	0.5	17	1	BD254622	ACCESSION:BD254622
3649	13.4	0.5	17	1	BD258292	ACCESSION:BD258292
3650	13.4	0.5	17	1	BD258507	ACCESSION:BD258507
3651	13.4	0.5	17	1	BD258508	ACCESSION:BD258508
3652	13.4	0.5	17	1	BD258509	ACCESSION:BD258509
3653	13.4	0.5	17	1	BD258577	ACCESSION:BD258577
c3654	13.4	0.5	17	1	I53884	ACCESSION:I53884
3655	13.4	0.5	17	1	I54166	ACCESSION:I54166
c3656	13.4	0.5	17	1	AR186544	ACCESSION:AR186544
c3657	13.4	0.5	17	1	AR186545	ACCESSION:AR186545
c3658	13.4	0.5	17	1	AR186546	ACCESSION:AR186546
3659	13.4	0.5	17	1	AR186701	ACCESSION:AR186701
3660	13.4	0.5	17	1	AR188379	ACCESSION:AR188379
c3661	13.4	0.5	17	1	AR192002	ACCESSION:AR192002
c3662	13.4	0.5	17	1	AR323175	ACCESSION:AR323175
c3663	13.4	0.5	17	1	AR323176	ACCESSION:AR323176
c3664	13.4	0.5	17	1	AR323177	ACCESSION:AR323177
3665	13.4	0.5	17	1	AR323332	ACCESSION:AR323332
3666	13.4	0.5	17	1	AR324232	ACCESSION:AR324232
c3667	13.4	0.5	17	1	AR325894	ACCESSION:AR325894
3668	13.4	0.5	17	1	AR328925	ACCESSION:AR328925
3669	13.4	0.5	17	1	AR434231	ACCESSION:AR434231
3670	13.4	0.5	17	1	AR434234	ACCESSION:AR434234
3671	13.4	0.5	17	1	AX099948	ACCESSION:AX099948
3672	13.4	0.5	17	1	AX214956	ACCESSION:AX214956
c3673	13.4	0.5	17	1	AX215487	ACCESSION:AX215487
c3674	13.4	0.5	17	1	AX215750	ACCESSION:AX215750
3675	13.4	0.5	17	1	AX216792	ACCESSION:AX216792
3676	13.4	0.5	17	1	AX216895	ACCESSION:AX216895
c3677	13.4	0.5	17	1	AX227073	ACCESSION:AX227073
c3678	13.4	0.5	17	1	AX227726	ACCESSION:AX227726
c3679	13.4	0.5	17	1	AX422050	ACCESSION:AX422050
c3680	13.4	0.5	17	1	AX422761	ACCESSION:AX422761
c3681	13.4	0.5	17	1	AX422762	ACCESSION:AX422762
3682	13.4	0.5	17	1	AX499271	ACCESSION:AX499271
3683	13.4	0.5	17	1	AX499272	ACCESSION:AX499272
3684	13.4	0.5	17	1	AX499273	ACCESSION:AX499273
c3685	13.4	0.5	17	1	AX500254	ACCESSION:AX500254
c3686	13.4	0.5	17	1	AX500255	ACCESSION:AX500255
c3687	13.4	0.5	17	1	AX500256	ACCESSION:AX500256
3688	13.4	0.5	17	1	AX600667	ACCESSION:AX600667
3689	13.4	0.5	17	1	AX672113	ACCESSION:AX672113
3690	13.4	0.5	17	1	AX673606	ACCESSION:AX673606
3691	13.4	0.5	17	1	AX674437	ACCESSION:AX674437
c3692	13.4	0.5	17	1	AX674708	ACCESSION:AX674708
3693	13.4	0.5	17	1	AX688047	ACCESSION:AX688047
3694	13.4	0.5	17	1	AX688048	ACCESSION:AX688048
3695	13.4	0.5	17	1	AX692521	ACCESSION:AX692521
c3696	13.4	0.5	17	1	AX692521	ACCESSION:AX692521
3697	13.4	0.5	17	1	AX692529	ACCESSION:AX692529
c3698	13.4	0.5	17	1	AX692529	ACCESSION:AX692529
c3699	13.4	0.5	17	1	AX708159	ACCESSION:AX708159
3700	13.4	0.5	17	1	AX722729	ACCESSION:AX722729
3701	13.4	0.5	17	1	AX723158	ACCESSION:AX723158
c3702	13.4	0.5	17	1	AX723265	ACCESSION:AX723265
3703	13.4	0.5	17	1	AX724168	ACCESSION:AX724168
c3704	13.4	0.5	17	1	AX725075	ACCESSION:AX725075
3705	13.4	0.5	17	1	AX725350	ACCESSION:AX725350
c3706	13.4	0.5	17	1	AX729187	ACCESSION:AX729187
3707	13.4	0.5	17	1	AX729876	ACCESSION:AX729876
c3708	13.4	0.5	17	1	AX732099	ACCESSION:AX732099
c3709	13.4	0.5	17	1	AX732979	ACCESSION:AX732979
c3710	13.4	0.5	17	1	AX737962	ACCESSION:AX737962
c3711	13.4	0.5	17	1	AX738283	ACCESSION:AX738283
3712	13.4	0.5	17	1	AX744261	ACCESSION:AX744261
c3713	13.4	0.5	17	1	AX750999	ACCESSION:AX750999
c3714	13.4	0.5	17	1	AX751000	ACCESSION:AX751000
3715	13.4	0.5	17	1	AX757727	ACCESSION:AX757727
c3716	13.4	0.5	17	1	AX758401	ACCESSION:AX758401
c3717	13.4	0.5	17	1	AX758644	ACCESSION:AX758644
3718	13.4	0.5	17	1	AX758703	ACCESSION:AX758703
c3719	13.4	0.5	17	1	AX759009	ACCESSION:AX759009
c3720	13.4	0.5	17	1	AX759584	ACCESSION:AX759584
3721	13.4	0.5	17	1	AX762667	ACCESSION:AX762667
c3722	13.4	0.5	17	1	BD015290	ACCESSION:BD015290
c3723	13.4	0.5	17	1	BD058091	ACCESSION:BD058091
c3724	13.4	0.5	17	1	BD058092	ACCESSION:BD058092
c3725	13.4	0.5	17	1	BD104958	ACCESSION:BD104958
c3726	13.4	0.5	17	1	BD105061	ACCESSION:BD105061
c3727	13.4	0.5	17	1	BD105063	ACCESSION:BD105063
c3728	13.4	0.5	17	1	BD105064	ACCESSION:BD105064
c3729	13.4	0.5	17	1	BD200954	ACCESSION:BD200954
3730	13.4	0.5	17	1	BD201172	ACCESSION:BD201172
3731	13.4	0.5	18	1	A64857	ACCESSION:A64857
3732	13.4	0.5	18	1	A87863	ACCESSION:A87863
c3733	13.4	0.5	18	1	A88146	ACCESSION:A88146
3734	13.4	0.5	18	1	A89830	ACCESSION:A89830
c3735	13.4	0.5	18	1	A90113	ACCESSION:A90113
c3736	13.4	0.5	18	1	AR080709	ACCESSION:AR080709
c3737	13.4	0.5	18	1	AR080713	ACCESSION:AR080713
c3738	13.4	0.5	18	1	AR087086	ACCESSION:AR087086
c3739	13.4	0.5	18	1	AR096351	ACCESSION:AR096351
c3740	13.4	0.5	18	1	AR112277	ACCESSION:AR112277
c3741	13.4	0.5	18	1	AR153218	ACCESSION:AR153218
c3742	13.4	0.5	18	1	AR162692	ACCESSION:AR162692
c3743	13.4	0.5	18	1	AR162696	ACCESSION:AR162696
c3744	13.4	0.5	18	1	AR163233	ACCESSION:AR163233
c3745	13.4	0.5	18	1	AR165895	ACCESSION:AR165895
c3746	13.4	0.5	18	1	AR176958	ACCESSION:AR176958
c3747	13.4	0.5	18	1	BD227752	ACCESSION:BD227752
c3748	13.4	0.5	18	1	BD227756	ACCESSION:BD227756
3749	13.4	0.5	18	1	I73187	ACCESSION:I73187
c3750	13.4	0.5	18	1	I73187	ACCESSION:I73187
c3751	13.4	0.5	18	1	AR181458	ACCESSION:AR181458
c3752	13.4	0.5	18	1	AR181460	ACCESSION:AR181460
c3753	13.4	0.5	18	1	AR187498	ACCESSION:AR187498
3754	13.4	0.5	18	1	AR187588	ACCESSION:AR187588
c3755	13.4	0.5	18	1	AR210977	ACCESSION:AR210977
c3756	13.4	0.5	18	1	AR229572	ACCESSION:AR229572

3465	13.6	0.5	20	1	AR203118	ACCESSION:AR203118
c3466	13.6	0.5	20	1	AR203152	ACCESSION:AR203152
3467	13.6	0.5	20	1	AR203166	ACCESSION:AR203166
3468	13.6	0.5	20	1	AR211368	ACCESSION:AR211368
c3469	13.6	0.5	20	1	AR212007	ACCESSION:AR212007
3470	13.6	0.5	20	1	AR217899	ACCESSION:AR217899
3471	13.6	0.5	20	1	AR220184	ACCESSION:AR220184
3472	13.6	0.5	20	1	AR221789	ACCESSION:AR221789
3473	13.6	0.5	20	1	AR222265	ACCESSION:AR222265
c3474	13.6	0.5	20	1	AR232339	ACCESSION:AR232339
3475	13.6	0.5	20	1	AR234640	ACCESSION:AR234640
c3476	13.6	0.5	20	1	AR234698	ACCESSION:AR234698
c3477	13.6	0.5	20	1	AR255963	ACCESSION:AR255963
c3478	13.6	0.5	20	1	AR255975	ACCESSION:AR255975
c3479	13.6	0.5	20	1	AR262371	ACCESSION:AR262371
c3480	13.6	0.5	20	1	AR262372	ACCESSION:AR262372
c3481	13.6	0.5	20	1	AR266944	ACCESSION:AR266944
3482	13.6	0.5	20	1	AR266945	ACCESSION:AR266945
c3483	13.6	0.5	20	1	AR277762	ACCESSION:AR277762
3484	13.6	0.5	20	1	AR294017	ACCESSION:AR294017
3485	13.6	0.5	20	1	AR297173	ACCESSION:AR297173
3486	13.6	0.5	20	1	AR298189	ACCESSION:AR298189
c3487	13.6	0.5	20	1	AR299111	ACCESSION:AR299111
c3488	13.6	0.5	20	1	AR300314	ACCESSION:AR300314
c3489	13.6	0.5	20	1	AR304441	ACCESSION:AR304441
3490	13.6	0.5	20	1	AR311041	ACCESSION:AR311041
c3491	13.6	0.5	20	1	AR311824	ACCESSION:AR311824
c3492	13.6	0.5	20	1	AR313463	ACCESSION:AR313463
c3493	13.6	0.5	20	1	AR313846	ACCESSION:AR313846
3494	13.6	0.5	20	1	AR343102	ACCESSION:AR343102
3495	13.6	0.5	20	1	AR360393	ACCESSION:AR360393
3496	13.6	0.5	20	1	AR360394	ACCESSION:AR360394
3497	13.6	0.5	20	1	AR360395	ACCESSION:AR360395
3498	13.6	0.5	20	1	AR360396	ACCESSION:AR360396
c3499	13.6	0.5	20	1	AR360397	ACCESSION:AR360397
c3500	13.6	0.5	20	1	AR360399	ACCESSION:AR360399
c3501	13.6	0.5	20	1	AR360402	ACCESSION:AR360402
3502	13.6	0.5	20	1	AR360420	ACCESSION:AR360420
3503	13.6	0.5	20	1	AR360421	ACCESSION:AR360421
3504	13.6	0.5	20	1	AR360422	ACCESSION:AR360422
3505	13.6	0.5	20	1	AR360423	ACCESSION:AR360423
c3506	13.6	0.5	20	1	AR360424	ACCESSION:AR360424
c3507	13.6	0.5	20	1	AR360426	ACCESSION:AR360426
c3508	13.6	0.5	20	1	AR360429	ACCESSION:AR360429
c3509	13.6	0.5	20	1	AR373481	ACCESSION:AR373481
c3510	13.6	0.5	20	1	AR373514	ACCESSION:AR373514
c3511	13.6	0.5	20	1	AR373631	ACCESSION:AR373631
c3512	13.6	0.5	20	1	AR373791	ACCESSION:AR373791
3513	13.6	0.5	20	1	AR382158	ACCESSION:AR382158
c3514	13.6	0.5	20	1	AR382159	ACCESSION:AR382159
3515	13.6	0.5	20	1	AR432267	ACCESSION:AR432267
c3516	13.6	0.5	20	1	AX010463	ACCESSION:AX010463
3517	13.6	0.5	20	1	AX048438	ACCESSION:AX048438
c3518	13.6	0.5	20	1	AX048438	ACCESSION:AX048438
3519	13.6	0.5	20	1	AX066409	ACCESSION:AX066409
c3520	13.6	0.5	20	1	AX077095	ACCESSION:AX077095
c3521	13.6	0.5	20	1	AX078027	ACCESSION:AX078027
c3522	13.6	0.5	20	1	AX078046	ACCESSION:AX078046
3523	13.6	0.5	20	1	AX099900	ACCESSION:AX099900
c3524	13.6	0.5	20	1	AX104161	ACCESSION:AX104161
c3525	13.6	0.5	20	1	AX104333	ACCESSION:AX104333
3526	13.6	0.5	20	1	AX104584	ACCESSION:AX104584
c3527	13.6	0.5	20	1	AX104663	ACCESSION:AX104663
3528	13.6	0.5	20	1	AX133293	ACCESSION:AX133293
3529	13.6	0.5	20	1	AX136904	ACCESSION:AX136904
c3530	13.6	0.5	20	1	AX148869	ACCESSION:AX148869
3531	13.6	0.5	20	1	AX149016	ACCESSION:AX149016
3532	13.6	0.5	20	1	AX149128	ACCESSION:AX149128
3533	13.6	0.5	20	1	AX167934	ACCESSION:AX167934
3534	13.6	0.5	20	1	AX167935	ACCESSION:AX167935
3535	13.6	0.5	20	1	AX231607	ACCESSION:AX231607
3536	13.6	0.5	20	1	AX231700	ACCESSION:AX231700
3537	13.6	0.5	20	1	AX252919	ACCESSION:AX252919
c3538	13.6	0.5	20	1	AX294124	ACCESSION:AX294124
3539	13.6	0.5	20	1	AX294426	ACCESSION:AX294426
c3540	13.6	0.5	20	1	AX298602	ACCESSION:AX298602
3541	13.6	0.5	20	1	AX298787	ACCESSION:AX298787
3542	13.6	0.5	20	1	AX349199	ACCESSION:AX349199
3543	13.6	0.5	20	1	AX354307	ACCESSION:AX354307
c3544	13.6	0.5	20	1	AX354976	ACCESSION:AX354976
c3545	13.6	0.5	20	1	AX354977	ACCESSION:AX354977
3546	13.6	0.5	20	1	AX354981	ACCESSION:AX354981
c3547	13.6	0.5	20	1	AX355514	ACCESSION:AX355514
c3548	13.6	0.5	20	1	AX418628	ACCESSION:AX418628
c3549	13.6	0.5	20	1	AX418788	ACCESSION:AX418788
3550	13.6	0.5	20	1	AX429779	ACCESSION:AX429779
3551	13.6	0.5	20	1	AX441504	ACCESSION:AX441504
3552	13.6	0.5	20	1	AX441505	ACCESSION:AX441505
3553	13.6	0.5	20	1	AX441506	ACCESSION:AX441506
3554	13.6	0.5	20	1	AX441507	ACCESSION:AX441507
c3555	13.6	0.5	20	1	AX441508	ACCESSION:AX441508
c3556	13.6	0.5	20	1	AX441510	ACCESSION:AX441510
c3557	13.6	0.5	20	1	AX441513	ACCESSION:AX441513
c3558	13.6	0.5	20	1	AX482057	ACCESSION:AX482057
3559	13.6	0.5	20	1	AX492793	ACCESSION:AX492793
c3560	13.6	0.5	20	1	AX511296	ACCESSION:AX511296
c3561	13.6	0.5	20	1	AX547214	ACCESSION:AX547214
c3562	13.6	0.5	20	1	AX547386	ACCESSION:AX547386
3563	13.6	0.5	20	1	AX547637	ACCESSION:AX547637
c3564	13.6	0.5	20	1	AX547716	ACCESSION:AX547716
3565	13.6	0.5	20	1	AX590963	ACCESSION:AX590963
3566	13.6	0.5	20	1	AX599049	ACCESSION:AX599049
3567	13.6	0.5	20	1	AX599172	ACCESSION:AX599172
3568	13.6	0.5	20	1	AX657302	ACCESSION:AX657302
3569	13.6	0.5	20	1	AX662867	ACCESSION:AX662867
3570	13.6	0.5	20	1	AX767571	ACCESSION:AX767571
3571	13.6	0.5	20	1	AX804600	ACCESSION:AX804600
3572	13.6	0.5	20	1	AX839715	ACCESSION:AX839715
3573	13.6	0.5	20	1	AX922674	ACCESSION:AX922674
3574	13.6	0.5	20	1	BD000413	ACCESSION:BD000413
3575	13.6	0.5	20	1	BD012474	ACCESSION:BD012474
3576	13.6	0.5	20	1	BD016578	ACCESSION:BD016578
c3577	13.6	0.5	20	1	BD065627	ACCESSION:BD065627
c3578	13.6	0.5	20	1	BD065818	ACCESSION:BD065818
c3579	13.6	0.5	20	1	BD073164	ACCESSION:BD073164
3580	13.6	0.5	20	1	BD088306	ACCESSION:BD088306
3581	13.6	0.5	20	1	BD088308	ACCESSION:BD088308
c3582	13.6	0.5	20	1	BD088771	ACCESSION:BD088771
c3583	13.6	0.5	20	1	BD094607	ACCESSION:BD094607
c3584	13.6	0.5	20	1	BD130033	ACCESSION:BD130033
c3585	13.6	0.5	20	1	BD138289	ACCESSION:BD138289
3586	13.6	0.5	20	1	BD144137	ACCESSION:BD144137
c3587	13.6	0.5	20	1	BD166405	ACCESSION:BD166405
3588	13.6	0.5	20	1	BD167996	ACCESSION:BD167996
3589	13.6	0.5	20	1	BD177804	ACCESSION:BD177804
c3590	13.6	0.5	20	1	BD177830	ACCESSION:BD177830
3591	13.6	0.5	20	1	BD195388	ACCESSION:BD195388
c3592	13.6	0.5	20	1	BD205800	ACCESSION:BD205800
3593	13.6	0.5	20	1	BD206090	ACCESSION:BD206090
c3594	13.6	0.5	20	1	HSTNRAS14	ACCESSION:Y13522 Y
3595	13.6	0.5	20	1	AB068343	ACCESSION:AB068343
3596	13.6	0.5	20	1	AB068345	ACCESSION:AB068345
c3597	13.6	0.5	20	1	AB069220	ACCESSION:AB069220
3598	13.6	0.5	21	1	AX713257	ACCESSION:AX713257
c3599	13.6	0.5	22	1	AR029876	ACCESSION:AR029876
c3600	13.6	0.5	22	1	AX267016	ACCESSION:AX267016
c3601	13.6	0.5	22	1	AX267017	ACCESSION:AX267017
c3602	13.6	0.5	24	1	I16929	ACCESSION:I16929
c3603	13.6	0.5	25	1	AX043318	ACCESSION:AX043318
3604	13.6	0.5	25	1	AX042955	ACCESSION:AX042955
3605	13.6	0.5	25	1	AX043216	ACCESSION:AX043216
3606	13.6	0.5	25	1	AX042614	ACCESSION:AX042614
3607	13.4	0.5	15	1	AR056160	ACCESSION:AR056160
3608	13.4	0.5	15	1	AR113918	ACCESSION:AR113918
3609	13.4	0.5	15	1	AX633203	ACCESSION:AX633203
3610	13.4	0.5	15	1	AR002256	ACCESSION:AR002256

c3319	13.8	0.5	20	1	AX462490	ACCESSION:AX462490
c3320	13.8	0.5	20	1	AX482700	ACCESSION:AX482700
c3321	13.8	0.5	20	1	AX511782	ACCESSION:AX511782
3322	13.8	0.5	20	1	AX547000	ACCESSION:AX547000
c3323	13.8	0.5	20	1	AX547000	ACCESSION:AX547000
c3324	13.8	0.5	20	1	AX613393	ACCESSION:AX613393
c3325	13.8	0.5	20	1	AX662602	ACCESSION:AX662602
c3326	13.8	0.5	20	1	AX671167	ACCESSION:AX671167
3327	13.8	0.5	20	1	AX810932	ACCESSION:AX810932
3328	13.8	0.5	20	1	AX810938	ACCESSION:AX810938
c3329	13.8	0.5	20	1	BD000131	ACCESSION:BD000131
3330	13.8	0.5	20	1	BD007718	ACCESSION:BD007718
c3331	13.8	0.5	20	1	BD012429	ACCESSION:BD012429
3332	13.8	0.5	20	1	BD074731	ACCESSION:BD074731
3333	13.8	0.5	20	1	BD079273	ACCESSION:BD079273
3334	13.8	0.5	20	1	BD087042	ACCESSION:BD087042
c3335	13.8	0.5	20	1	BD128029	ACCESSION:BD128029
3336	13.8	0.5	20	1	BD143073	ACCESSION:BD143073
3337	13.8	0.5	20	1	BD170783	ACCESSION:BD170783
3338	13.8	0.5	20	1	BD175645	ACCESSION:BD175645
c3339	13.8	0.5	20	1	BD181841	ACCESSION:BD181841
3340	13.8	0.5	21	1	DOGP41401	ACCESSION:L24302
3341	13.8	0.5	21	1	A20740	ACCESSION:A20740
3342	13.8	0.5	21	1	AR062638	ACCESSION:AR062638
c3343	13.8	0.5	21	1	AR081625	ACCESSION:AR081625
3344	13.8	0.5	21	1	AR093404	ACCESSION:AR093404
3345	13.8	0.5	21	1	AR104741	ACCESSION:AR104741
3346	13.8	0.5	21	1	AR105563	ACCESSION:AR105563
c3347	13.8	0.5	21	1	AR109833	ACCESSION:AR109833
c3348	13.8	0.5	21	1	AR109839	ACCESSION:AR109839
c3349	13.8	0.5	21	1	AR109840	ACCESSION:AR109840
c3350	13.8	0.5	21	1	AR109845	ACCESSION:AR109845
3351	13.8	0.5	21	1	AR123225	ACCESSION:AR123225
3352	13.8	0.5	21	1	AR139687	ACCESSION:AR139687
3353	13.8	0.5	21	1	AR152832	ACCESSION:AR152832
3354	13.8	0.5	21	1	AR168784	ACCESSION:AR168784
c3355	13.8	0.5	21	1	BD228621	ACCESSION:BD228621
3356	13.8	0.5	21	1	E30929	ACCESSION:E30929
c3357	13.8	0.5	21	1	E36587	ACCESSION:E36587
3358	13.8	0.5	21	1	I20640	ACCESSION:I20640
3359	13.8	0.5	21	1	I27778	ACCESSION:I27778
c3360	13.8	0.5	21	1	I29090	ACCESSION:I29090
3361	13.8	0.5	21	1	I33333	ACCESSION:I33333
c3362	13.8	0.5	21	1	I42137	ACCESSION:I42137
3363	13.8	0.5	21	1	AR200253	ACCESSION:AR200253
3364	13.8	0.5	21	1	AR212829	ACCESSION:AR212829
3365	13.8	0.5	21	1	AR262385	ACCESSION:AR262385
c3366	13.8	0.5	21	1	AR296500	ACCESSION:AR296500
3367	13.8	0.5	21	1	AR298436	ACCESSION:AR298436
3368	13.8	0.5	21	1	AR342463	ACCESSION:AR342463
c3369	13.8	0.5	21	1	AR344822	ACCESSION:AR344822
c3370	13.8	0.5	21	1	AR344857	ACCESSION:AR344857
3371	13.8	0.5	21	1	AR365046	ACCESSION:AR365046
3372	13.8	0.5	21	1	AR369458	ACCESSION:AR369458
3373	13.8	0.5	21	1	AR370563	ACCESSION:AR370563
c3374	13.8	0.5	21	1	AR404583	ACCESSION:AR404583
c3375	13.8	0.5	21	1	AX096072	ACCESSION:AX096072
c3376	13.8	0.5	21	1	AX096676	ACCESSION:AX096676
3377	13.8	0.5	21	1	AX097131	ACCESSION:AX097131
3378	13.8	0.5	21	1	AX097215	ACCESSION:AX097215
c3379	13.8	0.5	21	1	AX154141	ACCESSION:AX154141
c3380	13.8	0.5	21	1	AX183997	ACCESSION:AX183997
c3381	13.8	0.5	21	1	AX201193	ACCESSION:AX201193
3382	13.8	0.5	21	1	AX201215	ACCESSION:AX201215
3383	13.8	0.5	21	1	AX201233	ACCESSION:AX201233
3384	13.8	0.5	21	1	AX203169	ACCESSION:AX203169
c3385	13.8	0.5	21	1	AX397777	ACCESSION:AX397777
c3386	13.8	0.5	21	1	AX397812	ACCESSION:AX397812
c3387	13.8	0.5	21	1	AX555818	ACCESSION:AX555818
3388	13.8	0.5	21	1	AX594110	ACCESSION:AX594110
c3389	13.8	0.5	21	1	AX713257	ACCESSION:AX713257
3390	13.8	0.5	21	1	AX810933	ACCESSION:AX810933
3391	13.8	0.5	21	1	BD000358	ACCESSION:BD000358
c3392	13.8	0.5	21	1	BD056555	ACCESSION:BD056555
c3393	13.8	0.5	21	1	BD089006	ACCESSION:BD089006
3394	13.8	0.5	21	1	BD134288	ACCESSION:BD134288
3395	13.8	0.5	21	1	BD140134	ACCESSION:BD140134
c3396	13.8	0.5	21	1	BD161939	ACCESSION:BD161939
c3397	13.8	0.5	21	1	AB069141	ACCESSION:AB069141
c3398	13.8	0.5	22	1	AR066407	ACCESSION:AR066407
3399	13.8	0.5	22	1	AX011524	ACCESSION:AX011524
3400	13.8	0.5	22	1	BD226411	ACCESSION:BD226411
3401	13.8	0.5	25	1	AX042978	ACCESSION:AX042978
c3402	13.8	0.5	25	1	AX043019	ACCESSION:AX043019
3403	13.8	0.5	25	1	AX043461	ACCESSION:AX043461
c3404	13.8	0.5	25	1	AX042904	ACCESSION:AX042904
c3405	13.8	0.5	25	1	AX043257	ACCESSION:AX043257
c3406	13.6	0.5	20	1	AX048437	ACCESSION:AX048437
c3407	13.6	0.5	20	1	AX048435	ACCESSION:AX048435
c3408	13.6	0.5	20	1	BOVINE01	ACCESSION:D83281
c3409	13.6	0.5	20	1	BOVINE31	ACCESSION:D83311
3410	13.6	0.5	20	1	A69626	ACCESSION:A69626
c3411	13.6	0.5	20	1	A88114	ACCESSION:A88114
c3412	13.6	0.5	20	1	A88305	ACCESSION:A88305
c3413	13.6	0.5	20	1	A90081	ACCESSION:A90081
c3414	13.6	0.5	20	1	A90272	ACCESSION:A90272
3415	13.6	0.5	20	1	AR016151	ACCESSION:AR016151
3416	13.6	0.5	20	1	AR019149	ACCESSION:AR019149
c3417	13.6	0.5	20	1	AR036637	ACCESSION:AR036637
3418	13.6	0.5	20	1	AR052626	ACCESSION:AR052626
3419	13.6	0.5	20	1	AR060235	ACCESSION:AR060235
3420	13.6	0.5	20	1	AR086246	ACCESSION:AR086246
c3421	13.6	0.5	20	1	AR095027	ACCESSION:AR095027
3422	13.6	0.5	20	1	AR100486	ACCESSION:AR100486
c3423	13.6	0.5	20	1	AR100614	ACCESSION:AR100614
c3424	13.6	0.5	20	1	AR102419	ACCESSION:AR102419
c3425	13.6	0.5	20	1	AR103803	ACCESSION:AR103803
c3426	13.6	0.5	20	1	AR107635	ACCESSION:AR107635
c3427	13.6	0.5	20	1	AR107636	ACCESSION:AR107636
c3428	13.6	0.5	20	1	AR116415	ACCESSION:AR116415
3429	13.6	0.5	20	1	AR121022	ACCESSION:AR121022
3430	13.6	0.5	20	1	AR121320	ACCESSION:AR121320
c3431	13.6	0.5	20	1	AR121613	ACCESSION:AR121613
c3432	13.6	0.5	20	1	AR124459	ACCESSION:AR124459
c3433	13.6	0.5	20	1	AR126680	ACCESSION:AR126680
c3434	13.6	0.5	20	1	AR130120	ACCESSION:AR130120
3435	13.6	0.5	20	1	AR136423	ACCESSION:AR136423
3436	13.6	0.5	20	1	AR143173	ACCESSION:AR143173
3437	13.6	0.5	20	1	AR150141	ACCESSION:AR150141
c3438	13.6	0.5	20	1	AR153094	ACCESSION:AR153094
c3439	13.6	0.5	20	1	AR158732	ACCESSION:AR158732
3440	13.6	0.5	20	1	AR158929	ACCESSION:AR158929
c3441	13.6	0.5	20	1	AR159152	ACCESSION:AR159152
c3442	13.6	0.5	20	1	AR159153	ACCESSION:AR159153
c3443	13.6	0.5	20	1	AR159154	ACCESSION:AR159154
c3444	13.6	0.5	20	1	AR163820	ACCESSION:AR163820
3445	13.6	0.5	20	1	AR163962	ACCESSION:AR163962
c3446	13.6	0.5	20	1	AR164029	ACCESSION:AR164029
3447	13.6	0.5	20	1	AR173039	ACCESSION:AR173039
3448	13.6	0.5	20	1	AR176812	ACCESSION:AR176812
3449	13.6	0.5	20	1	BD228014	ACCESSION:BD228014
3450	13.6	0.5	20	1	BD249348	ACCESSION:BD249348
3451	13.6	0.5	20	1	BD251480	ACCESSION:BD251480
c3452	13.6	0.5	20	1	BD269458	ACCESSION:BD269458
3453	13.6	0.5	20	1	BD269459	ACCESSION:BD269459
3454	13.6	0.5	20	1	BD272643	ACCESSION:BD272643
c3455	13.6	0.5	20	1	E16129	ACCESSION:E16129
c3456	13.6	0.5	20	1	E29890	ACCESSION:E29890
3457	13.6	0.5	20	1	E29952	ACCESSION:E29952
3458	13.6	0.5	20	1	E39288	ACCESSION:E39288
3459	13.6	0.5	20	1	E39963	ACCESSION:E39963
3460	13.6	0.5	20	1	E58734	ACCESSION:E58734
c3461	13.6	0.5	20	1	I19926	ACCESSION:I19926
c3462	13.6	0.5	20	1	I72480	ACCESSION:I72480
c3463	13.6	0.5	20	1	I88040	ACCESSION:I88040
3464	13.6	0.5	20	1	AR199794	ACCESSION:AR199794

c3173	13.8	0.5	18	1	AX207025	ACCESSION:AX207025
3174	13.8	0.5	18	1	AX298581	ACCESSION:AX298581
3175	13.8	0.5	18	1	AX301867	ACCESSION:AX301867
c3176	13.8	0.5	18	1	AX327038	ACCESSION:AX327038
3177	13.8	0.5	18	1	AX404240	ACCESSION:AX404240
c3178	13.8	0.5	18	1	AX662307	ACCESSION:AX662307
3179	13.8	0.5	18	1	BD089251	ACCESSION:BD089251
3180	13.8	0.5	19	1	A25084	ACCESSION:A25084
3181	13.8	0.5	19	1	A85285	ACCESSION:A85285
3182	13.8	0.5	19	1	AR030969	ACCESSION:AR030969
3183	13.8	0.5	19	1	AR030972	ACCESSION:AR030972
3184	13.8	0.5	19	1	AR030974	ACCESSION:AR030974
3185	13.8	0.5	19	1	AR030975	ACCESSION:AR030975
3186	13.8	0.5	19	1	AR030976	ACCESSION:AR030976
3187	13.8	0.5	19	1	AR030977	ACCESSION:AR030977
3188	13.8	0.5	19	1	AR030978	ACCESSION:AR030978
3189	13.8	0.5	19	1	AR030981	ACCESSION:AR030981
3190	13.8	0.5	19	1	AR030982	ACCESSION:AR030982
3191	13.8	0.5	19	1	AR030983	ACCESSION:AR030983
3192	13.8	0.5	19	1	AR030984	ACCESSION:AR030984
3193	13.8	0.5	19	1	AR108814	ACCESSION:AR108814
3194	13.8	0.5	19	1	AR108817	ACCESSION:AR108817
3195	13.8	0.5	19	1	AR108819	ACCESSION:AR108819
3196	13.8	0.5	19	1	AR108820	ACCESSION:AR108820
3197	13.8	0.5	19	1	AR108821	ACCESSION:AR108821
3198	13.8	0.5	19	1	AR108822	ACCESSION:AR108822
3199	13.8	0.5	19	1	AR108823	ACCESSION:AR108823
3200	13.8	0.5	19	1	AR108826	ACCESSION:AR108826
3201	13.8	0.5	19	1	AR108827	ACCESSION:AR108827
3202	13.8	0.5	19	1	AR108828	ACCESSION:AR108828
3203	13.8	0.5	19	1	AR108829	ACCESSION:AR108829
3204	13.8	0.5	19	1	BD242593	ACCESSION:BD242593
3205	13.8	0.5	19	1	BD269034	ACCESSION:BD269034
3206	13.8	0.5	19	1	I38722	ACCESSION:I38722
3207	13.8	0.5	19	1	I62823	ACCESSION:I62823
3208	13.8	0.5	19	1	I81331	ACCESSION:I81331
3209	13.8	0.5	19	1	I88034	ACCESSION:I88034
3210	13.8	0.5	19	1	AR202164	ACCESSION:AR202164
3211	13.8	0.5	19	1	AR205763	ACCESSION:AR205763
3212	13.8	0.5	19	1	AR205766	ACCESSION:AR205766
3213	13.8	0.5	19	1	AR205768	ACCESSION:AR205768
3214	13.8	0.5	19	1	AR205769	ACCESSION:AR205769
3215	13.8	0.5	19	1	AR205770	ACCESSION:AR205770
3216	13.8	0.5	19	1	AR205771	ACCESSION:AR205771
3217	13.8	0.5	19	1	AR205772	ACCESSION:AR205772
3218	13.8	0.5	19	1	AR205775	ACCESSION:AR205775
3219	13.8	0.5	19	1	AR205776	ACCESSION:AR205776
3220	13.8	0.5	19	1	AR205777	ACCESSION:AR205777
3221	13.8	0.5	19	1	AR205778	ACCESSION:AR205778
3222	13.8	0.5	19	1	AR280183	ACCESSION:AR280183
3223	13.8	0.5	19	1	AR293201	ACCESSION:AR293201
3224	13.8	0.5	19	1	AR296121	ACCESSION:AR296121
3225	13.8	0.5	19	1	AR307194	ACCESSION:AR307194
3226	13.8	0.5	19	1	AX011598	ACCESSION:AX011598
c3227	13.8	0.5	19	1	AX130773	ACCESSION:AX130773
c3228	13.8	0.5	19	1	AX131091	ACCESSION:AX131091
c3229	13.8	0.5	19	1	AX132837	ACCESSION:AX132837
c3230	13.8	0.5	19	1	AX132840	ACCESSION:AX132840
3231	13.8	0.5	19	1	AX378760	ACCESSION:AX378760
3232	13.8	0.5	19	1	AX803976	ACCESSION:AX803976
3233	13.8	0.5	19	1	BD103645	ACCESSION:BD103645
3234	13.8	0.5	19	1	BD107601	ACCESSION:BD107601
3235	13.8	0.5	19	1	BD196445	ACCESSION:BD196445
3236	13.8	0.5	19	1	BD196765	ACCESSION:BD196765
c3237	13.8	0.5	20	1	AR107647	ACCESSION:AR107647
c3238	13.8	0.5	20	1	AX048444	ACCESSION:AX048444
3239	13.8	0.5	20	1	AR107644	ACCESSION:AR107644
3240	13.8	0.5	20	1	A40401	ACCESSION:A40401
c3241	13.8	0.5	20	1	AR010207	ACCESSION:AR010207
3242	13.8	0.5	20	1	AR011627	ACCESSION:AR011627
3243	13.8	0.5	20	1	AR030970	ACCESSION:AR030970
c3244	13.8	0.5	20	1	AR031542	ACCESSION:AR031542
3245	13.8	0.5	20	1	AR037329	ACCESSION:AR037329
3246	13.8	0.5	20	1	AR040612	ACCESSION:AR040612
c3247	13.8	0.5	20	1	AR052440	ACCESSION:AR052440
3248	13.8	0.5	20	1	AR068795	ACCESSION:AR068795
3249	13.8	0.5	20	1	AR075147	ACCESSION:AR075147
c3250	13.8	0.5	20	1	AR082428	ACCESSION:AR082428
3251	13.8	0.5	20	1	AR089233	ACCESSION:AR089233
3252	13.8	0.5	20	1	AR092669	ACCESSION:AR092669
c3253	13.8	0.5	20	1	AR100377	ACCESSION:AR100377
3254	13.8	0.5	20	1	AR103911	ACCESSION:AR103911
c3255	13.8	0.5	20	1	AR107643	ACCESSION:AR107643
3256	13.8	0.5	20	1	AR108815	ACCESSION:AR108815
c3257	13.8	0.5	20	1	AR109207	ACCESSION:AR109207
3258	13.8	0.5	20	1	AR116574	ACCESSION:AR116574
c3259	13.8	0.5	20	1	AR124483	ACCESSION:AR124483
3260	13.8	0.5	20	1	AR126737	ACCESSION:AR126737
3261	13.8	0.5	20	1	AR130999	ACCESSION:AR130999
c3262	13.8	0.5	20	1	AR150032	ACCESSION:AR150032
3263	13.8	0.5	20	1	AR158377	ACCESSION:AR158377
3264	13.8	0.5	20	1	AR163975	ACCESSION:AR163975
c3265	13.8	0.5	20	1	AR174366	ACCESSION:AR174366
c3266	13.8	0.5	20	1	BD227905	ACCESSION:BD227905
c3267	13.8	0.5	20	1	BD241888	ACCESSION:BD241888
c3268	13.8	0.5	20	1	E08391	ACCESSION:E08391
c3269	13.8	0.5	20	1	E39195	ACCESSION:E39195
c3270	13.8	0.5	20	1	I12653	ACCESSION:I12653
3271	13.8	0.5	20	1	I19623	ACCESSION:I19623
c3272	13.8	0.5	20	1	I43323	ACCESSION:I43323
c3273	13.8	0.5	20	1	I46642	ACCESSION:I46642
c3274	13.8	0.5	20	1	I95826	ACCESSION:I95826
3275	13.8	0.5	20	1	AR182905	ACCESSION:AR182905
c3276	13.8	0.5	20	1	AR182905	ACCESSION:AR182905
3277	13.8	0.5	20	1	AR205764	ACCESSION:AR205764
3278	13.8	0.5	20	1	AR207166	ACCESSION:AR207166
c3279	13.8	0.5	20	1	AR208724	ACCESSION:AR208724
c3280	13.8	0.5	20	1	AR228938	ACCESSION:AR228938
c3281	13.8	0.5	20	1	AR230963	ACCESSION:AR230963
3282	13.8	0.5	20	1	AR231782	ACCESSION:AR231782
3283	13.8	0.5	20	1	AR235921	ACCESSION:AR235921
c3284	13.8	0.5	20	1	AR264956	ACCESSION:AR264956
c3285	13.8	0.5	20	1	AR264957	ACCESSION:AR264957
c3286	13.8	0.5	20	1	AR264958	ACCESSION:AR264958
3287	13.8	0.5	20	1	AR268790	ACCESSION:AR268790
3288	13.8	0.5	20	1	AR271203	ACCESSION:AR271203
c3289	13.8	0.5	20	1	AR274662	ACCESSION:AR274662
c3290	13.8	0.5	20	1	AR275179	ACCESSION:AR275179
3291	13.8	0.5	20	1	AR278913	ACCESSION:AR278913
c3292	13.8	0.5	20	1	AR312181	ACCESSION:AR312181
3293	13.8	0.5	20	1	AR313789	ACCESSION:AR313789
3294	13.8	0.5	20	1	AR337182	ACCESSION:AR337182
c3295	13.8	0.5	20	1	AR344858	ACCESSION:AR344858
c3296	13.8	0.5	20	1	AR373535	ACCESSION:AR373535
3297	13.8	0.5	20	1	AR438112	ACCESSION:AR438112
3298	13.8	0.5	20	1	AX003426	ACCESSION:AX003426
c3299	13.8	0.5	20	1	AX008654	ACCESSION:AX008654
c3300	13.8	0.5	20	1	AX046104	ACCESSION:AX046104
3301	13.8	0.5	20	1	AX103947	ACCESSION:AX103947
c3302	13.8	0.5	20	1	AX103947	ACCESSION:AX103947
3303	13.8	0.5	20	1	AX117022	ACCESSION:AX117022
c3304	13.8	0.5	20	1	AX117942	ACCESSION:AX117942
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2718	14.4	0.5	22	1	AX592990
2719	14.4	0.5	22	1	AX593130
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2723	14.4	0.5	22	1	AX616971
2724	14.4	0.5	22	1	AX643845
2725	14.4	0.5	22	1	AX696030
2726	14.4	0.5	22	1	AX773003
2727	14.4	0.5	22	1	AX781387
2728	14.4	0.5	22	1	AX794404
2729	14.4	0.5	22	1	AX815443
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c2732	14.4	0.5	25	1	AX042547
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2395	15	0.5	22	1	BD206192	ACCESSION:BD206192
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c2406	15	0.5	23	1	A79730	ACCESSION:A79730
2407	15	0.5	23	1	BD250901	ACCESSION:BD250901
2408	15	0.5	23	1	BD260935	ACCESSION:BD260935
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2410	15	0.5	23	1	AR374920	ACCESSION:AR374920
2411	15	0.5	23	1	AR409907	ACCESSION:AR409907
2412	15	0.5	23	1	AX048427	ACCESSION:AX048427
c2413	15	0.5	23	1	AX048427	ACCESSION:AX048427
2414	15	0.5	23	1	AX226182	ACCESSION:AX226182
c2415	15	0.5	23	1	AX591818	ACCESSION:AX591818
c2416	15	0.5	23	1	BD009266	ACCESSION:BD009266
c2417	15	0.5	23	1	BD188565	ACCESSION:BD188565
c2418	15	0.5	23	1	BD225572	ACCESSION:BD225572
2419	15	0.5	24	1	A33476	ACCESSION:A33476
c2420	15	0.5	24	1	AX554007	ACCESSION:AX554007
2421	15	0.5	25	1	AX043309	ACCESSION:AX043309
c2422	15	0.5	25	1	I56670	ACCESSION:I56670
2423	15	0.5	25	1	AR211579	ACCESSION:AR211579
c2424	15	0.5	25	1	AX043206	ACCESSION:AX043206
2425	15	0.5	25	1	AX043296	ACCESSION:AX043296
2426	15	0.5	25	1	BD075857	ACCESSION:BD075857
c2427	15	0.5	25	1	AX042962	ACCESSION:AX042962
c2428	15	0.5	26	1	AR034927	ACCESSION:AR034927
c2429	15	0.5	26	1	AR145386	ACCESSION:AR145386
c2430	15	0.5	26	1	I18346	ACCESSION:I18346
c2431	15	0.5	26	1	I21333	ACCESSION:I21333
c2432	15	0.5	26	1	I35739	ACCESSION:I35739
c2433	15	0.5	26	1	I36757	ACCESSION:I36757
c2434	15	0.5	26	1	I40322	ACCESSION:I40322
c2435	15	0.5	30	1	I30206	ACCESSION:I30206
c2436	15	0.5	30	1	AX267026	ACCESSION:AX267026
c2437	14.8	0.5	18	1	AR085574	ACCESSION:AR085574
c2438	14.8	0.5	18	1	BD274799	ACCESSION:BD274799
c2439	14.8	0.5	18	1	I04805	ACCESSION:I04805
c2440	14.8	0.5	18	1	I18341	ACCESSION:I18341
c2441	14.8	0.5	18	1	AR205265	ACCESSION:AR205265
c2442	14.8	0.5	18	1	AR211095	ACCESSION:AR211095

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c2152	15	0.5	15	1	AR371280	ACCESSION:AR371280
2153	15	0.5	15	1	AR371281	ACCESSION:AR371281
c2154	15	0.5	15	1	AR371281	ACCESSION:AR371281
2155	15	0.5	15	1	AR410213	ACCESSION:AR410213
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2163	15	0.5	15	1	AX106973	ACCESSION:AX106973
c2164	15	0.5	15	1	AX106973	ACCESSION:AX106973
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c2170	15	0.5	15	1	AX180140	ACCESSION:AX180140
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c2172	15	0.5	15	1	AX180141	ACCESSION:AX180141
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c2184	15	0.5	15	1	AX633203	ACCESSION:AX633203
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2205	15	0.5	16	1	I16032	ACCESSION:I16032
2206	15	0.5	16	1	I28367	ACCESSION:I28367
2207	15	0.5	16	1	AR221693	ACCESSION:AR221693
c2208	15	0.5	16	1	AR221693	ACCESSION:AR221693
2209	15	0.5	16	1	AR221694	ACCESSION:AR221694
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2217	15	0.5	16	1	AR221698	ACCESSION:AR221698
c2218	15	0.5	16	1	AR221698	ACCESSION:AR221698
2219	15	0.5	16	1	AR221992	ACCESSION:AR221992
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2221	15	0.5	16	1	AR257438	ACCESSION:AR257438
c2222	15	0.5	16	1	AR257438	ACCESSION:AR257438
2223	15	0.5	16	1	AR257439	ACCESSION:AR257439
c2224	15	0.5	16	1	AR257439	ACCESSION:AR257439
2225	15	0.5	16	1	AR257440	ACCESSION:AR257440
c2226	15	0.5	16	1	AR257440	ACCESSION:AR257440
2227	15	0.5	16	1	AR257441	ACCESSION:AR257441
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2229	15	0.5	16	1	AR257442	ACCESSION:AR257442
c2230	15	0.5	16	1	AR257442	ACCESSION:AR257442
2231	15	0.5	16	1	AR257443	ACCESSION:AR257443
c2232	15	0.5	16	1	AR257443	ACCESSION:AR257443
2233	15	0.5	16	1	AR266619	ACCESSION:AR266619
2234	15	0.5	16	1	AR266620	ACCESSION:AR266620
2235	15	0.5	16	1	AR266646	ACCESSION:AR266646
2236	15	0.5	16	1	AR266647	ACCESSION:AR266647
2237	15	0.5	16	1	AR429378	ACCESSION:AR429378
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2245	15	0.5	16	1	AX253411	ACCESSION:AX253411
2246	15	0.5	16	1	AX306364	ACCESSION:AX306364
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2248	15	0.5	16	1	AX352388	ACCESSION:AX352388
c2249	15	0.5	16	1	AX359760	ACCESSION:AX359760
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c2259	15	0.5	17	1	E34258	ACCESSION:E34258
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c2261	15	0.5	17	1	AR187061	ACCESSION:AR187061
2262	15	0.5	17	1	AR187064	ACCESSION:AR187064
2263	15	0.5	17	1	AR241830	ACCESSION:AR241830
c2264	15	0.5	17	1	AR266625	ACCESSION:AR266625
c2265	15	0.5	17	1	AR323671	ACCESSION:AR323671
2266	15	0.5	17	1	AR323674	ACCESSION:AR323674
c2267	15	0.5	17	1	BD011730	ACCESSION:BD011730
2268	15	0.5	17	1	BD011731	ACCESSION:BD011731
c2269	15	0.5	17	1	BD091742	ACCESSION:BD091742
2270	15	0.5	17	1	BD091743	ACCESSION:BD091743
c2271	15	0.5	17	1	BD091750	ACCESSION:BD091750
2272	15	0.5	17	1	BD091751	ACCESSION:BD091751
c2273	15	0.5	17	1	BD091773	ACCESSION:BD091773
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c2285	15	0.5	17	1	BD168111	ACCESSION:BD168111
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c2287	15	0.5	17	1	BD171177	ACCESSION:BD171177
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2013	15.4	0.5	24	1	BD229208
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c2015	15.4	0.5	25	1	AX043281
2016	15.4	0.5	25	1	AX043100
c2017	15.4	0.5	25	1	AX043038
c2018	15.4	0.5	25	1	AX042684
c2019	15.4	0.5	25	1	AX043487
2020	15.4	0.5	25	1	AX042585
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c2023	15.4	0.5	29	1	AR409905
2024	15.2	0.5	16	1	E52143
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2028	15.2	0.5	17	1	AR183909
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c2038	15.2	0.5	20	1	AR163830
c2039	15.2	0.5	20	1	AR174362
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c2045	15.2	0.5	20	1	AR360398
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2052	15.2	0.5	20	1	AX004425
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c2070	15.2	0.5	21	1	AX000973
c2071	15.2	0.5	21	1	AX146093
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2074	15.2	0.5	21	1	BD089734
c2075	15.2	0.5	21	1	BD196252
c2076	15.2	0.5	22	1	AR135198
c2077	15.2	0.5	22	1	AR146694

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c2081	15.2	0.5	22	1	AX751620
2082	15.2	0.5	22	1	AX817759
2083	15.2	0.5	22	1	BD089101
c2084	15.2	0.5	22	1	BD191561
2085	15.2	0.5	22	1	AB067984
2086	15.2	0.5	23	1	AX164418
2087	15.2	0.5	23	1	AX698793
2088	15.2	0.5	23	1	AX771993
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c2092	15.2	0.5	25	1	AX043297
c2093	15.2	0.5	25	1	AX043310
c2094	15.2	0.5	25	1	AX043311
c2095	15.2	0.5	25	1	AX042593
c2096	15.2	0.5	25	1	AX043312
c2097	15.2	0.5	26	1	AR172578
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2099	15	0.5	15	1	AR029402
c2100	15	0.5	15	1	AR029402
2101	15	0.5	15	1	AR029403
c2102	15	0.5	15	1	AR029403
2103	15	0.5	15	1	AR034895
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c2110	15	0.5	15	1	AR049970
2111	15	0.5	15	1	AR049971
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c2114	15	0.5	15	1	AR056157
2115	15	0.5	15	1	AR056158
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2119	15	0.5	15	1	AR080676
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2121	15	0.5	15	1	AR084516
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2123	15	0.5	15	1	AR084520
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2125	15	0.5	15	1	AR105981
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2127	15	0.5	15	1	AR113915
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2133	15	0.5	15	1	AR170375
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2137	15	0.5	15	1	E12591
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2139	15	0.5	15	1	I29068
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2141	15	0.5	15	1	I38641
c2142	15	0.5	15	1	I38641
2143	15	0.5	15	1	AR200476
c2144	15	0.5	15	1	AR200476
2145	15	0.5	15	1	AR200477
c2146	15	0.5	15	1	AR200477
2147	15	0.5	15	1	AR222461
c2148	15	0.5	15	1	AR222461
2149	15	0.5	15	1	AR266630
c2150	15	0.5	15	1	AR266630

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c1861	15.8	0.6	21	1	AR084566	ACCESSION:AR084566
1862	15.8	0.6	21	1	AR084567	ACCESSION:AR084567
c1863	15.8	0.6	21	1	AR084578	ACCESSION:AR084578
1864	15.8	0.6	21	1	AR084579	ACCESSION:AR084579
1865	15.8	0.6	21	1	AR084582	ACCESSION:AR084582
1866	15.8	0.6	21	1	AR093142	ACCESSION:AR093142
c1867	15.8	0.6	21	1	AR103576	ACCESSION:AR103576
c1868	15.8	0.6	21	1	AX154293	ACCESSION:AX154293
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c1871	15.8	0.6	21	1	BD129806	ACCESSION:BD129806
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c1873	15.8	0.6	22	1	AX546922	ACCESSION:AX546922
1874	15.8	0.6	22	1	BD230925	ACCESSION:BD230925
c1875	15.8	0.6	22	1	AX011524	ACCESSION:AX011524
1876	15.8	0.6	22	1	AX352320	ACCESSION:AX352320
c1877	15.8	0.6	22	1	BD226411	ACCESSION:BD226411
1878	15.8	0.6	23	1	AR053253	ACCESSION:AR053253
c1879	15.8	0.6	23	1	AR053257	ACCESSION:AR053257
1880	15.8	0.6	23	1	AX084400	ACCESSION:AX084400
c1881	15.8	0.6	24	1	AX103868	ACCESSION:AX103868
c1882	15.8	0.6	24	1	AX546921	ACCESSION:AX546921
c1883	15.8	0.6	24	1	A33476	ACCESSION:A33476
c1884	15.8	0.6	24	1	AR078306	ACCESSION:AR078306
1885	15.8	0.6	24	1	AR078307	ACCESSION:AR078307
c1886	15.8	0.6	24	1	AR116903	ACCESSION:AR116903
c1887	15.8	0.6	24	1	BD229208	ACCESSION:BD229208
c1888	15.8	0.6	24	1	AR349460	ACCESSION:AR349460
1889	15.8	0.6	24	1	AX043137	ACCESSION:AX043137
c1890	15.8	0.6	24	1	BD085850	ACCESSION:BD085850
1891	15.8	0.6	24	1	S81366	ACCESSION:S81366
1892	15.8	0.6	25	1	BD090045	ACCESSION:BD090045
c1893	15.8	0.6	25	1	AX043131	ACCESSION:AX043131
c1894	15.8	0.6	25	1	AX115872	ACCESSION:AX115872
c1895	15.8	0.6	25	1	AX042590	ACCESSION:AX042590
c1896	15.8	0.6	25	1	AX042992	ACCESSION:AX042992
c1897	15.8	0.6	25	1	I45922	ACCESSION:I45922
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1899	15.8	0.6	25	1	AX042569	ACCESSION:AX042569
c1900	15.8	0.6	25	1	AX043112	ACCESSION:AX043112
1901	15.8	0.6	25	1	AX043284	ACCESSION:AX043284
1902	15.8	0.6	25	1	AX043413	ACCESSION:AX043413
c1903	15.8	0.6	34	1	AR098680	ACCESSION:AR098680
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1905	15.6	0.6	17	1	BD233654	ACCESSION:BD233654
c1906	15.6	0.6	17	1	BD233654	ACCESSION:BD233654
c1907	15.6	0.6	17	1	BD217905	ACCESSION:BD217905
c1908	15.6	0.6	22	1	A17252	ACCESSION:A17252
c1909	15.6	0.6	22	1	AR027635	ACCESSION:AR027635
1910	15.6	0.6	22	1	AR106296	ACCESSION:AR106296
1911	15.6	0.6	22	1	AR178618	ACCESSION:AR178618
1912	15.6	0.6	22	1	AX088188	ACCESSION:AX088188
c1913	15.6	0.6	22	1	AX283017	ACCESSION:AX283017
1914	15.6	0.6	22	1	AX922725	ACCESSION:AX922725
1915	15.6	0.6	22	1	BD073283	ACCESSION:BD073283
1916	15.6	0.6	23	1	AR085444	ACCESSION:AR085444
1917	15.6	0.6	23	1	AR088850	ACCESSION:AR088850
1918	15.6	0.6	23	1	AR167324	ACCESSION:AR167324
1919	15.6	0.6	23	1	I36707	ACCESSION:I36707
c1920	15.6	0.6	23	1	AX003445	ACCESSION:AX003445
c1921	15.6	0.6	23	1	BD087061	ACCESSION:BD087061
1922	15.6	0.6	24	1	AR162082	ACCESSION:AR162082
1923	15.6	0.6	24	1	AR166607	ACCESSION:AR166607
1924	15.6	0.6	24	1	BD238389	ACCESSION:BD238389
1925	15.6	0.6	24	1	AR279815	ACCESSION:AR279815
1926	15.6	0.6	24	1	A57515	ACCESSION:A57515
c1927	15.6	0.6	24	1	I30522	ACCESSION:I30522
c1928	15.6	0.6	24	1	AX207497	ACCESSION:AX207497
1929	15.6	0.6	24	1	AX291683	ACCESSION:AX291683
1930	15.6	0.6	24	1	AX451724	ACCESSION:AX451724
1931	15.6	0.6	24	1	AX493123	ACCESSION:AX493123
1932	15.6	0.6	24	1	AX493955	ACCESSION:AX493955
1933	15.6	0.6	24	1	AX554007	ACCESSION:AX554007
1934	15.6	0.6	24	1	BD082997	ACCESSION:BD082997
1935	15.6	0.6	24	1	BD091788	ACCESSION:BD091788
1936	15.6	0.6	25	1	AX042589	ACCESSION:AX042589
1937	15.6	0.6	25	1	AX043290	ACCESSION:AX043290
c1938	15.6	0.6	25	1	AX042902	ACCESSION:AX042902
1939	15.6	0.6	25	1	AX043108	ACCESSION:AX043108
1940	15.6	0.6	26	1	E31574	ACCESSION:E31574
1941	15.6	0.6	26	1	AX118414	ACCESSION:AX118414
c1942	15.4	0.5	17	1	AX692524	ACCESSION:AX692524
1943	15.4	0.5	17	1	AR187058	ACCESSION:AR187058
1944	15.4	0.5	17	1	AR187059	ACCESSION:AR187059
1945	15.4	0.5	17	1	AR187060	ACCESSION:AR187060
c1946	15.4	0.5	17	1	AR187065	ACCESSION:AR187065
c1947	15.4	0.5	17	1	AR187066	ACCESSION:AR187066
1948	15.4	0.5	17	1	AR323668	ACCESSION:AR323668
1949	15.4	0.5	17	1	AR323669	ACCESSION:AR323669
1950	15.4	0.5	17	1	AR323670	ACCESSION:AR323670
c1951	15.4	0.5	17	1	AR323675	ACCESSION:AR323675
c1952	15.4	0.5	17	1	AR323676	ACCESSION:AR323676
1953	15.4	0.5	17	1	AX692523	ACCESSION:AX692523
c1954	15.4	0.5	17	1	AX692523	ACCESSION:AX692523
1955	15.4	0.5	17	1	AX692527	ACCESSION:AX692527
c1956	15.4	0.5	17	1	AX692527	ACCESSION:AX692527
1957	15.4	0.5	17	1	AX728891	ACCESSION:AX728891
1958	15.4	0.5	17	1	AX732819	ACCESSION:AX732819
1959	15.4	0.5	17	1	AX760024	ACCESSION:AX760024
c1960	15.4	0.5	18	1	E32456	ACCESSION:E32456
1961	15.4	0.5	18	1	E32458	ACCESSION:E32458
c1962	15.4	0.5	18	1	E32453	ACCESSION:E32453
1963	15.4	0.5	18	1	E32455	ACCESSION:E32455
c1964	15.4	0.5	18	1	E32459	ACCESSION:E32459
1965	15.4	0.5	18	1	A67594	ACCESSION:A67594
1966	15.4	0.5	18	1	AR089732	ACCESSION:AR089732
1967	15.4	0.5	18	1	E32454	ACCESSION:E32454
c1968	15.4	0.5	18	1	E32454	ACCESSION:E32454
1969	15.4	0.5	18	1	E32457	ACCESSION:E32457
c1970	15.4	0.5	18	1	E32457	ACCESSION:E32457
c1971	15.4	0.5	18	1	E32460	ACCESSION:E32460
c1972	15.4	0.5	18	1	AX078832	ACCESSION:AX078832
c1973	15.4	0.5	18	1	AX804555	ACCESSION:AX804555
c1974	15.4	0.5	20	1	AR231312	ACCESSION:AR231312
c1975	15.4	0.5	20	1	AR086109	ACCESSION:AR086109
c1976	15.4	0.5	20	1	AR086110	ACCESSION:AR086110
c1977	15.4	0.5	20	1	E13187	ACCESSION:E13187
c1978	15.4	0.5	20	1	E13188	ACCESSION:E13188
1979	15.4	0.5	20	1	AX104239	ACCESSION:AX104239
c1980	15.4	0.5	20	1	AX294137	ACCESSION:AX294137
1981	15.4	0.5	20	1	AX355709	ACCESSION:AX355709
1982	15.4	0.5	20	1	AX547292	ACCESSION:AX547292
1983	15.4	0.5	20	1	AX613576	ACCESSION:AX613576
1984	15.4	0.5	20	1	BD171234	ACCESSION:BD171234
1985	15.4	0.5	20	1	BD185850	ACCESSION:BD185850
c1986	15.4	0.5	21	1	AR030787	ACCESSION:AR030787
c1987	15.4	0.5	21	1	AR045091	ACCESSION:AR045091
c1988	15.4	0.5	21	1	AR052947	ACCESSION:AR052947
c1989	15.4	0.5	21	1	AR122900	ACCESSION:AR122900
c1990	15.4	0.5	21	1	AR127822	ACCESSION:AR127822
c1991	15.4	0.5	21	1	AX038542	ACCESSION:AX038542
1992	15.4	0.5	21	1	AX094961	ACCESSION:AX094961
1993	15.4	0.5	21	1	AX095913	ACCESSION:AX095913
1994	15.4	0.5	21	1	AX810934	ACCESSION:AX810934
1995	15.4	0.5	21	1	BD185851	ACCESSION:BD185851
1996	15.4	0.5	22	1	AR003285	ACCESSION:AR003285
1997	15.4	0.5	22	1	AR003286	ACCESSION:AR003286
1998	15.4	0.5	22	1	AR003287	ACCESSION:AR003287
c1999	15.4	0.5	22	1	E36538	ACCESSION:E36538
c2000	15.4	0.5	22	1	E40160	ACCESSION:E40160
2001	15.4	0.5	22	1	I30196	ACCESSION:I30196
2002	15.4	0.5	22	1	I30197	ACCESSION:I30197
2003	15.4	0.5	22	1	I30198	ACCESSION:I30198
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c1714	16	0.6	16	1	BD167413	ACCESSION:BD167413
1715	16	0.6	16	1	BD167414	ACCESSION:BD167414
c1716	16	0.6	16	1	BD167414	ACCESSION:BD167414
c1717	16	0.6	17	1	AR187062	ACCESSION:AR187062
1718	16	0.6	17	1	AR187063	ACCESSION:AR187063
c1719	16	0.6	17	1	AR323672	ACCESSION:AR323672
1720	16	0.6	17	1	AR323673	ACCESSION:AR323673
1721	16	0.6	17	1	AX361606	ACCESSION:AX361606
c1722	16	0.6	17	1	AX692525	ACCESSION:AX692525
1723	16	0.6	17	1	AX814938	ACCESSION:AX814938
1724	16	0.6	17	1	AR172076	ACCESSION:AR172076
c1725	16	0.6	17	1	AR172076	ACCESSION:AR172076
1726	16	0.6	17	1	AR173367	ACCESSION:AR173367
c1727	16	0.6	17	1	AR173367	ACCESSION:AR173367
1728	16	0.6	17	1	E34258	ACCESSION:E34258
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1730	16	0.6	17	1	AR187061	ACCESSION:AR187061
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c1732	16	0.6	17	1	AR241830	ACCESSION:AR241830
1733	16	0.6	17	1	AR266625	ACCESSION:AR266625
1734	16	0.6	17	1	AR323671	ACCESSION:AR323671
c1735	16	0.6	17	1	AR323674	ACCESSION:AR323674
1736	16	0.6	17	1	AX146683	ACCESSION:AX146683
1737	16	0.6	17	1	AX692524	ACCESSION:AX692524
1738	16	0.6	17	1	AX692526	ACCESSION:AX692526
c1739	16	0.6	17	1	AX692526	ACCESSION:AX692526
1740	16	0.6	17	1	AX724426	ACCESSION:AX724426
1741	16	0.6	17	1	BD011730	ACCESSION:BD011730
c1742	16	0.6	17	1	BD011731	ACCESSION:BD011731
1743	16	0.6	17	1	BD091742	ACCESSION:BD091742
c1744	16	0.6	17	1	BD091743	ACCESSION:BD091743
1745	16	0.6	17	1	BD091750	ACCESSION:BD091750
c1746	16	0.6	17	1	BD091751	ACCESSION:BD091751
1747	16	0.6	17	1	BD091773	ACCESSION:BD091773
c1748	16	0.6	17	1	BD091774	ACCESSION:BD091774
1749	16	0.6	17	1	BD097334	ACCESSION:BD097334
c1750	16	0.6	17	1	BD097335	ACCESSION:BD097335
1751	16	0.6	17	1	BD142808	ACCESSION:BD142808
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1753	16	0.6	17	1	BD143834	ACCESSION:BD143834
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1755	16	0.6	17	1	BD167835	ACCESSION:BD167835
c1756	16	0.6	17	1	BD167836	ACCESSION:BD167836
1757	16	0.6	17	1	BD167907	ACCESSION:BD167907
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1761	16	0.6	17	1	BD171177	ACCESSION:BD171177
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1763	16	0.6	18	1	AX361600	ACCESSION:AX361600
1764	16	0.6	18	1	AX814932	ACCESSION:AX814932
c1765	16	0.6	18	1	A14689	ACCESSION:A14689
1766	16	0.6	18	1	AR208425	ACCESSION:AR208425
1767	16	0.6	18	1	AX085251	ACCESSION:AX085251
1768	16	0.6	18	1	E32450	ACCESSION:E32450
c1769	16	0.6	18	1	E32452	ACCESSION:E32452
1770	16	0.6	18	1	E32453	ACCESSION:E32453
c1771	16	0.6	18	1	E32455	ACCESSION:E32455
1772	16	0.6	18	1	E32459	ACCESSION:E32459
c1773	16	0.6	18	1	E32461	ACCESSION:E32461
c1774	16	0.6	20	1	AR086111	ACCESSION:AR086111
c1775	16	0.6	20	1	E13189	ACCESSION:E13189
1776	16	0.6	20	1	AR309844	ACCESSION:AR309844
c1777	16	0.6	20	1	AR309844	ACCESSION:AR309844
1778	16	0.6	20	1	AR312356	ACCESSION:AR312356
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c1780	16	0.6	20	1	AX048447	ACCESSION:AX048447
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1784	16	0.6	20	1	AX404077	ACCESSION:AX404077
c1785	16	0.6	20	1	AX404077	ACCESSION:AX404077
1786	16	0.6	20	1	BD143136	ACCESSION:BD143136
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c1789	16	0.6	21	1	E28097	ACCESSION:E28097
1790	16	0.6	21	1	AX394604	ACCESSION:AX394604
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1792	16	0.6	21	1	AX498247	ACCESSION:AX498247
1793	16	0.6	22	1	AX394605	ACCESSION:AX394605
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c1795	16	0.6	23	1	I79497	ACCESSION:I79497
c1796	16	0.6	23	1	BD133515	ACCESSION:BD133515
c1797	16	0.6	23	1	E12393	ACCESSION:E12393
c1798	16	0.6	23	1	E12391	ACCESSION:E12391
c1799	16	0.6	23	1	I79499	ACCESSION:I79499
c1800	16	0.6	23	1	BD187389	ACCESSION:BD187389
c1801	16	0.6	23	1	BD245241	ACCESSION:BD245241
c1802	16	0.6	23	1	BD245233	ACCESSION:BD245233
c1803	16	0.6	23	1	BD245237	ACCESSION:BD245237
1804	16	0.6	23	1	AX394606	ACCESSION:AX394606
c1805	16	0.6	23	1	AX394606	ACCESSION:AX394606
c1806	16	0.6	24	1	I33155	ACCESSION:I33155
1807	16	0.6	24	1	AR081684	ACCESSION:AR081684
c1808	16	0.6	24	1	AR140017	ACCESSION:AR140017
1809	16	0.6	24	1	BD235199	ACCESSION:BD235199
1810	16	0.6	24	1	AR364668	ACCESSION:AR364668
1811	16	0.6	24	1	AX300680	ACCESSION:AX300680
1812	16	0.6	24	1	AX394608	ACCESSION:AX394608
c1813	16	0.6	24	1	AX394608	ACCESSION:AX394608
c1814	16	0.6	24	1	BD187293	ACCESSION:BD187293
c1815	16	0.6	25	1	AX042549	ACCESSION:AX042549
c1816	16	0.6	25	1	AX043230	ACCESSION:AX043230
1817	16	0.6	25	1	AX042901	ACCESSION:AX042901
c1818	16	0.6	25	1	AX043067	ACCESSION:AX043067
1819	16	0.6	25	1	AX042691	ACCESSION:AX042691
1820	16	0.6	25	1	AX117632	ACCESSION:AX117632
c1821	16	0.6	25	1	AX043286	ACCESSION:AX043286
c1822	16	0.6	25	1	AX043616	ACCESSION:AX043616
1823	16	0.6	25	1	AX042714	ACCESSION:AX042714
c1824	16	0.6	25	1	AX042891	ACCESSION:AX042891
1825	16	0.6	25	1	AX043076	ACCESSION:AX043076
c1826	16	0.6	25	1	AX043747	ACCESSION:AX043747
c1827	16	0.6	26	1	E64577	ACCESSION:E64577
c1828	16	0.6	26	1	AR164510	ACCESSION:AR164510
1829	16	0.6	26	1	AR078461	ACCESSION:AR078461
1830	16	0.6	27	1	AX589115	ACCESSION:AX589115
1831	16	0.6	28	1	AX394618	ACCESSION:AX394618
1832	16	0.6	29	1	AX394620	ACCESSION:AX394620
c1833	15.8	0.6	20	1	AX067205	ACCESSION:AX067205
c1834	15.8	0.6	20	1	A40129	ACCESSION:A40129
c1835	15.8	0.6	20	1	AR065945	ACCESSION:AR065945
c1836	15.8	0.6	20	1	AR080767	ACCESSION:AR080767
1837	15.8	0.6	20	1	AR107646	ACCESSION:AR107646
c1838	15.8	0.6	20	1	AR157688	ACCESSION:AR157688
c1839	15.8	0.6	20	1	BD243970	ACCESSION:BD243970
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c1841	15.8	0.6	20	1	I50039	ACCESSION:I50039
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1843	15.8	0.6	20	1	AR182885	ACCESSION:AR182885
c1844	15.8	0.6	20	1	AR204058	ACCESSION:AR204058
c1845	15.8	0.6	20	1	AR264951	ACCESSION:AR264951
c1846	15.8	0.6	20	1	AR300019	ACCESSION:AR300019
c1847	15.8	0.6	20	1	AR309119	ACCESSION:AR309119
c1848	15.8	0.6	20	1	AR373534	ACCESSION:AR373534
1849	15.8	0.6	20	1	AX078047	ACCESSION:AX078047
1850	15.8	0.6	20	1	AX104051	ACCESSION:AX104051
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1856	15.8	0.6	20	1	BD069976	ACCESSION:BD069976
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1571	16.6	0.6	25	1	AX043286
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1573	16.6	0.6	25	1	AX043616
c1574	16.6	0.6	25	1	AX043642
1575	16.6	0.6	25	1	AX104992
1576	16.6	0.6	25	1	BD074369
1577	16.6	0.6	25	1	BD074392
c1578	16.6	0.6	25	1	BD088021
1579	16.6	0.6	25	1	AJ588309
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c1581	16.6	0.6	29	1	E04206
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1583	16.4	0.6	18	1	AX085253
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c1588	16.4	0.6	18	1	AX085251
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1605	16.4	0.6	23	1	AX053002
c1606	16.4	0.6	24	1	AR162082
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c1618	16.4	0.6	25	1	AX692829
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1623	16.4	0.6	25	1	AX042616
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1625	16.4	0.6	25	1	AX042891
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1634	16.4	0.6	25	1	AX692820
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1636	16.4	0.6	25	1	AX692830
c1637	16.4	0.6	25	1	AX692830
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1639	16.4	0.6	30	1	AX351711

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1642	16.2	0.6	21	1	BD246728
1643	16.2	0.6	21	1	E28097
c1644	16.2	0.6	21	1	AR241776
1645	16.2	0.6	21	1	AR296425
1646	16.2	0.6	21	1	AX026215
c1647	16.2	0.6	22	1	AX457060
1648	16.2	0.6	24	1	A93098
1649	16.2	0.6	24	1	AR091179
1650	16.2	0.6	24	1	AR174054
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1654	16.2	0.6	24	1	BD064144
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c1700	16	0.6	16	1	AX235176
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1428	17	0.6	23	1	AX496104
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c1511	16.8	0.6	20	1	AX441512
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1513	16.8	0.6	22	1	AR066407
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1515	16.8	0.6	23	1	BD245233
1516	16.8	0.6	23	1	BD245237
1517	16.8	0.6	23	1	AX053001
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1550	16.6	0.6	25	1	AX042831
1551	16.6	0.6	25	1	AR028113
1552	16.6	0.6	25	1	AR030289
c1553	16.6	0.6	25	1	AR065818
1554	16.6	0.6	25	1	AR146859
1555	16.6	0.6	25	1	E55072
1556	16.6	0.6	25	1	I42108
1557	16.6	0.6	25	1	AR435047
1558	16.6	0.6	25	1	AR435048
1559	16.6	0.6	25	1	AR435049
1560	16.6	0.6	25	1	AX000308
1561	16.6	0.6	25	1	AX000331
1562	16.6	0.6	25	1	AX042593
1563	16.6	0.6	25	1	AX042904
c1564	16.6	0.6	25	1	AX042952
c1565	16.6	0.6	25	1	AX042955
1566	16.6	0.6	25	1	AX042962

ACCESSION:AX118414
ACCESSION:BD169479
ACCESSION:AR055108
ACCESSION:AR055109
ACCESSION:AR068449
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ACCESSION:AR162868
ACCESSION:AR194018
ACCESSION:AR093063
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ACCESSION:AR163839
ACCESSION:E12411
ACCESSION:AR359565
ACCESSION:AR360401
ACCESSION:AR360428
ACCESSION:AR371269
ACCESSION:AX067205
ACCESSION:AX441512
ACCESSION:BD196314
ACCESSION:AR066407
ACCESSION:D50257
ACCESSION:BD245233
ACCESSION:BD245237
ACCESSION:AX053001
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ACCESSION:AX115478
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ACCESSION:AX803836
ACCESSION:AX692828
ACCESSION:I45922
ACCESSION:AR435374
ACCESSION:AX042527
ACCESSION:AX042543
ACCESSION:AX042569
ACCESSION:AX042831
ACCESSION:AX042902
ACCESSION:AX042933
ACCESSION:AX043112
ACCESSION:AX043114
ACCESSION:AX043119
ACCESSION:AX043218
ACCESSION:AX043284
ACCESSION:AX043295
ACCESSION:AX043297
ACCESSION:AX043310
ACCESSION:AX043311
ACCESSION:AX043318
ACCESSION:AX043413
ACCESSION:AX744661
ACCESSION:AX744667
ACCESSION:I16929
ACCESSION:AX093547
ACCESSION:BD143588
ACCESSION:AX043064
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ACCESSION:AR065818
ACCESSION:AR146859
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ACCESSION:AX000308
ACCESSION:AX000331
ACCESSION:AX042593
ACCESSION:AX042904
ACCESSION:AX042952
ACCESSION:AX042955
ACCESSION:AX042962

c1275	17.4	0.6	20	1	AX136903	ACCESSION:AX136903
c1276	17.4	0.6	20	1	E59328	ACCESSION:E59328
c1277	17.4	0.6	21	1	AR241831	ACCESSION:AR241831
1278	17.4	0.6	21	1	AX838821	ACCESSION:AX838821
1279	17.4	0.6	23	1	E12392	ACCESSION:E12392
c1280	17.4	0.6	23	1	E12392	ACCESSION:E12392
1281	17.4	0.6	23	1	I79498	ACCESSION:I79498
c1282	17.4	0.6	23	1	I79498	ACCESSION:I79498
c1283	17.4	0.6	24	1	AR431312	ACCESSION:AR431312
c1284	17.4	0.6	24	1	AR431308	ACCESSION:AR431308
c1285	17.4	0.6	25	1	AX043130	ACCESSION:AX043130
c1286	17.4	0.6	25	1	AX115988	ACCESSION:AX115988
1287	17.4	0.6	25	1	AX042590	ACCESSION:AX042590
c1288	17.4	0.6	25	1	AX043064	ACCESSION:AX043064
1289	17.4	0.6	25	1	AX043581	ACCESSION:AX043581
1290	17.4	0.6	25	1	AX117576	ACCESSION:AX117576
c1291	17.4	0.6	25	1	AX117576	ACCESSION:AX117576
1292	17.4	0.6	25	1	AX692821	ACCESSION:AX692821
c1293	17.4	0.6	25	1	AX692821	ACCESSION:AX692821
1294	17.4	0.6	25	1	AX692822	ACCESSION:AX692822
c1295	17.4	0.6	25	1	AX692822	ACCESSION:AX692822
c1296	17.4	0.6	25	1	BD006733	ACCESSION:BD006733
1297	17.4	0.6	28	1	AR055117	ACCESSION:AR055117
1298	17.4	0.6	28	1	AR068458	ACCESSION:AR068458
c1299	17.4	0.6	30	1	AR264925	ACCESSION:AR264925
c1300	17.4	0.6	30	1	BD072870	ACCESSION:BD072870
c1301	17.4	0.6	30	1	BD107497	ACCESSION:BD107497
c1302	17.4	0.6	30	1	BD145029	ACCESSION:BD145029
c1303	17.4	0.6	30	1	BD166029	ACCESSION:BD166029
c1304	17.4	0.6	30	1	AR264926	ACCESSION:AR264926
c1305	17.4	0.6	30	1	AR264927	ACCESSION:AR264927
c1306	17.4	0.6	30	1	BD072871	ACCESSION:BD072871
c1307	17.4	0.6	30	1	BD072872	ACCESSION:BD072872
c1308	17.4	0.6	30	1	BD107498	ACCESSION:BD107498
c1309	17.4	0.6	30	1	BD107499	ACCESSION:BD107499
c1310	17.4	0.6	30	1	BD145030	ACCESSION:BD145030
c1311	17.4	0.6	30	1	BD145031	ACCESSION:BD145031
c1312	17.4	0.6	30	1	BD166030	ACCESSION:BD166030
c1313	17.4	0.6	30	1	BD166031	ACCESSION:BD166031
c1314	17.4	0.6	30	1	AR264920	ACCESSION:AR264920
c1315	17.4	0.6	30	1	BD072865	ACCESSION:BD072865
c1316	17.4	0.6	30	1	BD107492	ACCESSION:BD107492
c1317	17.4	0.6	30	1	BD145024	ACCESSION:BD145024
c1318	17.4	0.6	30	1	BD166025	ACCESSION:BD166025
c1319	17.4	0.6	30	1	AR264921	ACCESSION:AR264921
c1320	17.4	0.6	30	1	AR264922	ACCESSION:AR264922
c1321	17.4	0.6	30	1	AR264923	ACCESSION:AR264923
c1322	17.4	0.6	30	1	AR264924	ACCESSION:AR264924
c1323	17.4	0.6	30	1	AR264928	ACCESSION:AR264928
c1324	17.4	0.6	30	1	AR264929	ACCESSION:AR264929
c1325	17.4	0.6	30	1	BD072866	ACCESSION:BD072866
c1326	17.4	0.6	30	1	BD072867	ACCESSION:BD072867
c1327	17.4	0.6	30	1	BD072868	ACCESSION:BD072868
c1328	17.4	0.6	30	1	BD072869	ACCESSION:BD072869
c1329	17.4	0.6	30	1	BD072873	ACCESSION:BD072873
c1330	17.4	0.6	30	1	BD072874	ACCESSION:BD072874
c1331	17.4	0.6	30	1	BD107493	ACCESSION:BD107493
c1332	17.4	0.6	30	1	BD107494	ACCESSION:BD107494
c1333	17.4	0.6	30	1	BD107495	ACCESSION:BD107495
c1334	17.4	0.6	30	1	BD107496	ACCESSION:BD107496
c1335	17.4	0.6	30	1	BD107500	ACCESSION:BD107500
c1336	17.4	0.6	30	1	BD107501	ACCESSION:BD107501
c1337	17.4	0.6	30	1	BD145025	ACCESSION:BD145025
c1338	17.4	0.6	30	1	BD145026	ACCESSION:BD145026
c1339	17.4	0.6	30	1	BD145027	ACCESSION:BD145027
c1340	17.4	0.6	30	1	BD145028	ACCESSION:BD145028
c1341	17.4	0.6	30	1	BD145032	ACCESSION:BD145032
c1342	17.4	0.6	30	1	BD145033	ACCESSION:BD145033
c1343	17.4	0.6	30	1	BD166026	ACCESSION:BD166026
c1344	17.4	0.6	30	1	BD166027	ACCESSION:BD166027
c1345	17.4	0.6	30	1	BD166028	ACCESSION:BD166028
c1346	17.4	0.6	30	1	BD166032	ACCESSION:BD166032
c1347	17.4	0.6	30	1	BD166033	ACCESSION:BD166033
c1348	17.4	0.6	30	1	BD166129	ACCESSION:BD166129
1349	17.2	0.6	19	1	AR163080	ACCESSION:AR163080
c1350	17.2	0.6	19	1	AR163080	ACCESSION:AR163080
1351	17.2	0.6	19	1	E08331	ACCESSION:E08331
c1352	17.2	0.6	19	1	E08331	ACCESSION:E08331
1353	17.2	0.6	20	1	E08332	ACCESSION:E08332
c1354	17.2	0.6	20	1	E08332	ACCESSION:E08332
1355	17.2	0.6	21	1	E08333	ACCESSION:E08333
c1356	17.2	0.6	21	1	E08333	ACCESSION:E08333
c1357	17.2	0.6	23	1	AX457061	ACCESSION:AX457061
c1358	17.2	0.6	23	1	BD245234	ACCESSION:BD245234
c1359	17.2	0.6	23	1	BD245238	ACCESSION:BD245238
c1360	17.2	0.6	23	1	BD245242	ACCESSION:BD245242
1361	17.2	0.6	23	1	I79499	ACCESSION:I79499
c1362	17.2	0.6	23	1	AX053000	ACCESSION:AX053000
c1363	17.2	0.6	23	1	AX119432	ACCESSION:AX119432
c1364	17.2	0.6	23	1	AX921569	ACCESSION:AX921569
1365	17.2	0.6	23	1	BD187389	ACCESSION:BD187389
1366	17.2	0.6	25	1	BD244864	ACCESSION:BD244864
c1367	17.2	0.6	25	1	AX042923	ACCESSION:AX042923
c1368	17.2	0.6	25	1	AX042823	ACCESSION:AX042823
c1369	17.2	0.6	25	1	AX042978	ACCESSION:AX042978
1370	17.2	0.6	25	1	AX042992	ACCESSION:AX042992
1371	17.2	0.6	25	1	AX043038	ACCESSION:AX043038
1372	17.2	0.6	25	1	AX043067	ACCESSION:AX043067
c1373	17.2	0.6	26	1	AX055876	ACCESSION:AX055876
1374	17.2	0.6	26	1	BD082357	ACCESSION:BD082357
c1375	17.2	0.6	28	1	AR022650	ACCESSION:AR022650
c1376	17.2	0.6	28	1	AR150988	ACCESSION:AR150988
c1377	17.2	0.6	28	1	AR156058	ACCESSION:AR156058
c1378	17.2	0.6	28	1	AR172065	ACCESSION:AR172065
c1379	17.2	0.6	28	1	AR173356	ACCESSION:AR173356
c1380	17.2	0.6	28	1	I87998	ACCESSION:I87998
c1381	17.2	0.6	28	1	AR340907	ACCESSION:AR340907
c1382	17.2	0.6	28	1	AX029525	ACCESSION:AX029525
c1383	17.2	0.6	35	1	I35032	ACCESSION:I35032
1384	17	0.6	17	1	A28997	ACCESSION:A28997
c1385	17	0.6	17	1	A28997	ACCESSION:A28997
1386	17	0.6	17	1	AR104585	ACCESSION:AR104585
c1387	17	0.6	17	1	AR104585	ACCESSION:AR104585
1388	17	0.6	17	1	AR141074	ACCESSION:AR141074
c1389	17	0.6	17	1	AR141074	ACCESSION:AR141074
1390	17	0.6	17	1	AR175846	ACCESSION:AR175846
c1391	17	0.6	17	1	AR175846	ACCESSION:AR175846
1392	17	0.6	17	1	AR187062	ACCESSION:AR187062
c1393	17	0.6	17	1	AR187063	ACCESSION:AR187063
1394	17	0.6	17	1	AR222463	ACCESSION:AR222463
c1395	17	0.6	17	1	AR222463	ACCESSION:AR222463
1396	17	0.6	17	1	AR236087	ACCESSION:AR236087
c1397	17	0.6	17	1	AR236087	ACCESSION:AR236087
1398	17	0.6	17	1	AR323672	ACCESSION:AR323672
c1399	17	0.6	17	1	AR323673	ACCESSION:AR323673
1400	17	0.6	17	1	AX146682	ACCESSION:AX146682
c1401	17	0.6	17	1	AX361606	ACCESSION:AX361606
1402	17	0.6	17	1	AX692525	ACCESSION:AX692525
1403	17	0.6	17	1	AX762112	ACCESSION:AX762112
c1404	17	0.6	17	1	AX814938	ACCESSION:AX814938
c1405	17	0.6	18	1	AX028843	ACCESSION:AX028843
1406	17	0.6	18	1	AX028844	ACCESSION:AX028844
c1407	17	0.6	18	1	BD190553	ACCESSION:BD190553
1408	17	0.6	18	1	E32456	ACCESSION:E32456
c1409	17	0.6	18	1	E32458	ACCESSION:E32458
1410	17	0.6	18	1	AX028845	ACCESSION:AX028845
c1411	17	0.6	18	1	AX028845	ACCESSION:AX028845
c1412	17	0.6	18	1	AX361600	ACCESSION:AX361600
c1413	17	0.6	18	1	AX814932	ACCESSION:AX814932
c1414	17	0.6	20	1	AR030917	ACCESSION:AR030917
c1415	17	0.6	20	1	I28309	ACCESSION:I28309
c1416	17	0.6	20	1	I47310	ACCESSION:I47310
1417	17	0.6	20	1	BD161924	ACCESSION:BD161924
c1418	17	0.6	20	1	BD161924	ACCESSION:BD161924
c1419	17	0.6	23	1	BD244863	ACCESSION:BD244863
c1420	17	0.6	23	1	BD244865	ACCESSION:BD244865

1129	18	0.6	21	1	AX825130	ACCESSION:AX825130
c1130	18	0.6	21	1	AX825132	ACCESSION:AX825132
1131	18	0.6	21	1	AX825123	ACCESSION:AX825123
c1132	18	0.6	21	1	AX825123	ACCESSION:AX825123
1133	18	0.6	21	1	AX825124	ACCESSION:AX825124
c1134	18	0.6	21	1	AX825124	ACCESSION:AX825124
1135	18	0.6	21	1	AX825125	ACCESSION:AX825125
c1136	18	0.6	21	1	AX825125	ACCESSION:AX825125
1137	18	0.6	21	1	AX825126	ACCESSION:AX825126
c1138	18	0.6	21	1	AX825126	ACCESSION:AX825126
1139	18	0.6	22	1	AR164318	ACCESSION:AR164318
c1140	18	0.6	22	1	AR164318	ACCESSION:AR164318
1141	18	0.6	22	1	AR164319	ACCESSION:AR164319
c1142	18	0.6	22	1	AR164319	ACCESSION:AR164319
1143	18	0.6	22	1	I31810	ACCESSION:I31810
c1144	18	0.6	22	1	I31810	ACCESSION:I31810
1145	18	0.6	22	1	I31811	ACCESSION:I31811
c1146	18	0.6	22	1	I31811	ACCESSION:I31811
1147	18	0.6	22	1	I69407	ACCESSION:I69407
c1148	18	0.6	22	1	I69407	ACCESSION:I69407
1149	18	0.6	22	1	I69408	ACCESSION:I69408
c1150	18	0.6	22	1	I69408	ACCESSION:I69408
1151	18	0.6	23	1	BD245230	ACCESSION:BD245230
1152	18	0.6	23	1	E12391	ACCESSION:E12391
1153	18	0.6	23	1	AX394607	ACCESSION:AX394607
c1154	18	0.6	23	1	AX394607	ACCESSION:AX394607
c1155	18	0.6	24	1	AR168453	ACCESSION:AR168453
1156	18	0.6	24	1	AX394609	ACCESSION:AX394609
c1157	18	0.6	24	1	AX394609	ACCESSION:AX394609
1158	18	0.6	24	1	BD097127	ACCESSION:BD097127
c1159	18	0.6	24	1	BD097127	ACCESSION:BD097127
1160	18	0.6	24	1	BD161931	ACCESSION:BD161931
c1161	18	0.6	24	1	BD161931	ACCESSION:BD161931
1162	18	0.6	25	1	AX394611	ACCESSION:AX394611
c1163	18	0.6	25	1	AX394611	ACCESSION:AX394611
c1164	18	0.6	26	1	AR144828	ACCESSION:AR144828
c1165	18	0.6	26	1	AR410280	ACCESSION:AR410280
c1166	18	0.6	26	1	AX191907	ACCESSION:AX191907
c1167	18	0.6	26	1	BD064385	ACCESSION:BD064385
c1168	18	0.6	26	1	AR013918	ACCESSION:AR013918
c1169	18	0.6	26	1	AR136778	ACCESSION:AR136778
1170	18	0.6	26	1	AR050239	ACCESSION:AR050239
1171	18	0.6	26	1	AR090583	ACCESSION:AR090583
c1172	18	0.6	26	1	AR106358	ACCESSION:AR106358
1173	18	0.6	26	1	AR164510	ACCESSION:AR164510
1174	18	0.6	26	1	AR197618	ACCESSION:AR197618
1175	18	0.6	26	1	AR259772	ACCESSION:AR259772
1176	18	0.6	26	1	AX394613	ACCESSION:AX394613
c1177	18	0.6	26	1	AX394613	ACCESSION:AX394613
1178	18	0.6	26	1	AX827015	ACCESSION:AX827015
c1179	18	0.6	26	1	AX827015	ACCESSION:AX827015
1180	18	0.6	26	1	AX839907	ACCESSION:AX839907
c1181	18	0.6	26	1	AX839907	ACCESSION:AX839907
c1182	18	0.6	27	1	AR142409	ACCESSION:AR142409
c1183	18	0.6	27	1	AR182555	ACCESSION:AR182555
c1184	18	0.6	27	1	AR027002	ACCESSION:AR027002
1185	18	0.6	27	1	AX394614	ACCESSION:AX394614
c1186	18	0.6	27	1	AX394614	ACCESSION:AX394614
c1187	18	0.6	28	1	AR055110	ACCESSION:AR055110
c1188	18	0.6	28	1	AR068451	ACCESSION:AR068451
c1189	18	0.6	28	1	AR371171	ACCESSION:AR371171
c1190	18	0.6	28	1	BD015304	ACCESSION:BD015304
1191	18	0.6	28	1	AX394616	ACCESSION:AX394616
1192	18	0.6	28	1	AX394617	ACCESSION:AX394617
1193	18	0.6	29	1	AX394619	ACCESSION:AX394619
1194	18	0.6	30	1	AX394621	ACCESSION:AX394621
c1195	18	0.6	30	1	AR242448	ACCESSION:AR242448
c1196	18	0.6	30	1	AR280216	ACCESSION:AR280216
c1197	18	0.6	30	1	AR322431	ACCESSION:AR322431
1198	18	0.6	31	1	AX394623	ACCESSION:AX394623
c1199	18	0.6	32	1	AR051291	ACCESSION:AR051291
c1200	18	0.6	32	1	I16939	ACCESSION:I16939
c1201	18	0.6	32	1	I45733	ACCESSION:I45733
1202	18	0.6	32	1	AX394625	ACCESSION:AX394625
c1203	18	0.6	32	1	AR014684	ACCESSION:AR014684
c1204	18	0.6	32	1	AR341692	ACCESSION:AR341692
c1205	18	0.6	32	1	AR366811	ACCESSION:AR366811
c1206	18	0.6	32	1	AR432384	ACCESSION:AR432384
c1207	18	0.6	32	1	AR409897	ACCESSION:AR409897
1208	17.8	0.6	19	1	A79657	ACCESSION:A79657
c1209	17.8	0.6	19	1	A79657	ACCESSION:A79657
1210	17.8	0.6	19	1	AR147331	ACCESSION:AR147331
c1211	17.8	0.6	19	1	AR147331	ACCESSION:AR147331
1212	17.8	0.6	22	1	AX103869	ACCESSION:AX103869
1213	17.8	0.6	22	1	AX457060	ACCESSION:AX457060
1214	17.8	0.6	22	1	AX546922	ACCESSION:AX546922
1215	17.8	0.6	23	1	AX457061	ACCESSION:AX457061
1216	17.8	0.6	24	1	AR431313	ACCESSION:AR431313
1217	17.8	0.6	24	1	AX103868	ACCESSION:AX103868
1218	17.8	0.6	24	1	AX546921	ACCESSION:AX546921
c1219	17.8	0.6	25	1	E36888	ACCESSION:E36888
1220	17.8	0.6	25	1	AR207710	ACCESSION:AR207710
c1221	17.8	0.6	25	1	AR243409	ACCESSION:AR243409
1222	17.8	0.6	25	1	AR265036	ACCESSION:AR265036
c1223	17.8	0.6	25	1	AR390565	ACCESSION:AR390565
c1224	17.8	0.6	25	1	AR393179	ACCESSION:AR393179
1225	17.8	0.6	25	1	AR435375	ACCESSION:AR435375
1226	17.8	0.6	25	1	AR435376	ACCESSION:AR435376
1227	17.8	0.6	25	1	AR435377	ACCESSION:AR435377
1228	17.8	0.6	25	1	AR435378	ACCESSION:AR435378
1229	17.8	0.6	25	1	AR435379	ACCESSION:AR435379
c1230	17.8	0.6	25	1	AX042571	ACCESSION:AX042571
1231	17.8	0.6	25	1	AX042981	ACCESSION:AX042981
1232	17.8	0.6	25	1	AX115872	ACCESSION:AX115872
1233	17.8	0.6	25	1	AX692823	ACCESSION:AX692823
c1234	17.8	0.6	25	1	AX692823	ACCESSION:AX692823
1235	17.8	0.6	25	1	AX692824	ACCESSION:AX692824
c1236	17.8	0.6	25	1	AX692824	ACCESSION:AX692824
1237	17.8	0.6	25	1	AX692825	ACCESSION:AX692825
c1238	17.8	0.6	25	1	AX692825	ACCESSION:AX692825
1239	17.8	0.6	25	1	AX692826	ACCESSION:AX692826
c1240	17.8	0.6	25	1	AX692826	ACCESSION:AX692826
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	661	19	0.7	19	1	AR124854
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	663	19	0.7	19	1	AR124856
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c	670	19	0.7	19	1	AR135291
	671	19	0.7	19	1	AR135292
c	672	19	0.7	19	1	AR135292
	673	19	0.7	19	1	AR135293
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	679	19	0.7	19	1	AR135296
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	681	19	0.7	19	1	AR135297
c	682	19	0.7	19	1	AR135297
	683	19	0.7	19	1	AR135298
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	685	19	0.7	19	1	AR135302
c	686	19	0.7	19	1	AR135302
	687	19	0.7	19	1	AR135304
c	688	19	0.7	19	1	AR135304
	689	19	0.7	19	1	AR135305
c	690	19	0.7	19	1	AR135305

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c 254	20.8	0.7	32	1	AX465307	ACCESSION:AX465307
c 255	20.8	0.7	32	1	AX556120	ACCESSION:AX556120
c 256	20.6	0.7	29	1	HSA241944	ACCESSION:AJ241944
257	20.6	0.7	31	1	A08914	ACCESSION:A08914
258	20.6	0.7	33	1	AR365237	ACCESSION:AR365237
259	20.6	0.7	36	1	AX495372	ACCESSION:AX495372
260	20.4	0.7	24	1	AR261539	ACCESSION:AR261539
261	20.4	0.7	24	1	AR431312	ACCESSION:AR431312
262	20.4	0.7	30	1	A79651	ACCESSION:A79651
263	20.4	0.7	30	1	AR264920	ACCESSION:AR264920
c 264	20.4	0.7	30	1	AX394621	ACCESSION:AX394621
265	20.4	0.7	30	1	BD072865	ACCESSION:BD072865
266	20.4	0.7	30	1	BD107492	ACCESSION:BD107492
267	20.4	0.7	30	1	BD145024	ACCESSION:BD145024
268	20.4	0.7	30	1	BD166025	ACCESSION:BD166025
269	20.2	0.7	22	1	AX583623	ACCESSION:AX583623
c 270	20.2	0.7	25	1	I29929	ACCESSION:I29929
c 271	20.2	0.7	25	1	AX338548	ACCESSION:AX338548
c 272	20.2	0.7	26	1	AR174582	ACCESSION:AR174582
c 273	20.2	0.7	26	1	BD248975	ACCESSION:BD248975
c 274	20.2	0.7	26	1	I79495	ACCESSION:I79495
c 275	20.2	0.7	26	1	AR279358	ACCESSION:AR279358
c 276	20.2	0.7	26	1	AR374074	ACCESSION:AR374074
c 277	20.2	0.7	26	1	AR404597	ACCESSION:AR404597
c 278	20.2	0.7	26	1	BD007174	ACCESSION:BD007174
279	20.2	0.7	26	1	AR144828	ACCESSION:AR144828
280	20.2	0.7	26	1	E33560	ACCESSION:E33560
281	20.2	0.7	26	1	AR410280	ACCESSION:AR410280
282	20.2	0.7	26	1	AX191907	ACCESSION:AX191907
283	20.2	0.7	26	1	BD064385	ACCESSION:BD064385
284	20.2	0.7	28	1	I06459	ACCESSION:I06459
285	20.2	0.7	28	1	AX184127	ACCESSION:AX184127
c 286	20.2	0.7	28	1	BD183015	ACCESSION:BD183015
287	20.2	0.7	30	1	AR016852	ACCESSION:AR016852
288	20.2	0.7	30	1	AR020878	ACCESSION:AR020878
289	20.2	0.7	30	1	AR027201	ACCESSION:AR027201
290	20.2	0.7	30	1	AR038488	ACCESSION:AR038488
291	20.2	0.7	30	1	AR064630	ACCESSION:AR064630
292	20.2	0.7	30	1	AR067555	ACCESSION:AR067555
293	20.2	0.7	30	1	I38507	ACCESSION:I38507
294	20.2	0.7	30	1	I56982	ACCESSION:I56982
295	20.2	0.7	30	1	I59848	ACCESSION:I59848
296	20.2	0.7	30	1	I75175	ACCESSION:I75175
297	20.2	0.7	30	1	AR242448	ACCESSION:AR242448
298	20.2	0.7	30	1	AR280216	ACCESSION:AR280216
299	20.2	0.7	30	1	AR322431	ACCESSION:AR322431
300	20.2	0.7	30	1	AR409723	ACCESSION:AR409723
301	20.2	0.7	32	1	AR222454	ACCESSION:AR222454
c 302	20.2	0.7	33	1	BD238394	ACCESSION:BD238394
c 303	20.2	0.7	33	1	AR279820	ACCESSION:AR279820
304	20	0.7	20	1	AR064875	ACCESSION:AR064875
c 305	20	0.7	20	1	AR080000	ACCESSION:AR080000
c 306	20	0.7	20	1	AR085926	ACCESSION:AR085926
307	20	0.7	20	1	AR087520	ACCESSION:AR087520
c 308	20	0.7	20	1	AR093312	ACCESSION:AR093312
309	20	0.7	20	1	AR118970	ACCESSION:AR118970
c 310	20	0.7	20	1	AR121692	ACCESSION:AR121692
c 311	20	0.7	20	1	AR123335	ACCESSION:AR123335
312	20	0.7	20	1	AR141070	ACCESSION:AR141070
313	20	0.7	20	1	AR154115	ACCESSION:AR154115
c 314	20	0.7	20	1	AR164658	ACCESSION:AR164658
315	20	0.7	20	1	E12676	ACCESSION:E12676
316	20	0.7	20	1	I36180	ACCESSION:I36180
c 317	20	0.7	20	1	AR213738	ACCESSION:AR213738
c 318	20	0.7	20	1	AR222466	ACCESSION:AR222466
319	20	0.7	20	1	AR236083	ACCESSION:AR236083
c 320	20	0.7	20	1	AR274394	ACCESSION:AR274394
321	20	0.7	20	1	AR343047	ACCESSION:AR343047
c 322	20	0.7	20	1	AR344936	ACCESSION:AR344936
c 323	20	0.7	20	1	AR365970	ACCESSION:AR365970
c 324	20	0.7	20	1	AR382312	ACCESSION:AR382312
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326	20	0.7	20	1	AX004876	ACCESSION:AX004876
327	20	0.7	20	1	AX045779	ACCESSION:AX045779
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330	20	0.7	20	1	AX104034	ACCESSION:AX104034
331	20	0.7	20	1	AX104364	ACCESSION:AX104364
c 332	20	0.7	20	1	AX104368	ACCESSION:AX104368
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c 338	20	0.7	20	1	AX440125	ACCESSION:AX440125
c 339	20	0.7	20	1	AX440140	ACCESSION:AX440140
c 340	20	0.7	20	1	AX465311	ACCESSION:AX465311
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c 345	20	0.7	20	1	AX556124	ACCESSION:AX556124
c 346	20	0.7	20	1	AX556139	ACCESSION:AX556139
c 347	20	0.7	20	1	AX664307	ACCESSION:AX664307
348	20	0.7	20	1	AX664308	ACCESSION:AX664308
349	20	0.7	20	1	AX741040	ACCESSION:AX741040
c 350	20	0.7	20	1	AX741052	ACCESSION:AX741052
c 351	20	0.7	20	1	BD008523	ACCESSION:BD008523
352	20	0.7	20	1	BD080522	ACCESSION:BD080522
353	20	0.7	20	1	BD107450	ACCESSION:BD107450
c 354	20	0.7	20	1	BD218101	ACCESSION:BD218101
c 355	20	0.7	21	1	AR153849	ACCESSION:AR153849
c 356	20	0.7	21	1	I36166	ACCESSION:I36166
357	20	0.7	21	1	AX825103	ACCESSION:AX825103
358	20	0.7	21	1	AX825104	ACCESSION:AX825104
359	20	0.7	21	1	AX825106	ACCESSION:AX825106
c 360	20	0.7	21	1	AX825136	ACCESSION:AX825136
c 361	20	0.7	21	1	AX825137	ACCESSION:AX825137
c 362	20	0.7	21	1	AX825138	ACCESSION:AX825138
363	20	0.7	21	1	AX825152	ACCESSION:AX825152
364	20	0.7	21	1	AX825153	ACCESSION:AX825153
365	20	0.7	21	1	AX825154	ACCESSION:AX825154
c 366	20	0.7	21	1	AX825160	ACCESSION:AX825160
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c 368	20	0.7	21	1	AX825162	ACCESSION:AX825162
369	20	0.7	21	1	AX825164	ACCESSION:AX825164
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c 371	20	0.7	21	1	AX825165	ACCESSION:AX825165
c 372	20	0.7	21	1	BD087491	ACCESSION:BD087491
c 373	20	0.7	24	1	AR241846	ACCESSION:AR241846
c 374	20	0.7	24	1	E13209	ACCESSION:E13209
c 375	20	0.7	25	1	AX708814	ACCESSION:AX708814
376	20	0.7	27	1	AR142409	ACCESSION:AR142409
377	20	0.7	27	1	AR182555	ACCESSION:AR182555
c 378	20	0.7	29	1	BD274321	ACCESSION:BD274321
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381	20	0.7	30	1	AR264922	ACCESSION:AR264922
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	411	19.8	0.7	25	1	AX338548	ACCESSION:AX338548
c	412	19.8	0.7	25	1	BD244864	ACCESSION:BD244864
	413	19.8	0.7	25	1	AX043282	ACCESSION:AX043282
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c	419	19.6	0.7	26	1	BD248974	ACCESSION:BD248974
c	420	19.6	0.7	26	1	I79494	ACCESSION:I79494
c	421	19.6	0.7	26	1	AR263648	ACCESSION:AR263648
c	422	19.6	0.7	26	1	AR374073	ACCESSION:AR374073
c	423	19.6	0.7	26	1	AX106717	ACCESSION:AX106717
c	424	19.6	0.7	26	1	AR137712	ACCESSION:AR137712
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	438	19.6	0.7	29	1	AR166605	ACCESSION:AR166605
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c	442	19.6	0.7	29	1	AX048408	ACCESSION:AX048408
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	444	19.6	0.7	29	1	AX052994	ACCESSION:AX052994
	445	19.6	0.7	29	1	AX353685	ACCESSION:AX353685
	446	19.6	0.7	29	1	AX662302	ACCESSION:AX662302
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	448	19.6	0.7	30	1	A43784	ACCESSION:A43784
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	450	19.6	0.7	30	1	A62995	ACCESSION:A62995
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	458	19.6	0.7	30	1	AX474674	ACCESSION:AX474674
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	460	19.6	0.7	30	1	BD105776	ACCESSION:BD105776
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	465	19.6	0.7	30	1	AR127791	ACCESSION:AR127791
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c	469	19.6	0.7	30	1	AR027201	ACCESSION:AR027201
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c	475	19.6	0.7	30	1	I59848	ACCESSION:I59848
c	476	19.6	0.7	30	1	I75175	ACCESSION:I75175
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	478	19.6	0.7	30	1	AR028195	ACCESSION:AR028195
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c	483	19.6	0.7	33	1	AR099615	ACCESSION:AR099615
c	484	19.6	0.7	33	1	AR120128	ACCESSION:AR120128
c	485	19.6	0.7	34	1	A63578	ACCESSION:A63578
	486	19.6	0.7	37	1	I29931	ACCESSION:I29931
c	487	19.6	0.7	37	1	AX106972	ACCESSION:AX106972
c	488	19.6	0.7	38	1	E50766	ACCESSION:E50766
	489	19.6	0.7	40	1	A48799	ACCESSION:A48799
	490	19.6	0.7	40	1	AR232955	ACCESSION:AR232955
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c	492	19.6	0.7	43	1	AX225198	ACCESSION:AX225198
	493	19.4	0.7	21	1	AX825135	ACCESSION:AX825135
c	494	19.4	0.7	21	1	AX825151	ACCESSION:AX825151
	495	19.4	0.7	21	1	AX825159	ACCESSION:AX825159
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c	497	19.4	0.7	21	1	AX825103	ACCESSION:AX825103
c	498	19.4	0.7	21	1	AX825106	ACCESSION:AX825106
	499	19.4	0.7	21	1	AX825137	ACCESSION:AX825137
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	502	19.4	0.7	21	1	AX825109	ACCESSION:AX825109
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	504	19.4	0.7	21	1	AX825113	ACCESSION:AX825113
	505	19.4	0.7	21	1	AX825114	ACCESSION:AX825114
	506	19.4	0.7	21	1	AX825115	ACCESSION:AX825115
	507	19.4	0.7	21	1	AX825117	ACCESSION:AX825117
	508	19.4	0.7	21	1	AX825118	ACCESSION:AX825118
	509	19.4	0.7	21	1	AX825119	ACCESSION:AX825119
c	510	19.4	0.7	21	1	AX825119	ACCESSION:AX825119
	511	19.4	0.7	21	1	AX825121	ACCESSION:AX825121
c	512	19.4	0.7	21	1	AX825127	ACCESSION:AX825127
	513	19.4	0.7	21	1	AX825131	ACCESSION:AX825131
	514	19.4	0.7	21	1	AX825134	ACCESSION:AX825134
c	515	19.4	0.7	21	1	AX825139	ACCESSION:AX825139
c	516	19.4	0.7	21	1	AX825143	ACCESSION:AX825143
	517	19.4	0.7	21	1	AX825147	ACCESSION:AX825147
c	518	19.4	0.7	21	1	AX825147	ACCESSION:AX825147
	519	19.4	0.7	21	1	AX825150	ACCESSION:AX825150
	520	19.4	0.7	21	1	AX825155	ACCESSION:AX825155
c	521	19.4	0.7	21	1	AX825155	ACCESSION:AX825155
	522	19.4	0.7	21	1	AX825158	ACCESSION:AX825158
	523	19.4	0.7	24	1	AR431308	ACCESSION:AR431308
	524	19.4	0.7	24	1	AX708815	ACCESSION:AX708815
c	525	19.4	0.7	24	1	AX708815	ACCESSION:AX708815
c	526	19.4	0.7	25	1	BD056964	ACCESSION:BD056964
	527	19.4	0.7	25	1	AX708814	ACCESSION:AX708814
c	528	19.4	0.7	26	1	BD237566	ACCESSION:BD237566
c	529	19.4	0.7	26	1	AR257336	ACCESSION:AR257336
c	530	19.4	0.7	26	1	AR263647	ACCESSION:AR263647
c	531	19.4	0.7	26	1	AX814950	ACCESSION:AX814950
c	532	19.4	0.7	26	1	BD062456	ACCESSION:BD062456
	533	19.4	0.7	26	1	AR013918	ACCESSION:AR013918
c	534	19.4	0.7	27	1	AX513052	ACCESSION:AX513052
	535	19.4	0.7	28	1	AR022650	ACCESSION:AR022650
	536	19.4	0.7	28	1	AR055108	ACCESSION:AR055108
	537	19.4	0.7	28	1	AR055109	ACCESSION:AR055109
	538	19.4	0.7	28	1	AR055110	ACCESSION:AR055110
	539	19.4	0.7	28	1	AR068449	ACCESSION:AR068449
	540	19.4	0.7	28	1	AR068450	ACCESSION:AR068450
	541	19.4	0.7	28	1	AR068451	ACCESSION:AR068451
	542	19.4	0.7	28	1	AR150988	ACCESSION:AR150988
	543	19.4	0.7	28	1	AR156058	ACCESSION:AR156058
	544	19.4	0.7	28	1	AR172065	ACCESSION:AR172065

c	107	22	0.8	30	1	AX079108	ACCESSION:AX079108
	108	22	0.8	30	1	BD072870	ACCESSION:BD072870
	109	22	0.8	30	1	BD107497	ACCESSION:BD107497
	110	22	0.8	30	1	BD145029	ACCESSION:BD145029
	111	22	0.8	30	1	BD166029	ACCESSION:BD166029
c	112	22	0.8	32	1	AX838502	ACCESSION:AX838502
	113	21.8	0.8	27	1	AR214918	ACCESSION:AR214918
	114	21.8	0.8	27	1	AX009609	ACCESSION:AX009609
	115	21.8	0.8	28	1	BD234335	ACCESSION:BD234335
	116	21.8	0.8	32	1	BD234356	ACCESSION:BD234356
c	117	21.8	0.8	35	1	AX556148	ACCESSION:AX556148
	118	21.6	0.8	29	1	AR098648	ACCESSION:AR098648
	119	21.6	0.8	29	1	AR204722	ACCESSION:AR204722
c	120	21.6	0.8	30	1	AR051244	ACCESSION:AR051244
c	121	21.6	0.8	30	1	AR127791	ACCESSION:AR127791
c	122	21.6	0.8	30	1	I28373	ACCESSION:I28373
	123	21.6	0.8	30	1	AR264926	ACCESSION:AR264926
	124	21.6	0.8	30	1	AR264927	ACCESSION:AR264927
	125	21.6	0.8	30	1	BD072871	ACCESSION:BD072871
	126	21.6	0.8	30	1	BD072872	ACCESSION:BD072872
	127	21.6	0.8	30	1	BD107498	ACCESSION:BD107498
	128	21.6	0.8	30	1	BD107499	ACCESSION:BD107499
	129	21.6	0.8	30	1	BD145030	ACCESSION:BD145030
	130	21.6	0.8	30	1	BD145031	ACCESSION:BD145031
	131	21.6	0.8	30	1	BD166030	ACCESSION:BD166030
	132	21.6	0.8	30	1	BD166031	ACCESSION:BD166031
	133	21.4	0.8	25	1	AX116188	ACCESSION:AX116188
	134	21.4	0.8	27	1	AX711956	ACCESSION:AX711956
	135	21.4	0.8	27	1	BD097128	ACCESSION:BD097128
	136	21.4	0.8	27	1	BD161932	ACCESSION:BD161932
c	137	21.4	0.8	28	1	AX427136	ACCESSION:AX427136
c	138	21.4	0.8	29	1	AR268128	ACCESSION:AR268128
c	139	21.4	0.8	31	1	AX394623	ACCESSION:AX394623
c	140	21.4	0.8	32	1	AX394625	ACCESSION:AX394625
	141	21.2	0.8	24	1	AX391871	ACCESSION:AX391871
	142	21.2	0.8	26	1	AR137712	ACCESSION:AR137712
	143	21.2	0.8	26	1	BD237566	ACCESSION:BD237566
	144	21.2	0.8	26	1	I79496	ACCESSION:I79496
	145	21.2	0.8	26	1	AR257336	ACCESSION:AR257336
	146	21.2	0.8	26	1	AR263647	ACCESSION:AR263647
c	147	21.2	0.8	26	1	AX338547	ACCESSION:AX338547
	148	21.2	0.8	26	1	AX427154	ACCESSION:AX427154
	149	21.2	0.8	26	1	AX528804	ACCESSION:AX528804
	150	21.2	0.8	26	1	AX814950	ACCESSION:AX814950
	151	21.2	0.8	26	1	BD062456	ACCESSION:BD062456
	152	21.2	0.8	26	1	BD192375	ACCESSION:BD192375
	153	21.2	0.8	27	1	AX327980	ACCESSION:AX327980
	154	21.2	0.8	27	1	AX513052	ACCESSION:AX513052
c	155	21.2	0.8	27	1	S64862S3	ACCESSION:S64864
	156	21.2	0.8	32	1	I29892	ACCESSION:I29892
c	157	21.2	0.8	32	1	AR222454	ACCESSION:AR222454
	158	21	0.7	21	1	AR080294	ACCESSION:AR080294
c	159	21	0.7	21	1	AR084521	ACCESSION:AR084521
	160	21	0.7	21	1	AR084524	ACCESSION:AR084524
	161	21	0.7	21	1	AR093143	ACCESSION:AR093143
	162	21	0.7	21	1	AR095412	ACCESSION:AR095412
	163	21	0.7	21	1	I65744	ACCESSION:I65744
	164	21	0.7	21	1	AR322245	ACCESSION:AR322245
	165	21	0.7	21	1	AX104720	ACCESSION:AX104720
	166	21	0.7	21	1	AX355812	ACCESSION:AX355812
	167	21	0.7	21	1	AX547773	ACCESSION:AX547773
	168	21	0.7	21	1	AX825105	ACCESSION:AX825105
c	169	21	0.7	21	1	AX825135	ACCESSION:AX825135
	170	21	0.7	21	1	AX825151	ACCESSION:AX825151
c	171	21	0.7	21	1	AX825159	ACCESSION:AX825159
	172	21	0.7	21	1	AX825163	ACCESSION:AX825163
	173	21	0.7	21	1	AX825166	ACCESSION:AX825166
	174	21	0.7	21	1	BD080832	ACCESSION:BD080832
	175	21	0.7	21	1	BD224108	ACCESSION:BD224108
c	176	21	0.7	22	1	AR164336	ACCESSION:AR164336
c	177	21	0.7	22	1	I31828	ACCESSION:I31828
c	178	21	0.7	22	1	I69425	ACCESSION:I69425
	179	21	0.7	23	1	BD244857	ACCESSION:BD244857
c	180	21	0.7	24	1	AR010037	ACCESSION:AR010037
c	181	21	0.7	24	1	AR034772	ACCESSION:AR034772
c	182	21	0.7	24	1	AR068465	ACCESSION:AR068465
c	183	21	0.7	24	1	AR105984	ACCESSION:AR105984
c	184	21	0.7	24	1	AR107972	ACCESSION:AR107972
	185	21	0.7	24	1	BD234330	ACCESSION:BD234330
c	186	21	0.7	24	1	I24762	ACCESSION:I24762
c	187	21	0.7	24	1	AR184443	ACCESSION:AR184443
c	188	21	0.7	24	1	AR202876	ACCESSION:AR202876
c	189	21	0.7	24	1	AR213697	ACCESSION:AR213697
c	190	21	0.7	24	1	AR232949	ACCESSION:AR232949
	191	21	0.7	24	1	AR241846	ACCESSION:AR241846
c	192	21	0.7	24	1	AR340571	ACCESSION:AR340571
c	193	21	0.7	24	1	AR345020	ACCESSION:AR345020
	194	21	0.7	24	1	AX104241	ACCESSION:AX104241
	195	21	0.7	24	1	AX104769	ACCESSION:AX104769
c	196	21	0.7	24	1	AX104770	ACCESSION:AX104770
c	197	21	0.7	24	1	AX354553	ACCESSION:AX354553
	198	21	0.7	24	1	AX355813	ACCESSION:AX355813
	199	21	0.7	24	1	AX427163	ACCESSION:AX427163
c	200	21	0.7	24	1	AX428574	ACCESSION:AX428574
	201	21	0.7	24	1	AX547294	ACCESSION:AX547294
	202	21	0.7	24	1	AX547822	ACCESSION:AX547822
c	203	21	0.7	24	1	AX547823	ACCESSION:AX547823
	204	21	0.7	24	1	AX684290	ACCESSION:AX684290
	205	21	0.7	24	1	AX750585	ACCESSION:AX750585
c	206	21	0.7	24	1	AX817782	ACCESSION:AX817782
	207	21	0.7	24	1	AX829247	ACCESSION:AX829247
c	208	21	0.7	24	1	AX838369	ACCESSION:AX838369
c	209	21	0.7	24	1	BD136714	ACCESSION:BD136714
	210	21	0.7	25	1	AR105982	ACCESSION:AR105982
	211	21	0.7	25	1	BD234336	ACCESSION:BD234336
	212	21	0.7	25	1	I58009	ACCESSION:I58009
	213	21	0.7	25	1	I96072	ACCESSION:I96072
	214	21	0.7	25	1	AR288252	ACCESSION:AR288252
c	215	21	0.7	25	1	BD187513	ACCESSION:BD187513
	216	21	0.7	25	1	BD187514	ACCESSION:BD187514
	217	21	0.7	25	1	BD204988	ACCESSION:BD204988
	218	21	0.7	26	1	AR174582	ACCESSION:AR174582
	219	21	0.7	26	1	BD248975	ACCESSION:BD248975
	220	21	0.7	26	1	I79495	ACCESSION:I79495
	221	21	0.7	26	1	AR279358	ACCESSION:AR279358
	222	21	0.7	26	1	AR374074	ACCESSION:AR374074
	223	21	0.7	26	1	AR404597	ACCESSION:AR404597
	224	21	0.7	26	1	BD007174	ACCESSION:BD007174
	225	21	0.7	27	1	AX492939	ACCESSION:AX492939
	226	21	0.7	27	1	BD175131	ACCESSION:BD175131
c	227	21	0.7	30	1	A79651	ACCESSION:A79651
c	228	21	0.7	30	1	AX351705	ACCESSION:AX351705
c	229	21	0.7	30	1	AX351706	ACCESSION:AX351706
c	230	21	0.7	30	1	AX351707	ACCESSION:AX351707
c	231	21	0.7	30	1	AX351708	ACCESSION:AX351708
c	232	21	0.7	30	1	AX351715	ACCESSION:AX351715
	233	21	0.7	32	1	AX430213	ACCESSION:AX430213
	234	21	0.7	32	1	BD165916	ACCESSION:BD165916
	235	21	0.7	32	1	AR014684	ACCESSION:AR014684
	236	21	0.7	32	1	AR341692	ACCESSION:AR341692
	237	21	0.7	32	1	AR366811	ACCESSION:AR366811
	238	21	0.7	32	1	AR432384	ACCESSION:AR432384
c	239	21	0.7	45	1	AX287571	ACCESSION:AX287571
c	240	21	0.7	45	1	AX287575	ACCESSION:AX287575
c	241	20.8	0.7	24	1	AR431307	ACCESSION:AR431307
	242	20.8	0.7	24	1	BD196419	ACCESSION:BD196419
c	243	20.8	0.7	24	1	BD196419	ACCESSION:BD196419
c	244	20.8	0.7	27	1	AR241865	ACCESSION:AR241865
c	245	20.8	0.7	27	1	AR214918	ACCESSION:AR214918
c	246	20.8	0.7	27	1	AX009609	ACCESSION:AX009609
c	247	20.8	0.7	32	1	AR274390	ACCESSION:AR274390
c	248	20.8	0.7	32	1	AR344932	ACCESSION:AR344932
c	249	20.8	0.7	32	1	AR382308	ACCESSION:AR382308
	250	20.8	0.7	32	1	AR409897	ACCESSION:AR409897
c	251	20.8	0.7	32	1	AR429649	ACCESSION:AR429649
c	252	20.8	0.7	32	1	AX196220	ACCESSION:AX196220

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OM nucleic - nucleic search, using sw model

Run on: June 10, 2004, 12:08:03 ; Search time 98 Seconds
(without alignments)
3.710 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgccgatgcgt.....gaaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 3135 seqs, 64831 residues

Total number of hits satisfying chosen parameters: 6270

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 4611 summaries

Database : rge3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30	1.1	45	1	AX287571	ACCESSION:AX287571
	2	30	1.1	45	1	AX287575	ACCESSION:AX287575
	3	29.2	1.0	43	1	AX225198	ACCESSION:AX225198
c	4	28.4	1.0	40	1	A48799	ACCESSION:A48799
c	5	28.4	1.0	40	1	AR232955	ACCESSION:AR232955
c	6	28	1.0	37	1	I29931	ACCESSION:I29931
	7	28	1.0	37	1	AX106972	ACCESSION:AX106972
	8	27.4	1.0	38	1	E50766	ACCESSION:E50766
	9	27.2	1.0	33	1	BD011883	ACCESSION:BD011883
c	10	27.2	1.0	40	1	BD170449	ACCESSION:BD170449
	11	26.8	1.0	41	1	AR309630	ACCESSION:AR309630
	12	26.8	1.0	41	1	AX516913	ACCESSION:AX516913
	13	26.8	1.0	41	1	AX519424	ACCESSION:AX519424
	14	26	0.9	34	1	A63578	ACCESSION:A63578
	15	25.6	0.9	33	1	AR099615	ACCESSION:AR099615
	16	25.6	0.9	33	1	AR120128	ACCESSION:AR120128
c	17	25.2	0.9	30	1	A43784	ACCESSION:A43784
	18	25.2	0.9	30	1	A62991	ACCESSION:A62991
c	19	25.2	0.9	30	1	A62995	ACCESSION:A62995
	20	25.2	0.9	30	1	AR179066	ACCESSION:AR179066
c	21	25.2	0.9	30	1	AR179070	ACCESSION:AR179070
	22	25.2	0.9	30	1	E04638	ACCESSION:E04638
c	23	25.2	0.9	30	1	I84450	ACCESSION:I84450
	24	25.2	0.9	30	1	AX104902	ACCESSION:AX104902
c	25	25.2	0.9	30	1	AX104903	ACCESSION:AX104903
	26	25.2	0.9	30	1	AX474673	ACCESSION:AX474673
c	27	25.2	0.9	30	1	AX474674	ACCESSION:AX474674
	28	25.2	0.9	30	1	AX521609	ACCESSION:AX521609
c	29	25.2	0.9	30	1	BD105776	ACCESSION:BD105776
	30	25.2	0.9	30	1	BD132851	ACCESSION:BD132851
	31	25.2	0.9	30	1	BD181358	ACCESSION:BD181358
c	32	25.2	0.9	30	1	BD181359	ACCESSION:BD181359
	33	24.8	0.9	40	1	BD170449	ACCESSION:BD170449
	34	24.6	0.9	35	1	AR029830	ACCESSION:AR029830
c	35	24.6	0.9	36	1	AX495372	ACCESSION:AX495372
	36	24.4	0.9	29	1	BD274321	ACCESSION:BD274321
	37	24.4	0.9	29	1	BD274339	ACCESSION:BD274339
	38	24	0.9	30	1	AX079109	ACCESSION:AX079109
	39	24	0.9	33	1	BD171339	ACCESSION:BD171339
	40	24	0.9	33	1	BD173750	ACCESSION:BD173750
	41	24	0.9	34	1	AR174572	ACCESSION:AR174572
	42	24	0.9	34	1	BD248965	ACCESSION:BD248965
	43	24	0.9	34	1	AR374064	ACCESSION:AR374064
	44	24	0.9	34	1	AX179588	ACCESSION:AX179588
c	45	23.6	0.8	31	1	A08914	ACCESSION:A08914
c	46	23.6	0.8	32	1	AX430213	ACCESSION:AX430213
c	47	23.6	0.8	32	1	BD165916	ACCESSION:BD165916
c	48	23.4	0.8	30	1	AX196237	ACCESSION:AX196237
c	49	23.4	0.8	30	1	AX440138	ACCESSION:AX440138
c	50	23.4	0.8	30	1	AX465324	ACCESSION:AX465324
c	51	23.4	0.8	30	1	AX556137	ACCESSION:AX556137
	52	23.4	0.8	36	1	BD238393	ACCESSION:BD238393
	53	23.4	0.8	36	1	AR279819	ACCESSION:AR279819
c	54	23.2	0.8	29	1	AX430216	ACCESSION:AX430216
c	55	23.2	0.8	29	1	BD165919	ACCESSION:BD165919
c	56	23.2	0.8	36	1	BD238393	ACCESSION:BD238393
c	57	23.2	0.8	36	1	AR279819	ACCESSION:AR279819
c	58	23	0.8	24	1	AR261539	ACCESSION:AR261539
	59	23	0.8	25	1	AX454028	ACCESSION:AX454028
	60	23	0.8	28	1	BD234339	ACCESSION:BD234339
	61	23	0.8	29	1	HSA241944	ACCESSION:AJ241944
	62	23	0.8	32	1	AR051291	ACCESSION:AR051291
	63	23	0.8	32	1	I16939	ACCESSION:I16939
	64	23	0.8	32	1	I45733	ACCESSION:I45733
	65	23	0.8	32	1	AX080522	ACCESSION:AX080522
	66	23	0.8	35	1	A63566	ACCESSION:A63566
	67	22.8	0.8	27	1	AR241865	ACCESSION:AR241865
c	68	22.8	0.8	29	1	AX052989	ACCESSION:AX052989
	69	22.8	0.8	35	1	I35032	ACCESSION:I35032
	70	22.8	0.8	35	1	AX556148	ACCESSION:AX556148
c	71	22.6	0.8	29	1	AR162080	ACCESSION:AR162080
c	72	22.6	0.8	29	1	AR166605	ACCESSION:AR166605
c	73	22.6	0.8	29	1	BD238387	ACCESSION:BD238387
	74	22.6	0.8	29	1	I65795	ACCESSION:I65795
c	75	22.6	0.8	29	1	AR279813	ACCESSION:AR279813
c	76	22.6	0.8	29	1	AR288232	ACCESSION:AR288232
	77	22.6	0.8	29	1	AX048408	ACCESSION:AX048408
c	78	22.6	0.8	29	1	AX048409	ACCESSION:AX048409
c	79	22.6	0.8	29	1	AX052994	ACCESSION:AX052994
c	80	22.6	0.8	29	1	AX353685	ACCESSION:AX353685
c	81	22.6	0.8	29	1	AX662302	ACCESSION:AX662302
c	82	22.6	0.8	29	1	BD204968	ACCESSION:BD204968
c	83	22.6	0.8	30	1	AX351711	ACCESSION:AX351711
	84	22.4	0.8	25	1	BD056964	ACCESSION:BD056964
	85	22.4	0.8	30	1	I30206	ACCESSION:I30206
	86	22.4	0.8	33	1	BD238394	ACCESSION:BD238394
	87	22.4	0.8	33	1	AR279820	ACCESSION:AR279820
	88	22.4	0.8	34	1	AR098680	ACCESSION:AR098680
	89	22.4	0.8	34	1	AR204754	ACCESSION:AR204754
c	90	22.2	0.8	27	1	E04985	ACCESSION:E04985
	91	22.2	0.8	27	1	AX104719	ACCESSION:AX104719
	92	22.2	0.8	27	1	AX355814	ACCESSION:AX355814
	93	22.2	0.8	27	1	AX547772	ACCESSION:AX547772
	94	22.2	0.8	32	1	I32124	ACCESSION:I32124
c	95	22.2	0.8	33	1	AR365237	ACCESSION:AR365237
	96	22	0.8	24	1	AR431307	ACCESSION:AR431307
	97	22	0.8	24	1	AR431310	ACCESSION:AR431310
c	98	22	0.8	25	1	AX394507	ACCESSION:AX394507
	99	22	0.8	25	1	AX394514	ACCESSION:AX394514
	100	22	0.8	26	1	AR174581	ACCESSION:AR174581
	101	22	0.8	26	1	BD248974	ACCESSION:BD248974
	102	22	0.8	26	1	I79494	ACCESSION:I79494
	103	22	0.8	26	1	AR263648	ACCESSION:AR263648
	104	22	0.8	26	1	AR374073	ACCESSION:AR374073
	105	22	0.8	26	1	AX106717	ACCESSION:AX106717
	106	22	0.8	30	1	AR264925	ACCESSION:AR264925

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 10, 2004, 12:17:18 ; Search time 116 Seconds
(without alignments)
3.649 Million cell updates/sec

Title: US-10-023-782A-3
Perfect score: 2804
Sequence: 1 tcgcagagccgccgatgcgt.....gaaaaaaaaaaaaaaaaaaa 2804

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 3579 seqs, 75484 residues

Total number of hits satisfying chosen parameters: 7158

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5590 summaries

Database : rng3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	31.4	1.1	47	1	AAL07489	Human reproductive
	2	30.4	1.1	44	1	ADD33791	Mouse mitochondria
	3	30	1.1	45	1	AAS95728	Allele discriminat
	4	30	1.1	45	1	AAS95724	Allele discriminat
c	5	29.4	1.0	33	1	ABQ80395	Probe APC 1-MUT.
	6	29.2	1.0	43	1	AAD17216	Human mRNA hybridi
c	7	29.2	1.0	44	1	AAV09273	Nucleotide sequenc
c	8	29	1.0	38	1	AAL07488	Human reproductive
c	9	28.8	1.0	43	1	AAL31948	Human SNP oligonuc
	10	28.4	1.0	40	1	AAQ25031	Oligonucleotide sp
	11	28.4	1.0	40	1	AAA39649	Primer used in con
c	12	28.2	1.0	36	1	ABK99273	Hepatitis C virus
c	13	28.2	1.0	36	1	AAD27117	RNA template, AU u
c	14	28.2	1.0	37	1	AAD27125	RNA template, (AU)
	15	28	1.0	28	1	AAL62267	Human TFAP2C DNA s
c	16	27.8	1.0	33	1	ABQ80394	Probe APC 1-WT. H
	17	27.8	1.0	42	1	AAA37946	DNA synthesis prim
	18	27.4	1.0	38	1	AAZ57404	Hepatitis C virus
	19	27.4	1.0	40	1	AAZ98722	PCR primer used fo
	20	27.2	1.0	32	1	AAN70278	Sequence of scissi
	21	27.2	1.0	32	1	AAN92244	SS probe MRCO68.
	22	27.2	1.0	32	1	ADC33445	Template oligonucl
	23	27.2	1.0	33	1	AAF29153	PCR primer SEQ ID
c	24	27.2	1.0	36	1	ABK99272	Hepatitis C virus
c	25	27.2	1.0	36	1	AAD27116	RNA template, AA u
c	26	27.2	1.0	38	1	AAL07487	Human reproductive
c	27	27.2	1.0	40	1	ABN89412	Polymorphism detec
	28	27.2	1.0	41	1	ABZ46327	Human aldehyde deh
	29	27.2	1.0	41	1	ABZ48839	Human aldehyde deh
	30	27	1.0	27	1	AAL62265	Human TFAP2C DNA s
c	31	27	1.0	37	1	AAD27124	RNA template, (AU)
	32	26.8	1.0	39	1	AAV12483	Oligonucleotide SE
	33	26.8	1.0	39	1	AAX30019	Multimer SEQ ID NO
	34	26.8	1.0	40	1	AAQ55168	Sequence of primer
	35	26.8	1.0	41	1	AAV03013	Aspergillus oryzae
	36	26.6	0.9	40	1	AAQ25023	Anti-sense oligonu
	37	26	0.9	34	1	AAT93827	Antitumoural phosp
	38	25.6	0.9	33	1	AAX88521	Conus stercusmusca
	39	25.4	0.9	31	1	AAS17761	Oligo d(T) PCR pri
	40	25.4	0.9	32	1	AAS09500	SMART PCR primer #
	41	25.4	0.9	32	1	ABA01204	Mamushi fibrinolyt
	42	25.2	0.9	30	1	AAN70277	Sequence of scissi
	43	25.2	0.9	30	1	AAN92243	SS probe MRCO64.
	44	25.2	0.9	30	1	AAQ36302	GST3anti, for GSTp
	45	25.2	0.9	30	1	AAQ36301	GST3par, for GSTpi
	46	25.2	0.9	30	1	AAX57020	WO9923258 oligonuc
c	47	25.2	0.9	30	1	AAF99889	Immunostimulatory
	48	25.2	0.9	30	1	AAF99888	Immunostimulatory
c	49	25.2	0.9	30	1	ABK10416	Synthetic primer s
	50	25.2	0.9	30	1	ABK10412	Synthetic primer s
	51	25.2	0.9	30	1	ABK70490	In-situ analysis s
	52	25.2	0.9	30	1	ABS53961	Method of measurin
	53	24.8	0.9	40	1	ABN89412	Polymorphism detec
	54	24.6	0.9	35	1	AAX14632	Triple helix formi
c	55	24.6	0.9	36	1	ABQ95487	Tumour suppression
	56	24.4	0.9	29	1	AAA71190	Molecular interact
	57	24.4	0.9	29	1	AAA71173	Molecular interact
c	58	24.4	0.9	36	1	AAD27121	RNA template, (AU)
	59	24.2	0.9	29	1	AAQ05003	Sequence binding t
	60	24.2	0.9	30	1	ADA26181	Rice semi-dwarf (s
	61	24.2	0.9	37	1	AAF85682	Pea blight resista
	62	24	0.9	30	1	AAF26222	APC binding protei
	63	24	0.9	33	1	AAL44170	Porphyra yezoensis
	64	24	0.9	34	1	AAA75564	PCR primer for DNA
	65	24	0.9	34	1	AAD09727	ZC18698 primer, to
	66	24	0.9	34	1	AAS20662	Primer ZC18698 ued
	67	24	0.9	34	1	ADD68172	PCR primer relatin
	68	23.8	0.8	34	1	ADC65905	DNA oligonucleotid
c	69	23.6	0.8	32	1	ABN83375	Mononucleotide rep
	70	23.6	0.8	35	1	AAD46356	Vp3 oligonucleotid
c	71	23.4	0.8	30	1	AAS63441	Oligonucleotide-na
c	72	23.4	0.8	30	1	AAS10385	Oligonucleotide-cy
c	73	23.4	0.8	30	1	ABK65048	Nanoparticle-oligo
c	74	23.4	0.8	30	1	ABS64686	Nucleic acid detec
c	75	23.4	0.8	30	1	AAL61658	Oligonucleotide #1
	76	23.4	0.8	36	1	AAA94321	RNA-protein fusion
c	77	23.4	0.8	36	1	ABK99274	Hepatitis C virus
c	78	23.4	0.8	36	1	AAD27118	RNA template, (AU)
	79	23.2	0.8	29	1	AAV15487	PR-1 promoter prim
c	80	23.2	0.8	29	1	ABN83378	Mononucleotide rep
c	81	23.2	0.8	32	1	ADA26489	DNA nanolithograph
c	82	23.2	0.8	36	1	AAA94321	RNA-protein fusion
	83	23	0.8	23	1	AAQ30431	Oligomer IL6804 fo
	84	23	0.8	25	1	AAI72268	P4 primer used in
	85	23	0.8	27	1	AAV71935	Anchored poly T RT
	86	23	0.8	28	1	AAA40362	pBluescriptSK+ pha
	87	23	0.8	32	1	AAQ87894	Normalised library
	88	23	0.8	32	1	AAF60568	Neuraminidase PCR
	89	23	0.8	35	1	AAT93816	Antitumoural phosp
	90	22.8	0.8	27	1	ABX79828	EST polymorphic DN
	91	22.8	0.8	35	1	AAQ52157	Breast cancer spec
	92	22.8	0.8	35	1	ABS64697	Nucleic acid detec
	93	22.8	0.8	35	1	AAL61669	Oligonucleotide #2
c	94	22.8	0.8	35	1	ABQ80396	Probe APC 2. Homo
	95	22.6	0.8	29	1	AAQ79096	Tobacco PMT PCR pr
c	96	22.6	0.8	29	1	AAA94315	RNA-protein fusion
c	97	22.6	0.8	29	1	AAS00066	Synthetic branched
c	98	22.6	0.8	29	1	AAH20990	C-myc epitope puro
c	99	22.6	0.8	29	1	AAK98637	S cerevisiae alpha
c	100	22.6	0.8	30	1	AAV48087	Oligonucleotide 30
c	101	22.6	0.8	30	1	ABL35101	Phosphorothioate s
c	102	22.4	0.8	24	1	ABK86169	Oligo dT primer #2
	103	22.4	0.8	24	1	ABK86168	Oligo dT primer #1
	104	22.4	0.8	25	1	AAV42215	Sequencing primer
	105	22.4	0.8	30	1	ADC16682	Aminoacylation RNA
	106	22.4	0.8	33	1	AAA94322	RNA-protein fusion

	107	22.4	0.8	34	1	AAV12929
	108	22.4	0.8	34	1	AAV59243
	109	22.4	0.8	34	1	AAV48094
	110	22.4	0.8	34	1	AAC90605
c	111	22.4	0.8	35	1	AAD46356
	112	22.2	0.8	27	1	AAN70281
	113	22.2	0.8	27	1	AAN70274
	114	22.2	0.8	27	1	AAN92240
	115	22.2	0.8	27	1	AAN92247
c	116	22.2	0.8	27	1	AAQ40854
	117	22.2	0.8	27	1	AAF99706
	118	22.2	0.8	27	1	ABS78427
	119	22.2	0.8	27	1	ABL39406
	120	22.2	0.8	27	1	ACH03245
	121	22.2	0.8	27	1	ADB37208
	122	22.2	0.8	33	1	ADC60749
	123	22.2	0.8	43	1	AAL31948
	124	22	0.8	23	1	AAQ30432
	125	22	0.8	23	1	AAQ30430
c	126	22	0.8	23	1	ABL01773
	127	22	0.8	24	1	AAI66361
	128	22	0.8	25	1	AAX84259
c	129	22	0.8	25	1	AAD34264
	130	22	0.8	26	1	AAD03682
	131	22	0.8	26	1	AAS20596
	132	22	0.8	26	1	ABS52638
	133	22	0.8	26	1	AAD45055
	134	22	0.8	26	1	AAS20671
	135	22	0.8	26	1	ABX93599
	136	22	0.8	30	1	AAX77343
	137	22	0.8	30	1	AAA90394
	138	22	0.8	30	1	ABL56893
c	139	22	0.8	30	1	AAF26221
	140	22	0.8	30	1	ABA97617
	141	22	0.8	30	1	ABL95890
	142	22	0.8	31	1	ABS55182
c	143	22	0.8	33	1	ACC42844
c	144	21.8	0.8	26	1	AAF16616
	145	21.8	0.8	27	1	AAZ43904
	146	21.8	0.8	28	1	AAA57856
	147	21.8	0.8	28	1	AAA40358
	148	21.8	0.8	31	1	AAQ43410
c	149	21.8	0.8	35	1	ABS64697
c	150	21.8	0.8	35	1	AAL61669
	151	21.6	0.8	29	1	AAV59216
	152	21.6	0.8	29	1	AAL44903
	153	21.6	0.8	29	1	ADC65873
c	154	21.6	0.8	30	1	AAQ83940
	155	21.6	0.8	30	1	ABL56894
	156	21.6	0.8	30	1	ABL56895
c	157	21.6	0.8	30	1	AAF60462
	158	21.6	0.8	30	1	AAD25661
	159	21.6	0.8	30	1	ABA97619
	160	21.6	0.8	30	1	ABA97618
	161	21.6	0.8	30	1	ABL95891
	162	21.6	0.8	30	1	ABL95892
	163	21.6	0.8	33	1	AAV06769
	164	21.6	0.8	33	1	ABK15694
c	165	21.6	0.8	40	1	AAQ25023
	166	21.4	0.8	25	1	AAH38515
	167	21.4	0.8	27	1	AAH43080
	168	21.4	0.8	27	1	ABQ79879
	169	21.4	0.8	27	1	ABX12469
	170	21.4	0.8	27	1	ADC75074
c	171	21.4	0.8	28	1	AAA57855
c	172	21.4	0.8	28	1	AAL43065
c	173	21.4	0.8	28	1	ADA39569
c	174	21.4	0.8	29	1	AAQ68614
c	175	21.4	0.8	29	1	AAT09934
c	176	21.4	0.8	31	1	AAD33519
c	177	21.4	0.8	32	1	AAD33521
	178	21.4	0.8	32	1	ABS53433
	179	21.2	0.8	24	1	ABK48140

Oligonucleotide SE
Small synthetic DN
Oligonucleotide 34
Tomato spotted wil
Vp3 oligonucleotid
Sequence of scissi
Sequence of scissi
SS probe MRCO46.
SS probe MRCO71.
DNA sequence used
Immunostimulatory
Angiogenesis inhib
Immunostimulatory
Immunostimulatory
Immunostimulatory
Termitomyces album
Human SNP oligonuc
Oligomer IL6805 fo
Oligomer IL6803 fo
Human MSH2 (hMSH2)
Human phosphatidyl
PCR primer for hum
Human CYP2D6 gene
Human full length
Human zsig63 cDNA
Human secreted sal
ZC7764a primer use
Human zalpha11 Lig
Human zsig63 PCR/s
Sindbis virus mRNA
Sindbis virus 3' R
Synthetic deoxyrib
APC binding protei
Poly f nucleotide
Probe poly f for a
Tumour-suppressor
Nuclear transition
Gastric acid produ
M. tuberculosis rp
Deoxy-T22-tagged s
pBluescriptSK+ pha
Structural product
Nucleic acid detec
Oligonucleotide #2
Linear multimer pr
Triplex forming ol
DNA oligonucleotid
Oligonucleotide cl
Synthetic deoxyrib
Synthetic deoxyrib
Oligonucleotide cl
Oligonucleotide #7
Poly h nucleotide
Poly g nucleotide
Probe poly g for a
Probe poly h for a
Oligonucleotide co
Human activating G
Anti-sense oligonu
SNP specific SNPE
Nucleotide sequenc
Nucleotide sequenc
Coxsackie B virus
Biosensor related
Deoxy-A22-tagged s
Regulatable, catal
Substrate RNA rela
tRNAPolyU reverse
Reverse tRNA prime
T7T18Apad_PS4-31-0
T7T18Apad_PS3-32-0
First strand synth
Aspergillus niger

	180	21.2	0.8	26	1	AAN70276
	181	21.2	0.8	26	1	AAN70275
	182	21.2	0.8	26	1	AAN92241
	183	21.2	0.8	26	1	AAN92242
	184	21.2	0.8	26	1	AAX07466
	185	21.2	0.8	26	1	AAX78723
	186	21.2	0.8	26	1	AAF77536
	187	21.2	0.8	26	1	AAF23526
	188	21.2	0.8	26	1	AAS20595
	189	21.2	0.8	26	1	ABS52637
	190	21.2	0.8	26	1	AAD45054
c	191	21.2	0.8	26	1	AAD26899
c	192	21.2	0.8	26	1	AAD39650
	193	21.2	0.8	26	1	AAD43853
	194	21.2	0.8	26	1	AAD55692
	195	21.2	0.8	26	1	ABZ24784
	196	21.2	0.8	26	1	ABX93598
	197	21.2	0.8	26	1	ACA62282
	198	21.2	0.8	26	1	ACF36382
	199	21.2	0.8	27	1	AAV71936
	200	21.2	0.8	27	1	ABQ76254
	201	21.2	0.8	30	1	ABX89953
	202	21	0.7	21	1	AAQ75733
c	203	21	0.7	21	1	AAQ75757
	204	21	0.7	21	1	AAX26973
	205	21	0.7	21	1	AAZ44350
	206	21	0.7	21	1	AAF99707
	207	21	0.7	21	1	AAH42480
	208	21	0.7	21	1	ABS78428
	209	21	0.7	21	1	ABL39404
	210	21	0.7	21	1	AAD51323
c	211	21	0.7	21	1	AAL62266
	212	21	0.7	21	1	ACH03246
	213	21	0.7	21	1	ADB37209
c	214	21	0.7	22	1	AAQ64724
c	215	21	0.7	22	1	AAF17413
	216	21	0.7	23	1	AAC62450
	217	21	0.7	23	1	AAC62451
	218	21	0.7	23	1	AAF16627
c	219	21	0.7	24	1	AAT99286
c	220	21	0.7	24	1	AAV31743
c	221	21	0.7	24	1	AAX04086
	222	21	0.7	24	1	AAA40359
	223	21	0.7	24	1	AAA40353
	224	21	0.7	24	1	AAF99756
	225	21	0.7	24	1	AAF99304
c	226	21	0.7	24	1	AAF99757
	227	21	0.7	24	1	ABV14842
	228	21	0.7	24	1	ABS78477
	229	21	0.7	24	1	ABS77949
c	230	21	0.7	24	1	ABS78478
	231	21	0.7	24	1	ABL39405
c	232	21	0.7	24	1	ABA98840
c	233	21	0.7	24	1	AAS17869
	234	21	0.7	24	1	ABK15639
	235	21	0.7	24	1	ACA58802
	236	21	0.7	24	1	ABX79809
	237	21	0.7	24	1	ABZ80181
	238	21	0.7	24	1	ACA62284
	239	21	0.7	24	1	ACD99729
c	240	21	0.7	24	1	ACH03285
	241	21	0.7	24	1	ACH03284
c	242	21	0.7	24	1	ADA66379
	243	21	0.7	24	1	ADB37258
	244	21	0.7	24	1	ADB36806
c	245	21	0.7	24	1	ADB37259
	246	21	0.7	24	1	ADD31867
	247	21	0.7	24	1	ADE25524
	248	21	0.7	25	1	AAQ95960
	249	21	0.7	25	1	AAX84258
	250	21	0.7	25	1	AAX84260
	251	21	0.7	25	1	AAA39306
	252	21	0.7	25	1	AAZ30267

Sequence of scissi
Sequence of scissi
SS probe MRCO59.
SS probe MRCO60.
Human BS124 specif
Human pancreatic P
CDNA library produ
Primer #4. Uniden
Human zsig63 cDNA
Human secreted sal
ZC7231 primer used
Bacterial PNP DNA
PolyPNP out-of-fra
Primer #2 used to
Bovine viral diarr
Oligodeoxynucleic
Human zsig63 PCR/s
Oligo (dT) primer
Nucleotide sequenc
Anchored poly T RT
Murine SCCE 5'-RAC
PolyA adapter DNA.
Reverse transcript
Reverse transcript
Primer used to rev
Protein kinase inh
Immunostimulatory
Oligonucleotide us
Angiogenesis inhib
Immunostimulatory
Regular oligo dT p
Human TFAP2C DNA s
Immunostimulatory
Immunostimulatory
2',5'-linked tetra
L1 cleavage site r
Cleavage of nuclei
Cleavage of nuclei
Gastric acid produ
POLYA, a competito
Nucleotide sequenc
Oligonucleotide PO
pBluescriptSK+ pha
pBluescriptSK+ pha
Immunostimulatory
Immunostimulatory
Immunostimulatory
Human prostate exp
Angiogenesis inhib
Angiogenesis inhib
Angiogenesis inhib
Immunostimulatory
A24 oligonucleotid
A24 oligonucleotid
RNA-PCR procedure
Gastric ulcer trea
EST polymorphic DN
Immunostimulatory
Oligo (dT)24 RT-PC
Immunostimulatory
Immunostimulatory
Immunostimulatory
mRNA poly A. Unid
Immunostimulatory
Immunostimulatory
Immunostimulatory
Butterfly biliverd
Rolling circle amp
Oligonucleotide bi
PCR primer for hum
PCR primer for hum
Rapid capture prob
Capture probe CP12

	253	21	0.7	25	1	ABK49986	Example oligonucle
	254	21	0.7	25	1	ADC54009	Oligonucleotide of
c	255	21	0.7	25	1	ADC54008	Oligonucleotide of
	256	21	0.7	26	1	AAI73048	Scaffold oligonucl
	257	21	0.7	26	1	AAS20672	Human zalphal1 Lig
	258	21	0.7	26	1	ABX93461	LS147-specific pol
	259	21	0.7	27	1	AAX15434	PCR primer used to
	260	21	0.7	27	1	ABS53863	Human androgen rec
	261	21	0.7	27	1	ABS54324	Human ARCAP associ
c	262	21	0.7	28	1	AAS11744	Human haemoglobin
	263	21	0.7	29	1	AAQ97396	Rat type I steroid
	264	21	0.7	29	1	AAT99803	Primer for rat ste
c	265	21	0.7	30	1	AAT69677	Downstream primer
c	266	21	0.7	30	1	ABL35095	RNA/DNA hybrid con
c	267	21	0.7	30	1	ABL35096	Phosphorothioate s
c	268	21	0.7	30	1	ABL35097	Phosphorothioate s
c	269	21	0.7	30	1	ABL35105	RNA/DNA hybrid ass
c	270	21	0.7	30	1	ABL35098	Phosphorothioate s
	271	21	0.7	32	1	ABN83375	Mononucleotide rep
	272	21	0.7	32	1	AAV03988	Primer B for Non-A
	273	21	0.7	32	1	AAQ43973	Triple helix formi
	274	21	0.7	32	1	AAT77235	Rat fibroblast gro
	275	21	0.7	32	1	AAT94579	Antifungal polypep
	276	21	0.7	32	1	ADC87763	F. culmorum FCWP1
c	277	21	0.7	45	1	AAS95728	Allele discriminat
c	278	21	0.7	45	1	AAS95724	Allele discriminat
	279	20.8	0.7	24	1	AAZ00877	PCR primer PGRT32
c	280	20.8	0.7	24	1	AAZ00877	PCR primer PGRT32
c	281	20.8	0.7	27	1	ABX79828	EST polymorphic DN
c	282	20.8	0.7	27	1	AAZ43904	M. tuberculosis rp
c	283	20.8	0.7	32	1	AAS63424	Oligonucleotide-na
c	284	20.8	0.7	32	1	AAS10367	Alkanethiol-modifi
	285	20.8	0.7	32	1	AAH28290	3' untranslated re
c	286	20.8	0.7	32	1	ABK65031	Nanoparticle-oligo
c	287	20.8	0.7	32	1	ABS64669	Nucleic acid detec
c	288	20.8	0.7	32	1	ACD27316	Nanotechnology nuc
c	289	20.8	0.7	32	1	AAL61641	Thiol-modified oli
c	290	20.8	0.7	32	1	ABX79177	Fluorescein-labell
c	291	20.8	0.7	32	1	ABX92173	Nanoparticle-assoc
c	292	20.8	0.7	32	1	ACD27251	Nanotechnology nuc
c	293	20.8	0.7	32	1	ACD27121	Nanotechnology nuc
c	294	20.8	0.7	32	1	ACD27381	Nanotechnology nuc
c	295	20.8	0.7	32	1	ACD27186	Nanotechnology nuc
c	296	20.8	0.7	32	1	ACD27056	Nanotechnology nuc
c	297	20.8	0.7	32	1	ACH00060	Nanotechnology nuc
c	298	20.8	0.7	32	1	ADA06155	Nanoparticle label
c	299	20.8	0.7	32	1	ACD26991	Nanotechnology nuc
c	300	20.8	0.7	32	1	ADE71592	Magneto-gold nanop
	301	20.8	0.7	47	1	AAL07489	Human reproductive
c	302	20.6	0.7	27	1	AAV71935	Anchored poly T RT
c	303	20.6	0.7	30	1	ABX89953	PolyA adapter DNA.
c	304	20.6	0.7	31	1	ABS55182	Tumour-suppressor
	305	20.6	0.7	36	1	ABQ95487	Tumour suppression
	306	20.4	0.7	24	1	ABK86169	Oligo dT primer #2
c	307	20.4	0.7	24	1	ABK86168	Oligo dT primer #1
c	308	20.4	0.7	24	1	AAI66361	Human phosphatidyl
c	309	20.4	0.7	30	1	AAD25661	Oligonucleotide #7
	310	20.4	0.7	30	1	AAT69677	Downstream primer
	311	20.4	0.7	30	1	ABL56888	Synthetic deoxyrib
	312	20.4	0.7	30	1	ABA97612	Poly a nucleotide
c	313	20.4	0.7	30	1	AAD33517	T7T18Apad_PS5-30-0
	314	20.4	0.7	30	1	ABL95885	Probe poly a for a
	315	20.4	0.7	31	1	AAQ99582	Human TPO anti-sen
	316	20.4	0.7	31	1	ABA97621	Poly j nucleotide
	317	20.2	0.7	22	1	AAL50570	Molecular array pr
	318	20.2	0.7	22	1	ABX74887	Oligo-dT primer us
	319	20.2	0.7	22	1	ACC48484	Locked nucleic aci
	320	20.2	0.7	22	1	ACC48485	Locked nucleic aci
	321	20.2	0.7	22	1	ACC48483	Locked nucleic aci
	322	20.2	0.7	22	1	AAD51324	Anchored oligo dT
	323	20.2	0.7	23	1	ABK13916	3'-PCR primer used
	324	20.2	0.7	24	1	ABK86172	Oligo dT primer #4
c	325	20.2	0.7	25	1	AAX84260	PCR primer for hum
	326	20.2	0.7	25	1	AAA47833	Adapter sequence f
c	327	20.2	0.7	25	1	AAD26900	Bacterial PNP DNA
	328	20.2	0.7	25	1	ABK86170	Oligo dT primer #3
c	329	20.2	0.7	26	1	AAI73048	Scaffold oligonucl
c	330	20.2	0.7	26	1	AAS20672	Human zalphal1 Lig
c	331	20.2	0.7	26	1	ABX93461	LS147-specific pol
	332	20.2	0.7	26	1	AAA13806	Yeast DOG2 stress
	333	20.2	0.7	26	1	AAD12516	Thuja sp. pinoresi
	334	20.2	0.7	28	1	AAH91554	Human inflammatory
	335	20.2	0.7	28	1	ACC83476	Oligo dT primer.
	336	20.2	0.7	28	1	ABZ59816	Potato gene PCR pr
c	337	20.2	0.7	28	1	ADD41445	Hepatitis C virus
c	338	20.2	0.7	29	1	AAV15487	PR-1 promoter prim
	339	20.2	0.7	30	1	AAV56638	Feline FLAF cDNA p
	340	20.2	0.7	30	1	AAV62858	Primer for PR-Q ge
	341	20.2	0.7	30	1	AAV81666	Oligonucleotide SE
c	342	20.2	0.7	30	1	AAF74908	CD40L poly-A tract
c	343	20.2	0.7	33	1	AAA94322	RNA-protein fusion
c	344	20.2	0.7	34	1	AAV48094	Oligonucleotide 34
	345	20.2	0.7	36	1	ABK99273	Hepatitis C virus
	346	20.2	0.7	36	1	AAD27117	RNA template, AU u
	347	20.2	0.7	36	1	ABK99272	Hepatitis C virus
	348	20.2	0.7	36	1	AAD27116	RNA template, AA u
	349	20.2	0.7	36	1	AAD27121	RNA template, (AU)
	350	20.2	0.7	36	1	ABK99274	Hepatitis C virus
	351	20.2	0.7	36	1	AAD27118	RNA template, (AU)
	352	20.2	0.7	37	1	AAD27125	RNA template, (AU)
	353	20.2	0.7	37	1	AAD27124	RNA template, (AU)
	354	20	0.7	20	1	AAQ25565	Dye-coupled 3'-ami
	355	20	0.7	20	1	AAQ33554	Microsatellite seq
c	356	20	0.7	20	1	AAQ58578	Sequence of synthe
	357	20	0.7	20	1	AAQ94205	Alpha-anomeric oli
c	358	20	0.7	20	1	AAQ75596	Reverse transcript
	359	20	0.7	20	1	AAQ75582	Reverse transcript
	360	20	0.7	20	1	AAQ90405	T2 (synthetic DNA
	361	20	0.7	20	1	AAV07752	Phosphorothioate o
	362	20	0.7	20	1	AAT63649	Anti-HTLV antisens
c	363	20	0.7	20	1	AAV34591	M. vaccae antigeni
	364	20	0.7	20	1	AAT86606	Oligonucleotide se
	365	20	0.7	20	1	AAX27533	Synthetic RNA sequ
c	366	20	0.7	20	1	AAZ11326	Mycobacterial 16S
c	367	20	0.7	20	1	AAA40449	Electochemical det
	368	20	0.7	20	1	AAA40448	Electochemical det
	369	20	0.7	20	1	AAZ91117	Oligonucleotide #5
	370	20	0.7	20	1	AAA50193	2'-Methoxyethoxy-m
	371	20	0.7	20	1	AAC87238	Phosphorothioate p
	372	20	0.7	20	1	AAC87230	Digoxigenin-labell
	373	20	0.7	20	1	AAC87241	Poly T oligonucleo
	374	20	0.7	20	1	AAS10402	DNA template for 3
	375	20	0.7	20	1	AAD16997	Capture probe CP5'
c	376	20	0.7	20	1	AAF60896	Conjugate forming
c	377	20	0.7	20	1	AAS63428	Oligonucleotide-na
c	378	20	0.7	20	1	AAF28481	Random oligonucleo
c	379	20	0.7	20	1	AAS10371	Oligonucleotide-cy
	380	20	0.7	20	1	AAF99427	Immunostimulatory
	381	20	0.7	20	1	AAF99099	Immunostimulatory
c	382	20	0.7	20	1	AAF99431	Immunostimulatory
	383	20	0.7	20	1	AAH46465	Oligonucleotide #1
c	384	20	0.7	20	1	AAH78547	Nucleotide sequenc
c	385	20	0.7	20	1	AAF28351	DNA oligomer #1.
	386	20	0.7	20	1	ABS77742	Angiogenesis inhib
	387	20	0.7	20	1	ABS78072	Angiogenesis inhib
c	388	20	0.7	20	1	ABS78076	Angiogenesis inhib
	389	20	0.7	20	1	ABL39402	Immunostimulatory
c	390	20	0.7	20	1	ABL38648	Immunostimulatory
	391	20	0.7	20	1	ABL39403	Immunostimulatory
	392	20	0.7	20	1	ABL54775	CD14 receptor PCR
c	393	20	0.7	20	1	ABK65035	Nanoparticle-oligo
c	394	20	0.7	20	1	ABK65050	Nanoparticle-oligo
	395	20	0.7	20	1	AAL45122	Oligonucleotide sy
c	396	20	0.7	20	1	ABL36232	M tuberculosis rRN
c	397	20	0.7	20	1	ABS64673	Nucleic acid detec
c	398	20	0.7	20	1	ABS64688	Nucleic acid detec

	399	20	0.7	20	1	ABN87103	Capture probe CP5'
c	400	20	0.7	20	1	ABZ88267	Human oligonucleot
c	401	20	0.7	20	1	ABZ88565	Human oligonucleot
c	402	20	0.7	20	1	ABZ88619	Human oligonucleot
c	403	20	0.7	20	1	ABZ89705	Human oligonucleot
c	404	20	0.7	20	1	ABZ85312	Human oligonucleot
c	405	20	0.7	20	1	ABZ88816	Human oligonucleot
c	406	20	0.7	20	1	ABZ88881	Human oligonucleot
c	407	20	0.7	20	1	ABZ89546	Human oligonucleot
c	408	20	0.7	20	1	ABZ89706	Human oligonucleot
c	409	20	0.7	20	1	ABZ88620	Human oligonucleot
c	410	20	0.7	20	1	ABZ88880	Human oligonucleot
c	411	20	0.7	20	1	ABZ89179	Human oligonucleot
c	412	20	0.7	20	1	ABZ88814	Human oligonucleot
c	413	20	0.7	20	1	ABZ89241	Human oligonucleot
c	414	20	0.7	20	1	ABZ90650	Human PDE4C oligon
c	415	20	0.7	20	1	ABZ99050	Human oligonucleot
c	416	20	0.7	20	1	ABZ88815	Human oligonucleot
	417	20	0.7	20	1	ABZ85311	Human oligonucleot
	418	20	0.7	20	1	ABZ85435	Human oligonucleot
c	419	20	0.7	20	1	ABZ88817	Human oligonucleot
c	420	20	0.7	20	1	ABZ88939	Human oligonucleot
c	421	20	0.7	20	1	ABZ89302	Human oligonucleot
c	422	20	0.7	20	1	ABZ87681	Human oligonucleot
c	423	20	0.7	20	1	ABZ88566	Human oligonucleot
c	424	20	0.7	20	1	ABZ89086	Human oligonucleot
c	425	20	0.7	20	1	ABZ85533	Human oligonucleot
c	426	20	0.7	20	1	ABZ89015	Human oligonucleot
c	427	20	0.7	20	1	ABZ89441	Human oligonucleot
c	428	20	0.7	20	1	ABZ89016	Human oligonucleot
c	429	20	0.7	20	1	ABZ89120	Human oligonucleot
c	430	20	0.7	20	1	ABZ89704	Human oligonucleot
c	431	20	0.7	20	1	ACD27320	Nanotechnology nuc
	432	20	0.7	20	1	ACC58867	Doubly labelled DN
	433	20	0.7	20	1	ABZ22916	Phosphorothioate 2
c	434	20	0.7	20	1	AAL61645	Thiol-modified oli
	435	20	0.7	20	1	ABZ59815	Potato gene PCR pr
c	436	20	0.7	20	1	ABX79181	Thio-modified 20dA
c	437	20	0.7	20	1	ABX92177	Nanoparticle-assoc
c	438	20	0.7	20	1	ACD27255	Nanotechnology nuc
c	439	20	0.7	20	1	ACD27125	Nanotechnology nuc
c	440	20	0.7	20	1	ACD27385	Nanotechnology nuc
c	441	20	0.7	20	1	ACD27190	Nanotechnology nuc
c	442	20	0.7	20	1	ACD27060	Nanotechnology nuc
c	443	20	0.7	20	1	AAL62273	Human transcriptio
c	444	20	0.7	20	1	AAL62303	Human transcriptio
c	445	20	0.7	20	1	AAL62320	Human transcriptio
c	446	20	0.7	20	1	AAL62343	Human transcriptio
c	447	20	0.7	20	1	AAL62284	Human transcriptio
c	448	20	0.7	20	1	AAL62290	Human transcriptio
c	449	20	0.7	20	1	AAL62301	Human transcriptio
c	450	20	0.7	20	1	AAL62306	Human transcriptio
c	451	20	0.7	20	1	AAL62312	Human transcriptio
c	452	20	0.7	20	1	AAL62325	Human transcriptio
c	453	20	0.7	20	1	AAL62327	Human transcriptio
c	454	20	0.7	20	1	AAL62341	Human transcriptio
c	455	20	0.7	20	1	AAL62272	Human transcriptio
c	456	20	0.7	20	1	AAL62288	Human transcriptio
c	457	20	0.7	20	1	AAL62292	Human transcriptio
c	458	20	0.7	20	1	AAL62307	Human transcriptio
c	459	20	0.7	20	1	AAL62314	Human transcriptio
c	460	20	0.7	20	1	AAL62313	Human transcriptio
c	461	20	0.7	20	1	AAL62331	Human transcriptio
c	462	20	0.7	20	1	AAL62286	Human transcriptio
c	463	20	0.7	20	1	AAL62339	Human transcriptio
c	464	20	0.7	20	1	AAL62340	Human transcriptio
c	465	20	0.7	20	1	AAL62348	Human transcriptio
c	466	20	0.7	20	1	AAL62293	Human transcriptio
c	467	20	0.7	20	1	AAL62308	Human transcriptio
c	468	20	0.7	20	1	AAL62316	Human transcriptio
c	469	20	0.7	20	1	AAL62294	Human transcriptio
c	470	20	0.7	20	1	AAL62298	Human transcriptio
c	471	20	0.7	20	1	AAL62305	Human transcriptio
c	472	20	0.7	20	1	AAL62309	Human transcriptio
c	473	20	0.7	20	1	AAL62315	Human transcriptio
c	474	20	0.7	20	1	AAL62333	Human transcriptio
c	475	20	0.7	20	1	AAL62278	Human transcriptio
c	476	20	0.7	20	1	AAL62310	Human transcriptio
c	477	20	0.7	20	1	AAL62319	Human transcriptio
c	478	20	0.7	20	1	AAL62336	Human transcriptio
c	479	20	0.7	20	1	AAL62276	Human transcriptio
c	480	20	0.7	20	1	AAL62282	Human transcriptio
c	481	20	0.7	20	1	AAL62285	Human transcriptio
c	482	20	0.7	20	1	AAL62302	Human transcriptio
c	483	20	0.7	20	1	AAL62347	Human transcriptio
c	484	20	0.7	20	1	AAL62283	Human transcriptio
c	485	20	0.7	20	1	AAL62323	Human transcriptio
c	486	20	0.7	20	1	AAL62330	Human transcriptio
c	487	20	0.7	20	1	AAL62342	Human transcriptio
c	488	20	0.7	20	1	AAL62346	Human transcriptio
c	489	20	0.7	20	1	AAL62277	Human transcriptio
c	490	20	0.7	20	1	AAL62287	Human transcriptio
c	491	20	0.7	20	1	AAL62300	Human transcriptio
c	492	20	0.7	20	1	AAL62304	Human transcriptio
c	493	20	0.7	20	1	AAL62317	Human transcriptio
c	494	20	0.7	20	1	AAL62334	Human transcriptio
c	495	20	0.7	20	1	AAL62337	Human transcriptio
c	496	20	0.7	20	1	AAL62289	Human transcriptio
c	497	20	0.7	20	1	AAL62291	Human transcriptio
c	498	20	0.7	20	1	AAL62296	Human transcriptio
c	499	20	0.7	20	1	AAL62321	Human transcriptio
c	500	20	0.7	20	1	AAL62324	Human transcriptio
c	501	20	0.7	20	1	AAL62326	Human transcriptio
c	502	20	0.7	20	1	AAL62329	Human transcriptio
c	503	20	0.7	20	1	AAL62344	Human transcriptio
c	504	20	0.7	20	1	AAL62279	Human transcriptio
c	505	20	0.7	20	1	AAL62280	Human transcriptio
c	506	20	0.7	20	1	AAL62281	Human transcriptio
c	507	20	0.7	20	1	AAL62297	Human transcriptio
c	508	20	0.7	20	1	AAL62318	Human transcriptio
c	509	20	0.7	20	1	AAL62322	Human transcriptio
c	510	20	0.7	20	1	AAL62274	Human transcriptio
c	511	20	0.7	20	1	AAL62299	Human transcriptio
c	512	20	0.7	20	1	AAL62332	Human transcriptio
c	513	20	0.7	20	1	AAL62338	Human transcriptio
c	514	20	0.7	20	1	AAL62271	Human transcriptio
c	515	20	0.7	20	1	AAL62275	Human transcriptio
c	516	20	0.7	20	1	AAL62295	Human transcriptio
c	517	20	0.7	20	1	AAL62311	Human transcriptio
c	518	20	0.7	20	1	AAL62328	Human transcriptio
c	519	20	0.7	20	1	AAL62335	Human transcriptio
c	520	20	0.7	20	1	AAL62345	Human transcriptio
c	521	20	0.7	20	1	ACH00064	Nanotechnology nuc
c	522	20	0.7	20	1	ACD99851	Immunostimulatory
	523	20	0.7	20	1	ACD99847	Immunostimulatory
	524	20	0.7	20	1	ACD99532	Immunostimulatory
c	525	20	0.7	20	1	ADA14838	Hairpin target seq
c	526	20	0.7	20	1	ADA06159	Nanoparticle label
c	527	20	0.7	20	1	ACD26995	Nanotechnology nuc
c	528	20	0.7	20	1	ADB36933	Immunostimulatory
	529	20	0.7	20	1	ADB36601	Immunostimulatory
	530	20	0.7	20	1	ADB36929	Immunostimulatory
	531	20	0.7	21	1	AAQ75732	Reverse transcript
c	532	20	0.7	21	1	AAQ75758	Reverse transcript
c	533	20	0.7	21	1	AAQ75756	Reverse transcript
	534	20	0.7	21	1	AAQ75731	Reverse transcript
	535	20	0.7	21	1	AAQ75734	Reverse transcript
c	536	20	0.7	21	1	AAQ75755	Reverse transcript
c	537	20	0.7	21	1	AAQ90391	CP-1 (synthetic DN
c	538	20	0.7	21	1	AAT10743	Oligonucleotide pr
c	539	20	0.7	21	1	AAX81302	3' ribonucleoside
c	540	20	0.7	23	1	AAQ30432	Oligomer IL6805 fo
c	541	20	0.7	24	1	ABX79809	EST polymorphic DN
c	542	20	0.7	24	1	AAT68615	DNA probe used in
c	543	20	0.7	24	1	ABK12409	RT-PCR primer #1 f
	544	20	0.7	25	1	AAZ99741	Primer used to rev

c	545	20	0.7	25	1	ABZ23535
	546	20	0.7	25	1	ACF79235
	547	20	0.7	27	1	AAT94842
	548	20	0.7	27	1	AAA59740
	549	20	0.7	27	1	AAF25224
	550	20	0.7	27	1	ABL41793
	551	20	0.7	27	1	ABX14927
	552	20	0.7	28	1	ADD35234
c	553	20	0.7	29	1	AAA71190
c	554	20	0.7	29	1	AAA71173
	555	20	0.7	29	1	AAQ85070
	556	20	0.7	29	1	AAQ83933
c	557	20	0.7	29	1	ACD18468
	558	20	0.7	29	1	ACD18467
	559	20	0.7	30	1	ABL56892
	560	20	0.7	30	1	ABL56896
	561	20	0.7	30	1	ABL56890
	562	20	0.7	30	1	ABL56891
	563	20	0.7	30	1	ABL56897
	564	20	0.7	30	1	ABL56889
	565	20	0.7	30	1	ABA97613
	566	20	0.7	30	1	ABA97620
	567	20	0.7	30	1	ABA97614
	568	20	0.7	30	1	ABA97615
	569	20	0.7	30	1	ABA97616
	570	20	0.7	30	1	ABL95886
	571	20	0.7	30	1	ABL95887
	572	20	0.7	30	1	ABL95894
	573	20	0.7	30	1	ABL95888
	574	20	0.7	30	1	ABL95889
	575	20	0.7	30	1	ABL95893
	576	20	0.7	30	1	ADA14837
c	577	20	0.7	30	1	ADA14837
	578	20	0.7	44	1	AAV09273
c	579	19.8	0.7	24	1	ABV77669
	580	19.8	0.7	25	1	AAD26900
	581	19.8	0.7	25	1	AAC96419
	582	19.8	0.7	26	1	AAD26899
	583	19.8	0.7	26	1	AAD39650
c	584	19.8	0.7	27	1	AAH43080
c	585	19.8	0.7	27	1	ABQ79879
c	586	19.8	0.7	27	1	ABX12469
c	587	19.8	0.7	27	1	ADC75074
	588	19.8	0.7	27	1	ADC75075
c	589	19.8	0.7	28	1	AAA57856
	590	19.8	0.7	29	1	AAA90025
c	591	19.8	0.7	31	1	AAS17761
c	592	19.8	0.7	32	1	AAS09500
c	593	19.8	0.7	32	1	ABA01204
	594	19.8	0.7	32	1	ADA26489
c	595	19.6	0.7	26	1	AAD03682
c	596	19.6	0.7	26	1	AAS20596
c	597	19.6	0.7	26	1	ABS52638
c	598	19.6	0.7	26	1	AAD45055
c	599	19.6	0.7	26	1	AAS20671
c	600	19.6	0.7	26	1	ABX93599
c	601	19.6	0.7	26	1	AAN70276
c	602	19.6	0.7	26	1	AAN70275
c	603	19.6	0.7	26	1	AAN92241
c	604	19.6	0.7	26	1	AAN92242
c	605	19.6	0.7	26	1	AAF77536
c	606	19.6	0.7	26	1	AAF23526
c	607	19.6	0.7	26	1	AAD43853
c	608	19.6	0.7	26	1	ABZ24784
c	609	19.6	0.7	26	1	ACA62282
	610	19.6	0.7	26	1	AAT99265
	611	19.6	0.7	26	1	AAT93819
c	612	19.6	0.7	26	1	AAV12482
c	613	19.6	0.7	26	1	AAV59215
	614	19.6	0.7	26	1	AAV31721
	615	19.6	0.7	26	1	AAX04087
c	616	19.6	0.7	26	1	AAX30018
c	617	19.6	0.7	26	1	ADC65872

fragment of a plas
Calix(a)arene-olig
Human ESF I 3' PCR
PCR primer for hES
3' primer for an e
Primer for human e
hESF I amplifying
Mouse mitochondria
Molecular interact
Molecular interact
Oligonucleotide cl
Oligonucleotide cl
Human zinc finger
Human zinc finger
Synthetic deoxyrib
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Poly b nucleotide
Poly i nucleotide
Poly c nucleotide
Poly d nucleotide
Poly e nucleotide
Probe poly b for a
Probe poly c for a
Probe poly j for a
Probe poly d for a
Probe poly e for a
Probe poly I for a
Hairpin oligonucle
Hairpin oligonucle
Nucleotide sequenc
Human zinc finger
Bacterial PNP DNA
HLA DQA1 gene PCR
Bacterial PNP DNA
PolyPNP out-of-fra
Nucleotide sequenc
Nucleotide sequenc
Coxsackie B virus
Biosensor related
Biosensor related
Deoxy-T22-tagged s
PCR primer for fat
Oligo d(T) PCR pri
SMART PCR primer #
Mamushi fibrinolyt
DNA nanolithograph
Human full length
Human zsig63 cDNA
Human secreted sal
ZC7764a primer use
Human zalpha11 Lig
Human zsig63 PCR/s
Sequence of scissi
Sequence of scissi
SS probe MRCO59.
SS probe MRCO60.
CDNA library produ
Primer #4. Uniden
Primer #2 used to
Oligodeoxynucleic
Oligo (dT) primer
Human PUR-alpha ge
Antitumoural phosp
Oligonucleotide SE
Circular template
Nucleotide sequenc
PUR-alpha RACE rea
Precircle DNA olig
DNA oligonucleotid

c	618	19.6	0.7	27	1	AAN70281
c	619	19.6	0.7	27	1	AAN70274
c	620	19.6	0.7	27	1	AAN92240
c	621	19.6	0.7	27	1	AAN92247
	622	19.6	0.7	27	1	AAQ40854
c	623	19.6	0.7	27	1	AAF99706
c	624	19.6	0.7	27	1	ABS78427
c	625	19.6	0.7	27	1	ABL39406
c	626	19.6	0.7	27	1	ACH03245
c	627	19.6	0.7	27	1	ADB37208
c	628	19.6	0.7	29	1	AAQ05003
	629	19.6	0.7	29	1	AAA94315
	630	19.6	0.7	29	1	AAS00066
	631	19.6	0.7	29	1	AAH20990
	632	19.6	0.7	29	1	AAK98637
c	633	19.6	0.7	30	1	AAN70277
c	634	19.6	0.7	30	1	AAN92243
c	635	19.6	0.7	30	1	AAQ36302
c	636	19.6	0.7	30	1	AAQ36301
c	637	19.6	0.7	30	1	AAX57020
	638	19.6	0.7	30	1	AAF99889
c	639	19.6	0.7	30	1	AAF99888
	640	19.6	0.7	30	1	ABK10416
c	641	19.6	0.7	30	1	ABK10412
c	642	19.6	0.7	30	1	ABK70490
c	643	19.6	0.7	30	1	ABS53961
	644	19.6	0.7	30	1	AAV48087
	645	19.6	0.7	30	1	AAQ83940
	646	19.6	0.7	30	1	AAF60462
c	647	19.6	0.7	30	1	AAV62858
c	648	19.6	0.7	30	1	AAV81666
	649	19.6	0.7	30	1	AAI65862
c	650	19.6	0.7	32	1	AAN70278
c	651	19.6	0.7	32	1	AAN92244
c	652	19.6	0.7	32	1	ADC33445
c	653	19.6	0.7	33	1	AAF29153
c	654	19.6	0.7	33	1	AAX88521
c	655	19.6	0.7	34	1	AAT93827
	656	19.6	0.7	38	1	AAL07488
c	657	19.6	0.7	38	1	AAZ57404
	658	19.6	0.7	38	1	AAL07487
c	659	19.6	0.7	40	1	AAQ25031
c	660	19.6	0.7	40	1	AAA39649
c	661	19.6	0.7	40	1	AAZ98722
c	662	19.6	0.7	40	1	AAQ55168
c	663	19.6	0.7	41	1	AAV03013
c	664	19.6	0.7	42	1	AAA37946
c	665	19.6	0.7	43	1	AAD17216
c	666	19.6	0.7	44	1	ADD33791
	667	19.4	0.7	21	1	AAQ75758
	668	19.4	0.7	21	1	AAQ75630
	669	19.4	0.7	21	1	AAQ75648
	670	19.4	0.7	21	1	AAQ75676
	671	19.4	0.7	21	1	AAQ75681
c	672	19.4	0.7	21	1	AAQ75629
	673	19.4	0.7	21	1	AAQ75725
c	674	19.4	0.7	21	1	AAQ75725
	675	19.4	0.7	21	1	AAQ75729
c	676	19.4	0.7	21	1	AAQ75729
c	677	19.4	0.7	21	1	AAQ75773
c	678	19.4	0.7	21	1	AAQ75780
c	679	19.4	0.7	21	1	AAQ75660
c	680	19.4	0.7	21	1	AAQ75684
c	681	19.4	0.7	21	1	AAQ75741
c	682	19.4	0.7	21	1	AAQ75652
c	683	19.4	0.7	21	1	AAQ75753
c	684	19.4	0.7	21	1	AAQ75788
	685	19.4	0.7	21	1	AAQ75680
	686	19.4	0.7	21	1	AAQ75649
	687	19.4	0.7	21	1	AAQ75726
c	688	19.4	0.7	21	1	AAQ75692
	689	19.4	0.7	21	1	AAQ75776
	690	19.4	0.7	21	1	AAQ75697

Sequence of scissi
Sequence of scissi
SS probe MRCO46.
SS probe MRCO71.
DNA sequence used
Immunostimulatory
Angiogenesis inhib
Immunostimulatory
Immunostimulatory
Immunostimulatory
Sequence binding t
RNA-protein fusion
Synthetic branched
C-myc epitope puro
S cerevisiae alpha
Sequence of scissi
SS probe MRCO64.
GST3anti, for GSTp
GST3par, for GSTpi
WO9923258 oligonuc
Immunostimulatory
Immunostimulatory
Synthetic primer s
Synthetic primer s
In-situ analysis s
Method of measurin
Oligonucleotide 30
Oligonucleotide cl
Oligonucleotide cl
Primer for PR-Q ge
Oligonucleotide SE
Nucleotide sequenc
Sequence of scissi
SS probe MRCO68.
Template oligonucl
PCR primer SEQ ID
Conus stercusmusca
Antitumoural phosp
Human reproductive
Hepatitis C virus
Human reproductive
Oligonucleotide sp
Primer used in con
PCR primer used fo
Sequence of primer
Aspergillus oryzae
DNA synthesis prim
Human mRNA hybridi
Mouse mitochondria
Reverse transcript
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	691	19.4	0.7	21	1	AAQ75637
	692	19.4	0.7	21	1	AAQ75685
	693	19.4	0.7	21	1	AAQ75717
	694	19.4	0.7	21	1	AAQ75777
	695	19.4	0.7	21	1	AAQ75644
c	696	19.4	0.7	21	1	AAQ75761
	697	19.4	0.7	21	1	AAQ75765
c	698	19.4	0.7	21	1	AAQ75765
	699	19.4	0.7	21	1	AAQ75772
c	700	19.4	0.7	21	1	AAQ75789
	701	19.4	0.7	21	1	AAQ75701
	702	19.4	0.7	21	1	AAQ75721
	703	19.4	0.7	21	1	AAF24290
	704	19.4	0.7	21	1	ABX79794
c	705	19.4	0.7	23	1	AAQ30431
c	706	19.4	0.7	23	1	AAQ30430
	707	19.4	0.7	23	1	ABL01773
	708	19.4	0.7	24	1	AAH24266
	709	19.4	0.7	24	1	ABN85073
c	710	19.4	0.7	24	1	ABK91269
	711	19.4	0.7	24	1	ABZ23536
c	712	19.4	0.7	24	1	ABZ23536
c	713	19.4	0.7	25	1	AAV42215
c	714	19.4	0.7	25	1	AAX84259
	715	19.4	0.7	25	1	ABZ23535
c	716	19.4	0.7	26	1	AAS20595
c	717	19.4	0.7	26	1	ABS52637
c	718	19.4	0.7	26	1	AAD45054
c	719	19.4	0.7	26	1	AAD55692
c	720	19.4	0.7	26	1	ABX93598
c	721	19.4	0.7	26	1	ACF36382
	722	19.4	0.7	26	1	AAV35002
c	723	19.4	0.7	26	1	AAF74913
c	724	19.4	0.7	27	1	ABQ76254
c	725	19.4	0.7	27	1	AAF74926
c	726	19.4	0.7	27	1	AAF74932
c	727	19.4	0.7	27	1	AAF74931
c	728	19.4	0.7	27	1	AAF74934
	729	19.4	0.7	28	1	AAT13977
	730	19.4	0.7	28	1	AAT70108
	731	19.4	0.7	28	1	AAT70106
	732	19.4	0.7	28	1	AAT70107
	733	19.4	0.7	28	1	AAV65735
	734	19.4	0.7	28	1	AAX05727
c	735	19.4	0.7	28	1	AAF74920
c	736	19.4	0.7	28	1	AAF74906
c	737	19.4	0.7	28	1	AAF74916
c	738	19.4	0.7	28	1	AAF74927
	739	19.4	0.7	28	1	AAF60450
	740	19.4	0.7	28	1	AAL45359
	741	19.4	0.7	28	1	ABZ70568
	742	19.4	0.7	29	1	AAQ49467
c	743	19.4	0.7	29	1	AAF74918
c	744	19.4	0.7	29	1	AAF74907
c	745	19.4	0.7	29	1	AAF74935
c	746	19.4	0.7	29	1	AAF74921
c	747	19.4	0.7	29	1	AAF74928
	748	19.4	0.7	29	1	AAH28298
c	749	19.4	0.7	29	1	AAD33515
c	750	19.4	0.7	29	1	AAD33516
c	751	19.4	0.7	30	1	ADC16682
	752	19.4	0.7	33	1	ACC42844
	753	19.2	0.7	21	1	ACC48482
c	754	19.2	0.7	21	1	ACC48482
	755	19.2	0.7	21	1	ACC99729
c	756	19.2	0.7	21	1	ACC99729
c	757	19.2	0.7	22	1	AAL50570
c	758	19.2	0.7	22	1	ABX74887
c	759	19.2	0.7	22	1	ACC48484
c	760	19.2	0.7	22	1	ACC48485
c	761	19.2	0.7	22	1	ACC48483
c	762	19.2	0.7	22	1	AAD51324
c	763	19.2	0.7	23	1	ABK13916

Reverse transcript
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Complementary nucl
EST polymorphic DN
Oligomer IL6804 fo
Oligomer IL6803 fo
Human MSH2 (hMSH2)
Human phosphatase
Human S4 ribosomal
Leukaemia related
fragment of a plas
fragment of a plas
Sequencing primer
PCR primer for hum
fragment of a plas
Human zsig63 cDNA
Human secreted sal
ZC7231 primer used
Bovine viral diarr
Human zsig63 PCR/s
Nucleotide sequenc
Human endothelin-b
CD40L poly-A tract
Murine SCCE 5'-RAC
CD40L poly-A tract
CD40L poly-A tract
CD40L poly-A tract
CD40L poly-A tract
E. spinifera fumon
PolyTV primer 3.
PolyTV primer 1.
PolyTV primer 2.
A. phoenices APOXD
E. spinifera fumon
CD40L poly-A tract
CD40L poly-A tract
CD40L poly-A tract
CD40L poly-A tract
RNA oligonucleotid
Puromycin linker D
5' RACE primer Bam
Oligo-dT primer "n
CD40L poly-A tract
CD40L poly-A tract
CD40L poly-A tract
CD40L poly-A tract
CD40L poly-A tract
3' untranslated re
T7T18Apad_PS6-29-0
T7T18Apad_PS18-29-
Aminoacylation RNA
Nuclear transition
Locked nucleic aci
Locked nucleic aci
Oligonucleotide.
Oligonucleotide.
Molecular array pr
Oligo-dT primer us
Locked nucleic aci
Locked nucleic aci
Locked nucleic aci
Anchored oligo dT
3'-PCR primer used

c	764	19.2	0.7	24	1	ABK48140
	765	19.2	0.7	24	1	AAT99286
	766	19.2	0.7	24	1	AAV31743
	767	19.2	0.7	24	1	AAX04086
c	768	19.2	0.7	24	1	AAA40359
c	769	19.2	0.7	24	1	AAA40353
c	770	19.2	0.7	24	1	AAF99756
c	771	19.2	0.7	24	1	AAF99304
	772	19.2	0.7	24	1	AAF99757
c	773	19.2	0.7	24	1	ABV14842
c	774	19.2	0.7	24	1	ABS78477
c	775	19.2	0.7	24	1	ABS77949
	776	19.2	0.7	24	1	ABS78478
c	777	19.2	0.7	24	1	ABL39405
	778	19.2	0.7	24	1	ABA98840
	779	19.2	0.7	24	1	AAS17869
c	780	19.2	0.7	24	1	ABK15639
c	781	19.2	0.7	24	1	ACA58802
c	782	19.2	0.7	24	1	ABZ80181
c	783	19.2	0.7	24	1	ACA62284
c	784	19.2	0.7	24	1	ACD99729
	785	19.2	0.7	24	1	ACH03285
c	786	19.2	0.7	24	1	ACH03284
	787	19.2	0.7	24	1	ADA66379
c	788	19.2	0.7	24	1	ADB37258
c	789	19.2	0.7	24	1	ADB36806
	790	19.2	0.7	24	1	ADB37259
c	791	19.2	0.7	24	1	ADD31867
c	792	19.2	0.7	24	1	ADE25524
	793	19.2	0.7	24	1	ABA97997
	794	19.2	0.7	24	1	ABL55130
	795	19.2	0.7	24	1	ABA98547
	796	19.2	0.7	24	1	ADD06134
c	797	19.2	0.7	25	1	AAQ95960
c	798	19.2	0.7	25	1	AAX84258
c	799	19.2	0.7	25	1	AAA39306
c	800	19.2	0.7	25	1	AAZ30267
c	801	19.2	0.7	25	1	ABK49986
c	802	19.2	0.7	25	1	ADC54009
	803	19.2	0.7	25	1	ADC54008
c	804	19.2	0.7	25	1	ABK86170
	805	19.2	0.7	25	1	AAC96700
c	806	19.2	0.7	25	1	ABL45245
c	807	19.2	0.7	26	1	AAX07466
c	808	19.2	0.7	26	1	AAX78723
c	809	19.2	0.7	27	1	AAV71936
c	810	19.2	0.7	27	1	ABS53863
c	811	19.2	0.7	27	1	ABS54324
	812	19.2	0.7	27	1	AAL47309
c	813	19.2	0.7	28	1	AAA40362
c	814	19.2	0.7	28	1	AAA40358
	815	19.2	0.7	28	1	AAQ52308
	816	19.2	0.7	29	1	ABN83378
c	817	19.2	0.7	29	1	AAL44903
	818	19.2	0.7	29	1	AAA71176
	819	19.2	0.7	29	1	AAA71193
c	820	19.2	0.7	29	1	AAF74917
c	821	19.2	0.7	29	1	AAF74929
c	822	19.2	0.7	32	1	ABS53433
c	823	19.2	0.7	32	1	AAQ43973
c	824	19.2	0.7	33	1	AAL44170
	825	19.2	0.7	35	1	ABQ80396
c	826	19.2	0.7	37	1	AAF85682
	827	19	0.7	19	1	AAQ75552
c	828	19	0.7	19	1	AAQ75556
	829	19	0.7	19	1	AAT10757
c	830	19	0.7	19	1	AAT10757
	831	19	0.7	19	1	AAV07878
c	832	19	0.7	19	1	AAV07878
	833	19	0.7	19	1	AAV06820
c	834	19	0.7	19	1	AAV06820
	835	19	0.7	19	1	AAX81316
c	836	19	0.7	19	1	AAX81316

Aspergillus niger
POLYA, a competito
Nucleotide sequenc
Oligonucleotide PO
pBluescriptSK+ pha
pBluescriptSK+ pha
Immunostimulatory
Immunostimulatory
Immunostimulatory
Human prostate exp
Angiogenesis inhib
Angiogenesis inhib
Angiogenesis inhib
Immunostimulatory
A24 oligonucleotid
A24 oligonucleotid
RNA-PCR procedure
Gastric ulcer trea
Immunostimulatory
Oligo (dT)24 RT-PC
Immunostimulatory
Immunostimulatory
Immunostimulatory
mRNA poly A. Unid
Immunostimulatory
Immunostimulatory
Immunostimulatory
Butterfly biliverd
Rolling circle amp
Human mitochondria
Human gonadotropin
Insulin-like growt
N-acetylgalactosam
Oligonucleotide bi
PCR primer for hum
Rapid capture prob
Capture probe CP12
Example oligonucle
Oligonucleotide of
Oligonucleotide of
Oligo dT primer #3
HLA HLA-A gene PCR
Human chromosome 1
Human BS124 specif
Human pancreatic p
Anchored poly T RT
Human androgen rec
Human ARCAP associ
Intracellular targ
pBluescriptSK+ pha
pBluescriptSK+ pha
FKBP12C PCR primer
Mononucleotide rep
Triplex forming ol
Molecular interact
Molecular interact
CD40L poly-A tract
CD40L poly-A tract
First strand synth
Triple helix formi
Porphyra yezoensis
Probe APC 2. Homo
Pea blight resista
Reverse transcript
Reverse transcript
Oligonucleotide pr
Oligonucleotide pr
Aminooxy-modified
Aminooxy-modified
Oligonucleotide co
Oligonucleotide co
5' amino oligonucl
5' amino oligonucl

	837	19	0.7	19	1	AAX81927
c	838	19	0.7	19	1	AAX81927
	839	19	0.7	19	1	AAZ01358
c	840	19	0.7	19	1	AAZ01358
	841	19	0.7	19	1	AAZ61390
c	842	19	0.7	19	1	AAZ61390
	843	19	0.7	19	1	AAZ61404
c	844	19	0.7	19	1	AAZ61404
	845	19	0.7	19	1	AAC62422
c	846	19	0.7	19	1	AAC62422
	847	19	0.7	19	1	AAZ95241
c	848	19	0.7	19	1	AAZ95241
	849	19	0.7	19	1	AAZ95240
c	850	19	0.7	19	1	AAZ95240
	851	19	0.7	19	1	AAA06839
c	852	19	0.7	19	1	AAA06839
	853	19	0.7	19	1	AAA88952
c	854	19	0.7	19	1	AAA88952
	855	19	0.7	19	1	AAA88965
c	856	19	0.7	19	1	AAA88965
	857	19	0.7	19	1	AAA88949
c	858	19	0.7	19	1	AAA88949
	859	19	0.7	19	1	AAA88950
c	860	19	0.7	19	1	AAA88950
	861	19	0.7	19	1	AAA88951
c	862	19	0.7	19	1	AAA88951
	863	19	0.7	19	1	AAA88947
c	864	19	0.7	19	1	AAA88947
	865	19	0.7	19	1	AAA88948
c	866	19	0.7	19	1	AAA88948
	867	19	0.7	19	1	AAA71630
c	868	19	0.7	19	1	AAA71630
	869	19	0.7	19	1	AAC62454
c	870	19	0.7	19	1	AAC62454
	871	19	0.7	19	1	AAF31458
c	872	19	0.7	19	1	AAF31458
	873	19	0.7	19	1	AAF31564
c	874	19	0.7	19	1	AAF31564
	875	19	0.7	19	1	AAH46460
c	876	19	0.7	19	1	AAH46460
	877	19	0.7	19	1	AAH25737
c	878	19	0.7	19	1	AAH25737
	879	19	0.7	19	1	AAH25738
c	880	19	0.7	19	1	AAH25738
	881	19	0.7	19	1	AAC83664
c	882	19	0.7	19	1	AAC83664
	883	19	0.7	19	1	AAK98526
c	884	19	0.7	19	1	AAK98526
	885	19	0.7	19	1	ABA91949
c	886	19	0.7	19	1	ABA91949
	887	19	0.7	19	1	ABA91951
c	888	19	0.7	19	1	ABA91951
	889	19	0.7	19	1	ABA91950
c	890	19	0.7	19	1	ABA91950
	891	19	0.7	19	1	ABL51520
c	892	19	0.7	19	1	ABL51520
	893	19	0.7	19	1	AAD42000
c	894	19	0.7	19	1	AAD42000
	895	19	0.7	19	1	AAD42002
c	896	19	0.7	19	1	AAD42002
	897	19	0.7	19	1	AAD42004
c	898	19	0.7	19	1	AAD42004
	899	19	0.7	19	1	AAD42010
c	900	19	0.7	19	1	AAD42010
	901	19	0.7	19	1	AAD42020
c	902	19	0.7	19	1	AAD42020
	903	19	0.7	19	1	AAD42001
c	904	19	0.7	19	1	AAD42001
	905	19	0.7	19	1	AAD42011
c	906	19	0.7	19	1	AAD42011
	907	19	0.7	19	1	AAD42005
c	908	19	0.7	19	1	AAD42005
	909	19	0.7	19	1	AAD42003

Polynucleotide str
Polynucleotide str
PCR primer for PG1
PCR primer for PG1
Uniform phosphodie
Uniform phosphodie
2'-O-modified ribo
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T19 diester for us
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Modified oligonucl
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Oligonucleotide IS
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2'-Modified chimer
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Phosphorothioate 2
Phosphorothioate 2
Cleavage of nuclei
Cleavage of nuclei
Oligonucleotide IS
Oligonucleotide IS
ISIS sequence 3232
ISIS sequence 3232
Oligonucleotide #8
Oligonucleotide #8
Human type II RNas
Human type II RNas
Human type II RNas
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2'-O-N-[2-(dimethy
2'-O-N-[2-(dimethy
Nucleic acid quant
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Methyl thioethyl m
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Dimethylaminopropy
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Methoxyethoxy modi
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Tailing reaction r
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Oligonucleotide #3
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Oligonucleotide #1
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Oligonucleotide #2
Oligonucleotide #2
Oligonucleotide #4
Oligonucleotide #4
Oligonucleotide #1
Oligonucleotide #1
Oligonucleotide #8
Oligonucleotide #8
Oligonucleotide #6

c	910	19	0.7	19	1	AAD42003
	911	19	0.7	19	1	AAD41998
c	912	19	0.7	19	1	AAD41998
	913	19	0.7	19	1	AAD41999
c	914	19	0.7	19	1	AAD41999
	915	19	0.7	19	1	AAD42009
c	916	19	0.7	19	1	AAD42009
	917	19	0.7	19	1	ABZ58336
c	918	19	0.7	19	1	ABZ58336
c	919	19	0.7	20	1	AAQ25565
c	920	19	0.7	20	1	AAQ33554
	921	19	0.7	20	1	AAQ58578
c	922	19	0.7	20	1	AAQ94205
c	923	19	0.7	20	1	AAQ90405
c	924	19	0.7	20	1	AAV07752
c	925	19	0.7	20	1	AAT63649
	926	19	0.7	20	1	AAV34591
c	927	19	0.7	20	1	AAT86606
c	928	19	0.7	20	1	AAX27533
	929	19	0.7	20	1	AAZ11326
	930	19	0.7	20	1	AAA40449
c	931	19	0.7	20	1	AAA40448
c	932	19	0.7	20	1	AAZ91117
c	933	19	0.7	20	1	AAA50193
c	934	19	0.7	20	1	AAC87238
c	935	19	0.7	20	1	AAC87230
c	936	19	0.7	20	1	AAC87241
c	937	19	0.7	20	1	AAS10402
c	938	19	0.7	20	1	AAD16997
	939	19	0.7	20	1	AAF60896
	940	19	0.7	20	1	AAS63428
	941	19	0.7	20	1	AAF28481
	942	19	0.7	20	1	AAS10371
c	943	19	0.7	20	1	AAF99427
c	944	19	0.7	20	1	AAF99099
	945	19	0.7	20	1	AAF99431
c	946	19	0.7	20	1	AAH46465
	947	19	0.7	20	1	AAH78547
	948	19	0.7	20	1	AAF28351
c	949	19	0.7	20	1	ABS77742
c	950	19	0.7	20	1	ABS78072
	951	19	0.7	20	1	ABS78076
c	952	19	0.7	20	1	ABL39402
	953	19	0.7	20	1	ABL38648
c	954	19	0.7	20	1	ABL39403
c	955	19	0.7	20	1	ABL54775
	956	19	0.7	20	1	ABK65035
	957	19	0.7	20	1	ABK65050
c	958	19	0.7	20	1	AAL45122
	959	19	0.7	20	1	ABL36232
	960	19	0.7	20	1	ABS64673
	961	19	0.7	20	1	ABS64688
c	962	19	0.7	20	1	ABN87103
	963	19	0.7	20	1	ABZ88267
	964	19	0.7	20	1	ABZ88565
	965	19	0.7	20	1	ABZ88619
	966	19	0.7	20	1	ABZ89705
	967	19	0.7	20	1	ABZ88816
	968	19	0.7	20	1	ABZ88881
	969	19	0.7	20	1	ABZ89706
	970	19	0.7	20	1	ABZ88620
	971	19	0.7	20	1	ABZ88880
	972	19	0.7	20	1	ABZ89179
	973	19	0.7	20	1	ABZ88814
	974	19	0.7	20	1	ABZ89241
	975	19	0.7	20	1	ABZ90650
	976	19	0.7	20	1	ABZ99050
	977	19	0.7	20	1	ABZ88815
c	978	19	0.7	20	1	ABZ85311
c	979	19	0.7	20	1	ABZ85435
	980	19	0.7	20	1	ABZ88817
	981	19	0.7	20	1	ABZ88939
	982	19	0.7	20	1	ABZ89302

Oligonucleotide #6
Oligonucleotide #1
Oligonucleotide #1
Oligonucleotide #2
Oligonucleotide #2
Oligonucleotide #1
Oligonucleotide #1
Oligonucleotide wi
Oligonucleotide wi
Dye-coupled 3'-ami
Microsatellite seq
Sequence of synthe
Alpha-anomeric oli
T2 (synthetic DNA
Phosphorothioate o
Anti-HTLV antisens
M. vaccae antigeni
Oligonucleotide se
Synthetic RNA sequ
Mycobacterial 16S
Electochemical det
Electochemical det
Oligonucleotide #5
2'-Methoxyethoxy-m
Phosphorothioate p
Digoxigenin-labell
Poly T oligonucleo
DNA template for 3
Capture probe CP5'
Conjugate forming
Oligonucleotide-na
Random oligonucleo
Oligonucleotide-cy
Immunostimulatory
Immunostimulatory
Immunostimulatory
Oligonucleotide #1
Nucleotide sequenc
DNA oligomer #1.
Angiogenesis inhib
Angiogenesis inhib
Angiogenesis inhib
Immunostimulatory
Immunostimulatory
Immunostimulatory
CD14 receptor PCR
Nanoparticle-oligo
Nanoparticle-oligo
Oligonucleotide sy
M tuberculosis rRN
Nucleic acid detec
Nucleic acid detec
Capture probe CP5'
Human oligonucleot
Human oligonucleot
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983	19	0.7	20	1	ABZ87681	Human oligonucleot
984	19	0.7	20	1	ABZ88566	Human oligonucleot
985	19	0.7	20	1	ABZ89086	Human oligonucleot
986	19	0.7	20	1	ABZ85533	Human oligonucleot
987	19	0.7	20	1	ABZ89015	Human oligonucleot
988	19	0.7	20	1	ABZ89441	Human oligonucleot
989	19	0.7	20	1	ABZ89016	Human oligonucleot
990	19	0.7	20	1	ABZ89120	Human oligonucleot
991	19	0.7	20	1	ABZ89704	Nanotechnology nuc
992	19	0.7	20	1	ACD27320	Doubly labelled DN
c 993	19	0.7	20	1	ACC58867	Phosphorothioate 2
c 994	19	0.7	20	1	ABZ22916	Thiol-modified oli
995	19	0.7	20	1	AAL61645	Potato gene PCR pr
c 996	19	0.7	20	1	ABZ59815	Thio-modified 20dA
997	19	0.7	20	1	ABX79181	Nanoparticle-assoc
998	19	0.7	20	1	ABX92177	Nanotechnology nuc
999	19	0.7	20	1	ACD27255	Nanotechnology nuc
1000	19	0.7	20	1	ACD27125	Nanotechnology nuc
1001	19	0.7	20	1	ACD27385	Nanotechnology nuc
1002	19	0.7	20	1	ACD27190	Nanotechnology nuc
1003	19	0.7	20	1	ACD27060	Nanotechnology nuc
1004	19	0.7	20	1	ACH00064	Immunostimulatory
1005	19	0.7	20	1	ACD99851	Immunostimulatory
c1006	19	0.7	20	1	ACD99847	Immunostimulatory
c1007	19	0.7	20	1	ACD99532	Hairpin target seq
1008	19	0.7	20	1	ADA14838	Nanoparticle label
1009	19	0.7	20	1	ADA06159	Nanotechnology nuc
1010	19	0.7	20	1	ACD26995	Immunostimulatory
1011	19	0.7	20	1	ADB36933	Immunostimulatory
c1012	19	0.7	20	1	ADB36601	Immunostimulatory
c1013	19	0.7	20	1	ADB36929	Reverse transcript
c1014	19	0.7	20	1	AAQ75598	Reverse transcript
1015	19	0.7	20	1	AAQ75579	Reverse transcript
c1016	19	0.7	20	1	AAQ75597	Reverse transcript
1017	19	0.7	20	1	AAQ75581	Reverse transcript
c1018	19	0.7	20	1	AAQ75595	Reverse transcript
1019	19	0.7	20	1	AAQ75580	Mammalian stem cel
1020	19	0.7	20	1	AAT04916	Mammalian stem cel
c1021	19	0.7	20	1	AAT04918	Stem cell factor u
1022	19	0.7	20	1	AAA13753	Stem cell factor u
c1023	19	0.7	20	1	AAA13754	Antisense IGFBP-5
c1024	19	0.7	20	1	AAA91207	Universal stem cel
1025	19	0.7	20	1	AAH41332	Universal stem cel
c1026	19	0.7	20	1	AAH41333	Human SCF (stem ce
1027	19	0.7	20	1	AAS04112	Human SCF (stem ce
c1028	19	0.7	20	1	AAS04113	Mammalian stem cel
1029	19	0.7	20	1	AAF89092	Mammalian stem cel
c1030	19	0.7	20	1	AAF89093	Aminopurine substi
c1031	19	0.7	20	1	AAS05714	8-aminopurine subs
1032	19	0.7	20	1	AAS05715	Human SCF (stem ce
c1033	19	0.7	20	1	AAH23891	Human SCF (stem ce
1034	19	0.7	20	1	AAH23890	Human SCF (stem ce
1035	19	0.7	20	1	AAS04213	Human SCF (stem ce
c1036	19	0.7	20	1	AAS04214	Human stem cell fa
c1037	19	0.7	20	1	AAS10449	Human stem cell fa
1038	19	0.7	20	1	AAS10448	Rat SCF 5' cDNA am
1039	19	0.7	20	1	AAD35465	Rat SCF 5' cDNA am
c1040	19	0.7	20	1	AAD35466	SCF universal olig
1041	19	0.7	20	1	ABS73849	SCF universal olig
c1042	19	0.7	20	1	ABS73850	Human oligonucleot
1043	19	0.7	20	1	ABZ88618	Human oligonucleot
c1044	19	0.7	20	1	ABZ88618	Human oligonucleot
c1045	19	0.7	20	1	ABZ89678	Human oligonucleot
c1046	19	0.7	20	1	ABZ89677	Human oligonucleot
1047	19	0.7	20	1	ABZ89085	Human oligonucleot
c1048	19	0.7	20	1	ABZ88694	Human oligonucleot
c1049	19	0.7	20	1	ABZ89240	Stem cell factor (
c1050	19	0.7	20	1	ADE52462	Stem cell factor (
1051	19	0.7	20	1	ADE52461	Primer used to rev
c1052	19	0.7	21	1	AAX26973	Protein kinase inh
c1053	19	0.7	21	1	AAZ44350	Immunostimulatory
c1054	19	0.7	21	1	AAF99707	Oligonucleotide us
c1055	19	0.7	21	1	AAH42480	Angiogenesis inhib
c1056	19	0.7	21	1	ABS78428	Immunostimulatory
c1057	19	0.7	21	1	ABL39404	Regular oligo dT p
c1058	19	0.7	21	1	AAD51323	Immunostimulatory
c1059	19	0.7	21	1	ACH03246	Immunostimulatory
c1060	19	0.7	21	1	ADB37209	CP-1 (synthetic DN
1061	19	0.7	21	1	AAQ90391	Oligonucleotide pr
1062	19	0.7	21	1	AAT10743	3' ribonucleoside
1063	19	0.7	21	1	AAX81302	Reverse transcript
1064	19	0.7	21	1	AAQ75724	Reverse transcript
c1065	19	0.7	21	1	AAQ75752	Reverse transcript
c1066	19	0.7	21	1	AAQ75762	Reverse transcript
1067	19	0.7	21	1	AAQ75719	Reverse transcript
1068	19	0.7	21	1	AAQ75730	Reverse transcript
c1069	19	0.7	21	1	AAQ75763	Reverse transcript
1070	19	0.7	21	1	AAQ75728	Reverse transcript
1071	19	0.7	21	1	AAQ75727	Reverse transcript
c1072	19	0.7	21	1	AAQ75764	Reverse transcript
1073	19	0.7	21	1	AAQ75722	Reverse transcript
1074	19	0.7	21	1	AAQ75723	Reverse transcript
c1075	19	0.7	21	1	AAQ75760	Reverse transcript
c1076	19	0.7	21	1	AAQ75751	Reverse transcript
c1077	19	0.7	21	1	AAQ75754	Reverse transcript
c1078	19	0.7	21	1	AAQ75759	Reverse transcript
1079	19	0.7	21	1	AAQ75720	HIV-1 gag protein
c1080	19	0.7	21	1	AAQ75766	HIV-1 gag protein
1081	19	0.7	21	1	AAV35395	2',5'-linked tetra
c1082	19	0.7	21	1	AAV35395	L1 cleavage site r
1083	19	0.7	22	1	AAQ64724	Amino modified oli
1084	19	0.7	22	1	AAF17413	Cleavage of nuclei
1085	19	0.7	22	1	AAT92356	Cleavage of nuclei
c1086	19	0.7	23	1	AAC62450	Gastric acid produ
c1087	19	0.7	23	1	AAC62451	Primer #1 for tiss
c1088	19	0.7	23	1	AAF16627	Double-anchored ol
1089	19	0.7	23	1	AAT33701	Synthetic oligonuc
1090	19	0.7	23	1	AAV61554	Oligonucleotide pr
1091	19	0.7	23	1	AAA29753	Murine osteoporosi
1092	19	0.7	23	1	AAA08407	Oligo dT primer #4
1093	19	0.7	23	1	ABA99682	DNA probe used in
c1094	19	0.7	24	1	ABK86172	Human gonadotropin
1095	19	0.7	24	1	AAT68615	Human CYP2D6 gene
c1096	19	0.7	24	1	ABL55130	SNP specific SNPE
1097	19	0.7	25	1	AAD34264	Cytochrome P450ox
c1098	19	0.7	25	1	AAH38515	Deoxy-A22-tagged s
1099	19	0.7	25	1	AAV57477	Regulatable, catal
1100	19	0.7	28	1	AAA57855	Substrate RNA rela
1101	19	0.7	28	1	AAL43065	Human haemoglobin
1102	19	0.7	28	1	ADA39569	HS/HIP reverse tra
1103	19	0.7	28	1	AAS11744	Oligo dT primer fo
1104	19	0.7	28	1	AAV61015	Single stranded DN
1105	19	0.7	28	1	AAZ61254	Tobacco PMT PCR pr
1106	19	0.7	28	1	AAI71210	tRNAPolyU reverse
c1107	19	0.7	29	1	AAQ79096	Reverse tRNA prime
1108	19	0.7	29	1	AAQ68614	Rat type I steroid
1109	19	0.7	29	1	AAT09934	Primer for rat ste
c1110	19	0.7	29	1	AAQ97396	Hepatitis E virus
c1111	19	0.7	29	1	AAT99803	Rice semi-dwarf (s
1112	19	0.7	29	1	AAI69697	APC binding protei
1113	19	0.7	29	1	ADA26182	Oligonucleotide-na
c1114	19	0.7	30	1	AAF26222	Oligonucleotide-cy
1115	19	0.7	30	1	AAS63441	Nanoparticle-oligo
1116	19	0.7	30	1	AAS10385	Nucleic acid detec
1117	19	0.7	30	1	ABK65048	Oligonucleotide #1
1118	19	0.7	30	1	ABS64686	Sindbis virus mRNA
1119	19	0.7	30	1	AAL61658	Sindbis virus 3' R
c1120	19	0.7	30	1	AAX77343	APC binding protei
c1121	19	0.7	30	1	AAA90394	Structural product
1122	19	0.7	30	1	AAF26221	Neuraminidase PCR
c1123	19	0.7	31	1	AAQ43410	Primer B for Non-A
c1124	19	0.7	32	1	AAF60568	Rat fibroblast gro
c1125	19	0.7	32	1	AAV03988	Oligonucleotide-na
c1126	19	0.7	32	1	AAT77235	Alkanethiol-modifi
1127	19	0.7	32	1	AAS63424	
1128	19	0.7	32	1	AAS10367	

1129	19	0.7	32	1	ABK65031	Nanoparticle-oligo
1130	19	0.7	32	1	ABS64669	Nucleic acid detec
1131	19	0.7	32	1	ACD27316	Nanotechnology nuc
1132	19	0.7	32	1	AAL61641	Thiol-modified oli
1133	19	0.7	32	1	ABX79177	Fluorescein-labell
1134	19	0.7	32	1	ABX92173	Nanoparticle-assoc
1135	19	0.7	32	1	ACD27251	Nanotechnology nuc
1136	19	0.7	32	1	ACD27121	Nanotechnology nuc
1137	19	0.7	32	1	ACD27381	Nanotechnology nuc
1138	19	0.7	32	1	ACD27186	Nanotechnology nuc
1139	19	0.7	32	1	ACD27056	Nanotechnology nuc
1140	19	0.7	32	1	ACH00060	Nanotechnology nuc
1141	19	0.7	32	1	ADA06155	Nanoparticle label
1142	19	0.7	32	1	ACD26991	Nanotechnology nuc
1143	19	0.7	32	1	ADE71592	Magneto-gold nanop
1144	19	0.7	33	1	ABQ80395	Probe APC 1-MUT.
1145	19	0.7	33	1	ABQ80394	Probe APC 1-WT. H
c1146	19	0.7	33	1	ADC60749	Termitomyces album
c1147	19	0.7	33	1	ABK15694	Human activating G
c1148	19	0.7	34	1	AAA75564	PCR primer for DNA
c1149	19	0.7	34	1	AAD09727	ZC18698 primer, to
c1150	19	0.7	34	1	AAS20662	Primer ZC18698 ued
c1151	19	0.7	34	1	ADD68172	PCR primer relatin
c1152	19	0.7	35	1	AAX14632	Triple helix formi
c1153	19	0.7	41	1	ABZ46327	Human aldehyde deh
c1154	19	0.7	41	1	ABZ48839	Human aldehyde deh
c1155	18.8	0.7	22	1	ABA93238	PolyA adaptor olig
1156	18.8	0.7	24	1	ABV77669	Human zinc finger
1157	18.8	0.7	24	1	AAH75510	Human CCR4 related
1158	18.8	0.7	24	1	AAH44623	Human FD 17 PCR pr
1159	18.8	0.7	24	1	ABK13715	RT-PCR primer #2 f
1160	18.8	0.7	25	1	AAC96267	HLA DPA1 gene PCR
1161	18.8	0.7	25	1	AAC96268	HLA DPA1 gene PCR
1162	18.8	0.7	25	1	ABA03917	Human connexin 9 P
c1163	18.8	0.7	27	1	AAF74933	CD40L poly-A tract
1164	18.6	0.7	25	1	AAC96079	16s rRNA gene PCR
1165	18.6	0.7	25	1	AAC95686	HLA DPB1 gene PCR
c1166	18.6	0.7	25	1	AAC96214	16s rRNA gene PCR
1167	18.6	0.7	25	1	AAC96367	HLA DPB1 gene PCR
c1168	18.6	0.7	25	1	ACI00608	Human microarray D
c1169	18.6	0.7	25	1	ACI61005	Human microarray D
1170	18.6	0.7	26	1	AAA88688	Oligo-dT-XhoI prim
1171	18.4	0.7	20	1	AAQ75596	Reverse transcript
1172	18.4	0.7	20	1	ABZ85312	Human oligonucleot
1173	18.4	0.7	20	1	ABZ89546	Human oligonucleot
1174	18.4	0.7	20	1	AAQ75598	Reverse transcript
c1175	18.4	0.7	20	1	AAQ75581	Reverse transcript
c1176	18.4	0.7	20	1	AAQ75580	Reverse transcript
c1177	18.4	0.7	20	1	ABZ89085	Human oligonucleot
1178	18.4	0.7	20	1	ABZ88694	Human oligonucleot
1179	18.4	0.7	20	1	AAQ49436	Cytochrome P450 se
1180	18.4	0.7	20	1	AAQ75566	Reverse transcript
1181	18.4	0.7	20	1	AAQ75569	Reverse transcript
1182	18.4	0.7	20	1	AAQ75584	Reverse transcript
1183	18.4	0.7	20	1	AAQ75585	Reverse transcript
1184	18.4	0.7	20	1	AAQ75568	Reverse transcript
c1185	18.4	0.7	20	1	AAQ75570	Reverse transcript
c1186	18.4	0.7	20	1	AAQ75572	Reverse transcript
1187	18.4	0.7	20	1	AAQ75586	Reverse transcript
c1188	18.4	0.7	20	1	AAQ75586	Reverse transcript
1189	18.4	0.7	20	1	AAQ75589	Reverse transcript
c1190	18.4	0.7	20	1	AAQ75604	Reverse transcript
c1191	18.4	0.7	20	1	AAQ75588	Reverse transcript
1192	18.4	0.7	20	1	AAQ75601	Reverse transcript
1193	18.4	0.7	20	1	AAQ75564	Reverse transcript
c1194	18.4	0.7	20	1	AAQ75564	Reverse transcript
1195	18.4	0.7	20	1	AAQ75600	Reverse transcript
c1196	18.4	0.7	20	1	AAQ75600	Reverse transcript
1197	18.4	0.7	20	1	AAQ75578	Reverse transcript
1198	18.4	0.7	20	1	AAQ75590	Reverse transcript
c1199	18.4	0.7	20	1	AAQ75602	Reverse transcript
c1200	18.4	0.7	20	1	AAQ75592	Reverse transcript
c1201	18.4	0.7	20	1	ABZ88266	Human oligonucleot
c1202	18.4	0.7	20	1	ABZ85534	Human oligonucleot
c1203	18.4	0.7	20	1	ABZ92865	Human oligonucleot
c1204	18.4	0.7	20	1	ABZ88938	Human oligonucleot
1205	18.4	0.7	20	1	ABZ88813	Reverse transcript
1206	18.4	0.7	21	1	AAQ75757	Reverse transcript
1207	18.4	0.7	21	1	AAQ75756	Reverse transcript
1208	18.4	0.7	21	1	AAQ75755	Reverse transcript
c1209	18.4	0.7	21	1	AAQ75630	Reverse transcript
1210	18.4	0.7	21	1	AAQ75629	Reverse transcript
1211	18.4	0.7	21	1	AAQ75773	Reverse transcript
1212	18.4	0.7	21	1	AAQ75684	Reverse transcript
c1213	18.4	0.7	21	1	AAQ75726	Reverse transcript
c1214	18.4	0.7	21	1	AAQ75685	Reverse transcript
c1215	18.4	0.7	21	1	AAQ75772	Reverse transcript
c1216	18.4	0.7	21	1	AAQ75724	Reverse transcript
c1217	18.4	0.7	21	1	AAQ75730	Reverse transcript
1218	18.4	0.7	21	1	AAQ75763	Reverse transcript
c1219	18.4	0.7	21	1	AAQ75728	Reverse transcript
c1220	18.4	0.7	21	1	AAQ75727	Reverse transcript
1221	18.4	0.7	21	1	AAQ75764	Reverse transcript
c1222	18.4	0.7	21	1	AAQ75723	Reverse transcript
1223	18.4	0.7	21	1	AAQ75766	Reverse transcript
c1224	18.4	0.7	21	1	AAQ75651	Reverse transcript
1225	18.4	0.7	21	1	AAQ75702	Reverse transcript
c1226	18.4	0.7	21	1	AAQ75661	Reverse transcript
1227	18.4	0.7	21	1	AAQ75675	Reverse transcript
1228	18.4	0.7	21	1	AAQ75771	Reverse transcript
c1229	18.4	0.7	21	1	AAQ75771	Reverse transcript
1230	18.4	0.7	21	1	AAQ75627	Reverse transcript
c1231	18.4	0.7	21	1	AAQ75627	Reverse transcript
c1232	18.4	0.7	21	1	AAQ75693	Reverse transcript
c1233	18.4	0.7	21	1	AAQ75739	Reverse transcript
1234	18.4	0.7	21	1	AAQ75778	Reverse transcript
c1235	18.4	0.7	21	1	AAQ75778	Reverse transcript
c1236	18.4	0.7	21	1	AAQ75787	Reverse transcript
1237	18.4	0.7	21	1	AAQ75643	Reverse transcript
c1238	18.4	0.7	21	1	AAQ75781	Reverse transcript
1239	18.4	0.7	21	1	AAQ75695	Reverse transcript
1240	18.4	0.7	21	1	AAQ75718	Reverse transcript
1241	18.4	0.7	21	1	AAQ75646	Reverse transcript
1242	18.4	0.7	21	1	AAQ75650	Reverse transcript
c1243	18.4	0.7	21	1	AAQ75650	Reverse transcript
1244	18.4	0.7	21	1	AAQ75682	Reverse transcript
c1245	18.4	0.7	21	1	AAQ75682	Reverse transcript
1246	18.4	0.7	21	1	AAQ75678	Reverse transcript
c1247	18.4	0.7	21	1	AAQ75694	Reverse transcript
1248	18.4	0.7	21	1	AAQ75700	Reverse transcript
c1249	18.4	0.7	21	1	AAQ75742	Reverse transcript
c1250	18.4	0.7	21	1	AAQ75659	Reverse transcript
1251	18.4	0.7	21	1	AAQ75715	Reverse transcript
1252	18.4	0.7	21	1	AAQ75716	Reverse transcript
c1253	18.4	0.7	21	1	AAQ75740	Reverse transcript
c1254	18.4	0.7	21	1	AAQ75779	Reverse transcript
1255	18.4	0.7	21	1	AAQ75628	Reverse transcript
c1256	18.4	0.7	21	1	AAQ75628	Reverse transcript
1257	18.4	0.7	21	1	AAQ75636	Reverse transcript
1258	18.4	0.7	21	1	AAQ75686	Reverse transcript
c1259	18.4	0.7	21	1	AAQ75686	Reverse transcript
1260	18.4	0.7	21	1	AAQ75775	Reverse transcript
c1261	18.4	0.7	21	1	AAQ75790	Reverse transcript
1262	18.4	0.7	21	1	AAQ75698	Reverse transcript
1263	18.4	0.7	21	1	AAQ75699	Reverse transcript
1264	18.4	0.7	21	1	AAQ75635	Reverse transcript
1265	18.4	0.7	21	1	AAQ75645	Reverse transcript
c1266	18.4	0.7	21	1	AAQ75691	Reverse transcript
c1267	18.4	0.7	21	1	AAQ75782	Reverse transcript
c1268	18.4	0.7	21	1	AAQ75662	Reverse transcript
1269	18.4	0.7	21	1	AAQ75679	Reverse transcript
1270	18.4	0.7	21	1	AAQ75774	Reverse transcript
c1271	18.4	0.7	21	1	AAQ75774	Reverse transcript
1272	18.4	0.7	21	1	AAQ75638	Reverse transcript
c1273	18.4	0.7	21	1	AAQ75653	Reverse transcript
1274	18.4	0.7	21	1	AAQ75677	Reverse transcript

1275	18.4	0.7	21	1	AAQ75683	Reverse transcript
c1276	18.4	0.7	21	1	AAQ75683	Reverse transcript
1277	18.4	0.7	21	1	AAQ75696	Reverse transcript
1278	18.4	0.7	21	1	AAQ75647	Reverse transcript
c1279	18.4	0.7	21	1	AAQ75654	Reverse transcript
1280	18.4	0.7	22	1	ABA93238	PolyA adaptor olig
1281	18.4	0.7	24	1	ABK12409	RT-PCR primer #1 f
1282	18.4	0.7	24	1	AAL47515	Human cyclophilin-
c1283	18.4	0.7	25	1	AAF74925	CD40L poly-A tract
c1284	18.4	0.7	25	1	AAF74930	CD40L poly-A tract
1285	18.4	0.7	26	1	AAA62140	A. auricaliformis
1286	18.4	0.7	26	1	AAC93128	Stephania tetrandr
1287	18.4	0.7	28	1	AAQ36362	GL6anti, targetted
c1288	18.4	0.7	28	1	AAD33514	T7T18Apad_PS19-28-
c1289	18.4	0.7	28	1	AAD33512	T7T18Apad_PS8-28-0
1290	18.2	0.6	19	1	AAX06572	(-)-limonene-6-hyd
c1291	18.2	0.6	19	1	AAX06572	(-)-limonene-6-hyd
1292	18.2	0.6	19	1	AAZ99489	Primer HOOK for cD
c1293	18.2	0.6	19	1	AAZ99489	Primer HOOK for cD
1294	18.2	0.6	19	1	AAD15201	3' sequencing prim
c1295	18.2	0.6	19	1	AAD15201	3' sequencing prim
1296	18.2	0.6	19	1	AAH21968	Mouse total gene e
c1297	18.2	0.6	19	1	AAH21968	Mouse total gene e
1298	18.2	0.6	19	1	AAF76617	Spearmint (-)-limo
c1299	18.2	0.6	19	1	AAF76617	Spearmint (-)-limo
1300	18.2	0.6	19	1	AAS06525	Mouse microglia an
c1301	18.2	0.6	19	1	AAS06525	Mouse microglia an
1302	18.2	0.6	19	1	ABK71509	CNS related 3' seq
c1303	18.2	0.6	19	1	ABK71509	CNS related 3' seq
1304	18.2	0.6	19	1	ABQ73231	Rabbit atheroscler
c1305	18.2	0.6	19	1	ABQ73231	Rabbit atheroscler
1306	18.2	0.6	19	1	AAD34663	PCR primer #4 used
c1307	18.2	0.6	19	1	AAD34663	PCR primer #4 used
1308	18.2	0.6	19	1	AAD40279	HOOK PCR primer us
c1309	18.2	0.6	19	1	AAD40279	HOOK PCR primer us
1310	18.2	0.6	19	1	ABZ68389	Reverse transcript
c1311	18.2	0.6	19	1	ABZ68389	Reverse transcript
1312	18.2	0.6	19	1	ACC79402	M13 sequencing pri
c1313	18.2	0.6	19	1	ACC79402	M13 sequencing pri
1314	18.2	0.6	19	1	AAD49149	3' sequencing prim
c1315	18.2	0.6	19	1	AAD49149	3' sequencing prim
1316	18.2	0.6	19	1	AAD50267	3' sequencing prim
c1317	18.2	0.6	19	1	AAD50267	3' sequencing prim
1318	18.2	0.6	19	1	ADC21495	Human PRDI-BF1 RT-
c1319	18.2	0.6	19	1	ADC21495	Human PRDI-BF1 RT-
1320	18.2	0.6	20	1	AAZ09197	Oligonucleotide 9
c1321	18.2	0.6	20	1	AAZ09197	Oligonucleotide 9
1322	18.2	0.6	23	1	AAQ45360	Human protein-tyro
1323	18.2	0.6	23	1	AAT37316	RT-PCR Primer for
1324	18.2	0.6	23	1	AAZ28229	Second round PCR p
1325	18.2	0.6	23	1	AAA29299	Second round prime
1326	18.2	0.6	23	1	ABA97431	Glycosyltransferas
c1327	18.2	0.6	24	1	ABA97997	Human mitochondria
c1328	18.2	0.6	25	1	AAI72268	P4 primer used in
c1329	18.2	0.6	25	1	ACF79235	Calix(a)arene-olig
c1330	18.2	0.6	25	1	AAC96079	16s rRNA gene PCR
1331	18.2	0.6	25	1	AAT27193	Stem loop oligonuc
1332	18.2	0.6	25	1	AAC96418	HLA DQA1 gene PCR
1333	18.2	0.6	25	1	AAC96060	16s rRNA gene PCR
1334	18.2	0.6	25	1	AAH38315	SNP specific SNPE
1335	18.2	0.6	26	1	AAX89364	Chromosomal bindin
1336	18.2	0.6	26	1	ABS54659	Human p53 protein
c1337	18.2	0.6	27	1	ADC75075	Biosensor related
1338	18.2	0.6	27	1	AAT90275	Pyrimidine ring mo
1339	18.2	0.6	27	1	ADC75076	Biosensor related
c1340	18.2	0.6	28	1	AAF60450	RNA oligonucleotid
c1341	18.2	0.6	28	1	AAL45359	Puromycin linker D
c1342	18.2	0.6	28	1	AAT70113	PolyAB primer 2.
1343	18.2	0.6	28	1	ABK52626	Minority genome me
1344	18.2	0.6	28	1	AAD41903	ON-41 oligonucleot
c1345	18.2	0.6	29	1	AAA71176	Molecular interact
c1346	18.2	0.6	29	1	AAA71193	Molecular interact
1347	18	0.6	18	1	AAQ34110	Sequence of a micr
c1348	18	0.6	18	1	AAQ34110	Sequence of a micr
1349	18	0.6	18	1	AAQ75025	PCR primer. Synth
c1350	18	0.6	18	1	AAQ75025	PCR primer. Synth
1351	18	0.6	18	1	AAT94667	Anchored poly(T) o
c1352	18	0.6	18	1	AAT94668	Anchored poly(T) o
1353	18	0.6	18	1	AAV37712	Human protein AQ2_
1354	18	0.6	18	1	AAV21970	Nuclease resistant
c1355	18	0.6	18	1	AAV21970	Nuclease resistant
1356	18	0.6	18	1	AAX19943	Primer SEQ ID NO:3
c1357	18	0.6	18	1	AAX19943	Primer SEQ ID NO:3
1358	18	0.6	18	1	AAX19942	Primer SEQ ID NO:2
c1359	18	0.6	18	1	AAX19942	Primer SEQ ID NO:2
1360	18	0.6	18	1	AAX18372	RT-PCR primer of t
1361	18	0.6	18	1	AAA40563	Human adult ovary
1362	18	0.6	18	1	AAZ87161	Oligoarabinonucleo
c1363	18	0.6	18	1	AAZ87161	Oligoarabinonucleo
1364	18	0.6	18	1	AAZ87162	Oligoarabinonucleo
c1365	18	0.6	18	1	AAZ87162	Oligoarabinonucleo
1366	18	0.6	18	1	AAZ87166	Deoxyarabinonucleo
c1367	18	0.6	18	1	AAZ87166	Deoxyarabinonucleo
1368	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
c1369	18	0.6	18	1	AAZ87167	Deoxyarabinonucleo
1370	18	0.6	18	1	AAD03565	Oligonucleotide #6
c1371	18	0.6	18	1	AAD03565	Oligonucleotide #6
1372	18	0.6	18	1	AAD17014	Oligonucleotide A1
c1373	18	0.6	18	1	AAD17014	Oligonucleotide A1
c1374	18	0.6	18	1	AAF75598	Binary encoded seq
1375	18	0.6	18	1	AAF99708	Immunostimulatory
c1376	18	0.6	18	1	AAF99708	Immunostimulatory
1377	18	0.6	18	1	AAF99734	Immunostimulatory
c1378	18	0.6	18	1	AAF99734	Immunostimulatory
1379	18	0.6	18	1	AAF82472	Phagemid vector pC
c1380	18	0.6	18	1	AAF82472	Phagemid vector pC
1381	18	0.6	18	1	AAS94743	Rat secreted facto
c1382	18	0.6	18	1	AAS94743	Rat secreted facto
1383	18	0.6	18	1	ABS78455	Angiogenesis inhib
c1384	18	0.6	18	1	ABS78455	Angiogenesis inhib
1385	18	0.6	18	1	ABS78429	Angiogenesis inhib
c1386	18	0.6	18	1	ABS78429	Angiogenesis inhib
1387	18	0.6	18	1	ABL39401	Immunostimulatory
c1388	18	0.6	18	1	ABL39401	Immunostimulatory
1389	18	0.6	18	1	AAD41497	Oligonucleotide us
c1390	18	0.6	18	1	AAD41497	Oligonucleotide us
1391	18	0.6	18	1	ABS53437	Poly d(T) primer.
c1392	18	0.6	18	1	ABS53437	Poly d(T) primer.
1393	18	0.6	18	1	ABA93239	Adaptor oligonucle
c1394	18	0.6	18	1	ABA93239	Adaptor oligonucle
1395	18	0.6	18	1	AAD56466	Target RNA #1 used
c1396	18	0.6	18	1	AAD56466	Target RNA #1 used
1397	18	0.6	18	1	AAD56440	Antisense oligo #1
c1398	18	0.6	18	1	AAD56440	Antisense oligo #1
1399	18	0.6	18	1	AAD56446	2'F-ANA antisense
c1400	18	0.6	18	1	AAD56446	2'F-ANA antisense
1401	18	0.6	18	1	ACH03247	Immunostimulatory
c1402	18	0.6	18	1	ACH03247	Immunostimulatory
1403	18	0.6	18	1	AAD57871	Antisense oligo #1
c1404	18	0.6	18	1	AAD57871	Antisense oligo #1
1405	18	0.6	18	1	AAD57878	Antisense DNA-RNA
c1406	18	0.6	18	1	AAD57878	Antisense DNA-RNA
1407	18	0.6	18	1	AAD57879	Antisense DNA-RNA
c1408	18	0.6	18	1	AAD57879	Antisense DNA-RNA
1409	18	0.6	18	1	AAD57877	Antisense DNA-RNA
c1410	18	0.6	18	1	AAD57877	Target RNA #1 used
1411	18	0.6	18	1	AAD57890	Target RNA #1 used
c1412	18	0.6	18	1	AAD57890	Immunostimulatory
1413	18	0.6	18	1	ADB37210	Immunostimulatory
c1414	18	0.6	18	1	ADB37210	Immunostimulatory
1415	18	0.6	18	1	ADB37236	Immunostimulatory
c1416	18	0.6	18	1	ADB37236	Human probe NEG fo
1417	18	0.6	18	1	ADE77617	Human probe NEG fo
c1418	18	0.6	18	1	ADE77617	Reverse transcript
1419	18	0.6	19	1	AAQ75553	Reverse transcript
c1420	18	0.6	19	1	AAQ75558	

1421	18	0.6	19	1	AAQ75551	Reverse transcript
1422	18	0.6	19	1	AAQ75554	Reverse transcript
c1423	18	0.6	19	1	AAQ75555	Reverse transcript
c1424	18	0.6	19	1	AAQ75557	Reverse transcript
1425	18	0.6	19	1	ABL51521	Tailing reaction r
c1426	18	0.6	19	1	ABL51521	Tailing reaction r
1427	18	0.6	19	1	ABZ75398	Synthetic nuclease
c1428	18	0.6	19	1	ABZ75398	Synthetic nuclease
1429	18	0.6	19	1	ABZ75399	Synthetic nuclease
c1430	18	0.6	19	1	ABZ75399	Synthetic nuclease
c1431	18	0.6	20	1	AAT04916	Mammalian stem cel
1432	18	0.6	20	1	AAT04918	Mammalian stem cel
c1433	18	0.6	20	1	AAA13753	Stem cell factor u
1434	18	0.6	20	1	AAA13754	Stem cell factor u
c1435	18	0.6	20	1	AAH41332	Universal stem cel
1436	18	0.6	20	1	AAH41333	Universal stem cel
c1437	18	0.6	20	1	AAS04112	Human SCF (stem ce
1438	18	0.6	20	1	AAS04113	Human SCF (stem ce
c1439	18	0.6	20	1	AAF89092	Mammalian stem cel
1440	18	0.6	20	1	AAF89093	Mammalian stem cel
1441	18	0.6	20	1	AAS05714	Aminopurine substi
c1442	18	0.6	20	1	AAS05715	8-aminopurine subs
1443	18	0.6	20	1	AAH23891	Human SCF (stem ce
c1444	18	0.6	20	1	AAH23890	Human SCF (stem ce
c1445	18	0.6	20	1	AAS04213	Human SCF (stem ce
1446	18	0.6	20	1	AAS04214	Human SCF (stem ce
1447	18	0.6	20	1	AAS10449	Human stem cell fa
c1448	18	0.6	20	1	AAS10448	Human stem cell fa
c1449	18	0.6	20	1	AAD35465	Rat SCF 5' cDNA am
1450	18	0.6	20	1	AAD35466	Rat SCF 5' cDNA am
c1451	18	0.6	20	1	ABS73849	SCF universal olig
1452	18	0.6	20	1	ABS73850	SCF universal olig
1453	18	0.6	20	1	ABZ89678	Human oligonucleot
1454	18	0.6	20	1	ABZ89677	Human oligonucleot
1455	18	0.6	20	1	ABZ89240	Human oligonucleot
1456	18	0.6	20	1	ADE52462	Stem cell factor (
c1457	18	0.6	20	1	ADE52461	Stem cell factor (
1458	18	0.6	20	1	AAQ75588	Reverse transcript
c1459	18	0.6	20	1	AAQ75601	Reverse transcript
c1460	18	0.6	20	1	AAQ75591	Reverse transcript
c1461	18	0.6	20	1	AAQ75605	Reverse transcript
1462	18	0.6	20	1	AAQ75575	Reverse transcript
1463	18	0.6	20	1	AAQ75577	Reverse transcript
c1464	18	0.6	20	1	AAQ75593	Reverse transcript
c1465	18	0.6	20	1	AAQ75594	Reverse transcript
1466	18	0.6	20	1	AAQ75583	Reverse transcript
c1467	18	0.6	20	1	AAQ75606	Reverse transcript
c1468	18	0.6	20	1	AAQ75603	Reverse transcript
1469	18	0.6	20	1	AAQ75576	Reverse transcript
1470	18	0.6	20	1	AAQ75587	Reverse transcript
c1471	18	0.6	20	1	AAQ75599	Reverse transcript
1472	18	0.6	20	1	AAT04917	Mammalian stem cel
c1473	18	0.6	20	1	AAT04917	Mammalian stem cel
1474	18	0.6	20	1	AAA13752	Stem cell factor u
c1475	18	0.6	20	1	AAA13752	Stem cell factor u
1476	18	0.6	20	1	AAH41331	Universal stem cel
c1477	18	0.6	20	1	AAH41331	Universal stem cel
1478	18	0.6	20	1	AAS04111	Human SCF (stem ce
c1479	18	0.6	20	1	AAS04111	Human SCF (stem ce
1480	18	0.6	20	1	AAF89091	Mammalian stem cel
c1481	18	0.6	20	1	AAF89091	Mammalian stem cel
1482	18	0.6	20	1	AAH23889	Human SCF (stem ce
c1483	18	0.6	20	1	AAH23889	Human SCF (stem ce
1484	18	0.6	20	1	AAS04212	Human SCF (stem ce
c1485	18	0.6	20	1	AAS04212	Human SCF (stem ce
1486	18	0.6	20	1	AAS10447	Human stem cell fa
c1487	18	0.6	20	1	AAS10447	Human stem cell fa
1488	18	0.6	20	1	AAD35464	Rat SCF 5' cDNA am
c1489	18	0.6	20	1	AAD35464	Rat SCF 5' cDNA am
1490	18	0.6	20	1	ABS73848	SCF universal olig
c1491	18	0.6	20	1	ABS73848	SCF universal olig
1492	18	0.6	20	1	ABZ89896	Human oligonucleot
c1493	18	0.6	20	1	ABZ89703	Human oligonucleot
c1494	18	0.6	20	1	ABZ89719	Human oligonucleot
1495	18	0.6	20	1	ADE52460	Stem cell factor (
c1496	18	0.6	20	1	ADE52460	Stem cell factor (
1497	18	0.6	21	1	AAQ75692	Reverse transcript
c1498	18	0.6	21	1	AAQ75776	Reverse transcript
c1499	18	0.6	21	1	AAQ75777	Reverse transcript
1500	18	0.6	21	1	AAQ75693	Reverse transcript
1501	18	0.6	21	1	AAQ75694	Reverse transcript
c1502	18	0.6	21	1	AAQ75775	Reverse transcript
1503	18	0.6	21	1	AAQ75691	Reverse transcript
c1504	18	0.6	21	1	AAQ75735	Reverse transcript
c1505	18	0.6	21	1	AAQ75738	Reverse transcript
c1506	18	0.6	21	1	AAQ75748	Reverse transcript
c1507	18	0.6	21	1	AAQ75795	Reverse transcript
1508	18	0.6	21	1	AAQ75671	Reverse transcript
c1509	18	0.6	21	1	AAQ75736	Reverse transcript
c1510	18	0.6	21	1	AAQ75798	Reverse transcript
1511	18	0.6	21	1	AAQ75674	Reverse transcript
1512	18	0.6	21	1	AAQ75687	Reverse transcript
c1513	18	0.6	21	1	AAQ75793	Reverse transcript
c1514	18	0.6	21	1	AAQ75794	Reverse transcript
1515	18	0.6	21	1	AAQ75690	Reverse transcript
c1516	18	0.6	21	1	AAQ75767	Reverse transcript
1517	18	0.6	21	1	AAQ75688	Reverse transcript
1518	18	0.6	21	1	AAQ75713	Reverse transcript
c1519	18	0.6	21	1	AAQ75747	Reverse transcript
c1520	18	0.6	21	1	AAQ75786	Reverse transcript
c1521	18	0.6	21	1	AAQ75791	Reverse transcript
c1522	18	0.6	21	1	AAQ75743	Reverse transcript
c1523	18	0.6	21	1	AAQ75769	Reverse transcript
c1524	18	0.6	21	1	AAQ75796	Reverse transcript
c1525	18	0.6	21	1	AAQ75797	Reverse transcript
1526	18	0.6	21	1	AAQ75689	Reverse transcript
1527	18	0.6	21	1	AAQ75703	Reverse transcript
1528	18	0.6	21	1	AAQ75714	Reverse transcript
1529	18	0.6	21	1	AAQ75705	Reverse transcript
1530	18	0.6	21	1	AAQ75712	Reverse transcript
c1531	18	0.6	21	1	AAQ75737	Reverse transcript
1532	18	0.6	21	1	AAQ75672	Reverse transcript
1533	18	0.6	21	1	AAQ75706	Reverse transcript
c1534	18	0.6	21	1	AAQ75746	Reverse transcript
c1535	18	0.6	21	1	AAQ75784	Reverse transcript
c1536	18	0.6	21	1	AAQ75785	Reverse transcript
1537	18	0.6	21	1	AAQ75704	Reverse transcript
1538	18	0.6	21	1	AAQ75708	Reverse transcript
1539	18	0.6	21	1	AAQ75673	Reverse transcript
c1540	18	0.6	21	1	AAQ75768	Reverse transcript
1541	18	0.6	21	1	AAQ75707	Reverse transcript
c1542	18	0.6	21	1	AAQ75750	Reverse transcript
1543	18	0.6	21	1	AAQ75710	Reverse transcript
c1544	18	0.6	21	1	AAQ75745	Reverse transcript
c1545	18	0.6	21	1	AAQ75749	Reverse transcript
c1546	18	0.6	21	1	AAQ75770	Reverse transcript
1547	18	0.6	21	1	AAQ75709	Reverse transcript
1548	18	0.6	21	1	AAQ75711	Reverse transcript
c1549	18	0.6	21	1	AAQ75744	Reverse transcript
c1550	18	0.6	21	1	AAQ75783	Reverse transcript
c1551	18	0.6	21	1	AAQ75792	Reverse transcript
1552	18	0.6	22	1	AAQ64706	2',5'-linked tetra
c1553	18	0.6	22	1	AAQ64706	2',5'-linked tetra
1554	18	0.6	22	1	AAA98276	Human mismatch rep
1555	18	0.6	23	1	AAQ75028	LCR oligo 2. Synt
c1556	18	0.6	23	1	AAQ75028	LCR oligo 2. Synt
1557	18	0.6	23	1	AAQ75029	LCR oligo 3. Synt
c1558	18	0.6	23	1	AAQ75029	LCR oligo 3. Synt
1559	18	0.6	23	1	AAF85497	PCR primer for DNA
1560	18	0.6	23	1	AAD33503	T7T18Apad_PS13-23-
c1561	18	0.6	23	1	AAD33503	T7T18Apad_PS13-23-
c1562	18	0.6	23	1	ABL95973	Probe #48 for assa
c1563	18	0.6	24	1	ABN85073	Human S4 ribosomal
1564	18	0.6	24	1	AAH76998	Human amyloid prec
1565	18	0.6	24	1	AAH43079	Nucleotide sequenc
c1566	18	0.6	24	1	AAH43079	Nucleotide sequenc

1567	18	0.6	24	1	ABQ79878	Nucleotide sequenc
c1568	18	0.6	24	1	ABQ79878	Nucleotide sequenc
1569	18	0.6	24	1	AAD33505	T7T18Apad_PS12-24-
c1570	18	0.6	24	1	AAD33505	T7T18Apad_PS12-24-
1571	18	0.6	24	1	ADC75073	Biosensor related
c1572	18	0.6	24	1	ADC75073	Biosensor related
c1573	18	0.6	25	1	AAA47833	Adapter sequence f
1574	18	0.6	25	1	ABK87633	BamT15G PCR primer
1575	18	0.6	25	1	ABK87631	BamT15A PCR primer
1576	18	0.6	25	1	ABK87632	BamT15C PCR primer
1577	18	0.6	25	1	AAD33507	T7T18Apad_PS11-25-
c1578	18	0.6	25	1	AAD33507	T7T18Apad_PS11-25-
c1579	18	0.6	26	1	AAD12516	Thuja sp. pinoresi
c1580	18	0.6	26	1	AAV35002	Human endothelin-b
c1581	18	0.6	26	1	AAA88688	Oligo-dT-XhoI prim
c1582	18	0.6	26	1	AAC93128	Stephania tetrandr
1583	18	0.6	26	1	AAQ47178	MHC DR A intron bi
1584	18	0.6	26	1	AAZ25387	Infectious pancrea
c1585	18	0.6	26	1	AAA91664	HCV(+)RNA oligonuc
c1586	18	0.6	26	1	AAS01617	Human MINT31/CACNA
c1587	18	0.6	26	1	AAS01577	Human T-type calci
1588	18	0.6	26	1	AAS01670	Human MINT31/CACNA
1589	18	0.6	26	1	ABK66615	Human gene specifi
1590	18	0.6	26	1	AAD33509	T7T18Apad_PS10-26-
c1591	18	0.6	26	1	AAD33509	T7T18Apad_PS10-26-
c1592	18	0.6	27	1	AAX15434	PCR primer used to
c1593	18	0.6	27	1	AAT94842	Human ESF I 3' PCR
c1594	18	0.6	27	1	AAA59740	PCR primer for hES
c1595	18	0.6	27	1	AAF25224	3' primer for an e
c1596	18	0.6	27	1	ABL41793	Primer for human e
c1597	18	0.6	27	1	ABX14927	hESF I amplifying
c1598	18	0.6	27	1	AAL47309	Intracellular targ
c1599	18	0.6	27	1	AAX23568	Deletion sequence
c1600	18	0.6	27	1	AAX23572	Deletion sequence
1601	18	0.6	27	1	AAD33510	T7T18Apad_PS9-27-0
c1602	18	0.6	27	1	AAD33510	T7T18Apad_PS9-27-0
c1603	18	0.6	28	1	ACC83476	Oligo dT primer.
c1604	18	0.6	28	1	ABZ59816	Potato gene PCR pr
c1605	18	0.6	28	1	ADD35234	Mouse mitochondria
c1606	18	0.6	28	1	AAT70108	PolyTV primer 3.
c1607	18	0.6	28	1	AAV61015	HS/HIP reverse tra
c1608	18	0.6	28	1	AAZ61254	Oligo dT primer fo
c1609	18	0.6	28	1	AAI71210	Single stranded DN
1610	18	0.6	28	1	AAD33512	T7T18Apad_PS8-28-0
c1611	18	0.6	29	1	AAA90025	PCR primer for fat
1612	18	0.6	29	1	AAD33515	T7T18Apad_PS6-29-0
c1613	18	0.6	29	1	AAI69697	Hepatitis E virus
1614	18	0.6	30	1	AAD33517	T7T18Apad_PS5-30-0
c1615	18	0.6	30	1	AAV56638	Feline FLAF cDNA p
1616	18	0.6	30	1	AAF74908	CD40L poly-A tract
1617	18	0.6	31	1	AAD33519	T7T18Apad_PS4-31-0
c1618	18	0.6	31	1	AAQ99582	Human TPO anti-sen
c1619	18	0.6	32	1	AAQ87894	Normalised library
1620	18	0.6	32	1	AAD33521	T7T18Apad_PS3-32-0
c1621	18	0.6	32	1	AAT94579	Antifungal polypep
c1622	18	0.6	32	1	ADC87763	F. culmorum FCWP1
c1623	18	0.6	32	1	AAH28290	3' untranslated re
c1624	18	0.6	34	1	AAC90605	Tomato spotted wil
c1625	18	0.6	39	1	AAV12483	Oligonucleotide SE
c1626	18	0.6	39	1	AAX30019	Multimer SEQ ID NO
1627	17.8	0.6	19	1	AAT69640	Telomerase Oligo-d
c1628	17.8	0.6	19	1	AAT69640	Telomerase Oligo-d
c1629	17.8	0.6	21	1	AAQ75733	Reverse transcript
c1630	17.8	0.6	21	1	AAQ75732	Reverse transcript
c1631	17.8	0.6	21	1	AAQ75648	Reverse transcript
c1632	17.8	0.6	21	1	AAQ75676	Reverse transcript
c1633	17.8	0.6	21	1	AAQ75681	Reverse transcript
1634	17.8	0.6	21	1	AAQ75780	Reverse transcript
1635	17.8	0.6	21	1	AAQ75660	Reverse transcript
1636	17.8	0.6	21	1	AAQ75652	Reverse transcript
1637	17.8	0.6	21	1	AAQ75753	Reverse transcript
1638	17.8	0.6	21	1	AAQ75788	Reverse transcript
c1639	17.8	0.6	21	1	AAQ75680	Reverse transcript
c1640	17.8	0.6	21	1	AAQ75697	Reverse transcript
c1641	17.8	0.6	21	1	AAQ75637	Reverse transcript
c1642	17.8	0.6	21	1	AAQ75644	Reverse transcript
1643	17.8	0.6	21	1	AAQ75761	Reverse transcript
c1644	17.8	0.6	21	1	AAQ75721	Reverse transcript
1645	17.8	0.6	21	1	AAQ75762	Reverse transcript
1646	17.8	0.6	21	1	AAQ75760	Reverse transcript
1647	17.8	0.6	21	1	AAQ75754	Reverse transcript
1648	17.8	0.6	21	1	AAQ75781	Reverse transcript
c1649	17.8	0.6	21	1	AAQ75700	Reverse transcript
1650	17.8	0.6	21	1	AAQ75742	Reverse transcript
c1651	17.8	0.6	21	1	AAQ75716	Reverse transcript
1652	17.8	0.6	21	1	AAQ75740	Reverse transcript
c1653	17.8	0.6	21	1	AAQ75636	Reverse transcript
1654	17.8	0.6	21	1	AAQ75790	Reverse transcript
c1655	17.8	0.6	21	1	AAQ75645	Reverse transcript
1656	17.8	0.6	21	1	AAQ75662	Reverse transcript
1657	17.8	0.6	21	1	AAQ75653	Reverse transcript
c1658	17.8	0.6	21	1	AAQ75677	Reverse transcript
c1659	17.8	0.6	21	1	AAQ75696	Reverse transcript
1660	17.8	0.6	21	1	AAQ75793	Reverse transcript
c1661	17.8	0.6	21	1	AAQ75688	Reverse transcript
c1662	17.8	0.6	21	1	AAQ75713	Reverse transcript
1663	17.8	0.6	21	1	AAQ75769	Reverse transcript
1664	17.8	0.6	21	1	AAQ75797	Reverse transcript
c1665	17.8	0.6	21	1	AAQ75672	Reverse transcript
c1666	17.8	0.6	21	1	AAQ75708	Reverse transcript
1667	17.8	0.6	21	1	AAQ75768	Reverse transcript
1668	17.8	0.6	21	1	AAQ75745	Reverse transcript
1669	17.8	0.6	21	1	AAQ75749	Reverse transcript
c1670	17.8	0.6	21	1	AAQ75709	Reverse transcript
1671	17.8	0.6	21	1	AAQ75744	Reverse transcript
1672	17.8	0.6	21	1	AAQ75792	Reverse transcript
1673	17.8	0.6	21	1	AAQ75633	Reverse transcript
c1674	17.8	0.6	21	1	AAQ75633	Reverse transcript
c1675	17.8	0.6	21	1	AAQ75620	Reverse transcript
1676	17.8	0.6	21	1	AAQ75626	Reverse transcript
1677	17.8	0.6	21	1	AAQ75664	Reverse transcript
c1678	17.8	0.6	21	1	AAQ75664	Reverse transcript
1679	17.8	0.6	21	1	AAQ75669	Reverse transcript
c1680	17.8	0.6	21	1	AAQ75668	Reverse transcript
1681	17.8	0.6	21	1	AAQ75625	Reverse transcript
c1682	17.8	0.6	21	1	AAQ75625	Reverse transcript
1683	17.8	0.6	21	1	AAQ75634	Reverse transcript
1684	17.8	0.6	21	1	AAQ75614	Reverse transcript
1685	17.8	0.6	21	1	AAQ75665	Reverse transcript
1686	17.8	0.6	21	1	AAQ75612	Reverse transcript
c1687	17.8	0.6	21	1	AAQ75612	Reverse transcript
1688	17.8	0.6	21	1	AAQ75641	Reverse transcript
1689	17.8	0.6	21	1	AAQ75632	Reverse transcript
1690	17.8	0.6	21	1	AAQ75621	Reverse transcript
c1691	17.8	0.6	21	1	AAQ75656	Reverse transcript
1692	17.8	0.6	21	1	AAQ75617	Reverse transcript
1693	17.8	0.6	21	1	AAQ75640	Reverse transcript
c1694	17.8	0.6	21	1	AAQ75640	Reverse transcript
c1695	17.8	0.6	21	1	AAQ75613	Reverse transcript
1696	17.8	0.6	21	1	AAQ75616	Reverse transcript
c1697	17.8	0.6	21	1	AAZ26563	Human polymorphic
1698	17.8	0.6	22	1	AAF98936	Immunostimulatory
1699	17.8	0.6	22	1	ABS77577	Angiogenesis inhib
1700	17.8	0.6	22	1	ACD99369	Immunostimulatory
1701	17.8	0.6	22	1	ADB36438	Immunostimulatory
1702	17.8	0.6	23	1	AAH91823	Human inflammatory
1703	17.8	0.6	24	1	AAF98935	Immunostimulatory
1704	17.8	0.6	24	1	AAI64873	Human serine/threo
c1705	17.8	0.6	24	1	AAI64873	Human serine/threo
1706	17.8	0.6	24	1	AAI65187	Human gap connexin
1707	17.8	0.6	24	1	ABS77576	Angiogenesis inhib
1708	17.8	0.6	24	1	ABA01048	Human sodium pump
1709	17.8	0.6	24	1	ABN86902	Human macroprotein
1710	17.8	0.6	24	1	ACD99368	Immunostimulatory
1711	17.8	0.6	24	1	ADB36437	Immunostimulatory
c1712	17.8	0.6	25	1	AAV30657	Telomerase reverse

1713	17.8	0.6	25	1	AAC96118	16s rRNA gene PCR
c1714	17.8	0.6	25	1	AAC95708	HLA DQA1 gene PCR
1715	17.8	0.6	25	1	AAH38199	SNP specific SNPE
1716	17.8	0.6	25	1	ABS98709	Human p53 PCR prim
1717	17.8	0.6	25	1	AAD44166	Probe 261 targette
1718	17.8	0.6	25	1	ABS76275	Human PAPP-E exon
1719	17.8	0.6	25	1	ABS76276	Human PAPP-E exon
1720	17.8	0.6	25	1	ABS76274	Human PAPP-E exon
1721	17.8	0.6	25	1	ABS76273	Human PAPP-E exon
1722	17.8	0.6	25	1	ABS76272	Human PAPP-E exon
1723	17.8	0.6	25	1	ABK99538	Human p53 gene hyb
1724	17.8	0.6	25	1	AAD39915	Human PCR primer #
1725	17.8	0.6	25	1	ACD00131	G-protein coupled
1726	17.8	0.6	25	1	ACD00133	G-protein coupled
1727	17.8	0.6	25	1	ACD00132	G-protein coupled
1728	17.8	0.6	25	1	ACD00130	G-protein coupled
1729	17.8	0.6	25	1	ACD00134	G-protein coupled
1730	17.8	0.6	25	1	ADB04569	Human MDZ7 scannin
c1731	17.8	0.6	25	1	ADB04569	Human MDZ7 scannin
1732	17.8	0.6	25	1	ADB04572	Human MDZ7 scannin
c1733	17.8	0.6	25	1	ADB04572	Human MDZ7 scannin
1734	17.8	0.6	25	1	ADB04573	Human MDZ7 scannin
c1735	17.8	0.6	25	1	ADB04573	Human MDZ7 scannin
1736	17.8	0.6	25	1	ADB04571	Human MDZ7 scannin
c1737	17.8	0.6	25	1	ADB04571	Human MDZ7 scannin
1738	17.8	0.6	25	1	ADB04570	Human MDZ7 scannin
c1739	17.8	0.6	25	1	ADB04570	Human MDZ7 scannin
1740	17.8	0.6	25	1	ABX79024	Electronic microar
c1741	17.8	0.6	26	1	AAA13806	Yeast DOG2 stress
1742	17.8	0.6	27	1	AAQ05023	Sequence binding t
1743	17.8	0.6	27	1	AAQ36361	GL6par, targetted
c1744	17.8	0.6	27	1	ABK52620	Minority genome me
1745	17.6	0.6	24	1	ABA05517	Human Tre carcinog
1746	17.6	0.6	24	1	ABQ73262	Human ribosomal pr
1747	17.6	0.6	24	1	ABQ04183	Oligonucleotide ad
1748	17.6	0.6	24	1	ABQ00107	Oligonucleotide ad
c1749	17.6	0.6	24	1	ABQ04224	Oligonucleotide ad
1750	17.6	0.6	24	1	ABA99264	Human tra oncogene
1751	17.6	0.6	24	1	ABK11020	Gamma-COP13 polype
1752	17.6	0.6	25	1	AAV27258	Sunflower antifung
1753	17.6	0.6	25	1	AAA68966	Bacteriophage 96 O
c1754	17.6	0.6	25	1	AAC96038	16s rRNA gene PCR
c1755	17.6	0.6	25	1	AAC96289	HLA DPB1 gene PCR
1756	17.6	0.6	25	1	AAC96549	HLA DRB345 gene PC
c1757	17.6	0.6	25	1	AAC96427	HLA DQA1 gene PCR
c1758	17.6	0.6	25	1	AAC95726	HLA DQA1 gene PCR
c1759	17.6	0.6	25	1	AAC96237	16s rRNA gene PCR
c1760	17.6	0.6	25	1	AAC96446	HLA DQA1 gene PCR
c1761	17.6	0.6	25	1	AAH38027	SNP specific SNPE
c1762	17.6	0.6	25	1	ACK08350	Human microarray D
1763	17.6	0.6	25	1	ACI33260	Human microarray D
c1764	17.6	0.6	25	1	ACK08351	Human microarray D
1765	17.6	0.6	26	1	AAV12482	Oligonucleotide SE
1766	17.6	0.6	26	1	AAV59215	Circular template
1767	17.6	0.6	26	1	AAX30018	Precircle DNA olig
1768	17.6	0.6	26	1	ADC65872	DNA oligonucleotid
1769	17.6	0.6	26	1	AAS01617	Human MINT31/CACNA
1770	17.6	0.6	26	1	AAS01577	Human T-type calci
c1771	17.6	0.6	26	1	AAS01670	Human MINT31/CACNA
1772	17.6	0.6	26	1	AAS01630	Human CACNA1G R6 3
c1773	17.6	0.6	27	1	AAD49491	Oligonucleotide #2
c1774	17.6	0.6	29	1	AAV59216	Linear multimer pr
c1775	17.6	0.6	29	1	ADC65873	DNA oligonucleotid
1776	17.6	0.6	29	1	AAF74918	CD40L poly-A tract
1777	17.6	0.6	29	1	AAF74907	CD40L poly-A tract
1778	17.6	0.6	29	1	AAF74935	CD40L poly-A tract
1779	17.6	0.6	29	1	AAF74921	CD40L poly-A tract
1780	17.6	0.6	29	1	AAF74928	CD40L poly-A tract
c1781	17.6	0.6	31	1	ABA97621	Poly j nucleotide
c1782	17.4	0.6	19	1	AAQ75552	Reverse transcript
1783	17.4	0.6	19	1	AAQ75556	Reverse transcript
c1784	17.4	0.6	19	1	AAQ75553	Reverse transcript
c1785	17.4	0.6	19	1	AAQ75554	Reverse transcript
1786	17.4	0.6	19	1	AAQ75557	Reverse transcript
1787	17.4	0.6	19	1	AAQ75549	Reverse transcript
c1788	17.4	0.6	19	1	AAQ75549	Reverse transcript
1789	17.4	0.6	19	1	AAQ75548	Reverse transcript
c1790	17.4	0.6	19	1	AAQ75548	Reverse transcript
c1791	17.4	0.6	19	1	AAQ75550	Reverse transcript
1792	17.4	0.6	19	1	ADE29541	Mitogen activated
c1793	17.4	0.6	19	1	ADE29541	Mitogen activated
1794	17.4	0.6	19	1	ADE29704	Mitogen activated
c1795	17.4	0.6	19	1	ADE29704	Mitogen activated
c1796	17.4	0.6	20	1	AAQ75582	Reverse transcript
c1797	17.4	0.6	20	1	AAQ75579	Reverse transcript
1798	17.4	0.6	20	1	AAQ75597	Reverse transcript
1799	17.4	0.6	20	1	AAQ75595	Reverse transcript
1800	17.4	0.6	20	1	AAA91207	Antisense IGFBP-5
c1801	17.4	0.6	20	1	AAQ75566	Reverse transcript
c1802	17.4	0.6	20	1	AAQ75569	Reverse transcript
c1803	17.4	0.6	20	1	AAQ75584	Reverse transcript
c1804	17.4	0.6	20	1	AAQ75585	Reverse transcript
c1805	17.4	0.6	20	1	AAQ75568	Reverse transcript
1806	17.4	0.6	20	1	AAQ75570	Reverse transcript
c1807	17.4	0.6	20	1	AAQ75589	Reverse transcript
c1808	17.4	0.6	20	1	AAQ75590	Reverse transcript
1809	17.4	0.6	20	1	AAQ75602	Reverse transcript
1810	17.4	0.6	20	1	ABZ85534	Human oligonucleot
1811	17.4	0.6	20	1	ABZ88938	Human oligonucleot
c1812	17.4	0.6	20	1	ABZ88813	Human oligonucleot
c1813	17.4	0.6	20	1	AAQ75583	Reverse transcript
c1814	17.4	0.6	20	1	AAQ75587	Reverse transcript
1815	17.4	0.6	20	1	AAQ75599	Reverse transcript
1816	17.4	0.6	20	1	ABZ89703	Human oligonucleot
c1817	17.4	0.6	20	1	AAQ75574	Reverse transcript
1818	17.4	0.6	20	1	AAQ75563	Reverse transcript
c1819	17.4	0.6	20	1	AAQ75563	Reverse transcript
1820	17.4	0.6	20	1	AAQ75565	Reverse transcript
c1821	17.4	0.6	20	1	AAQ75565	Reverse transcript
c1822	17.4	0.6	20	1	AAQ75573	Reverse transcript
1823	17.4	0.6	20	1	AAQ75567	Reverse transcript
c1824	17.4	0.6	20	1	AAQ75567	Reverse transcript
c1825	17.4	0.6	20	1	AAQ75571	Reverse transcript
c1826	17.4	0.6	20	1	AAF99943	Synthetic oligonuc
1827	17.4	0.6	20	1	ABA05917	Hepatitis B virus
c1828	17.4	0.6	20	1	ABZ88879	Human oligonucleot
c1829	17.4	0.6	20	1	ABZ85669	Human oligonucleot
1830	17.4	0.6	20	1	ABZ90829	Human oligonucleot
1831	17.4	0.6	20	1	ABZ89301	Human oligonucleot
c1832	17.4	0.6	20	1	ABZ89301	Human oligonucleot
c1833	17.4	0.6	21	1	AAQ75731	Reverse transcript
c1834	17.4	0.6	21	1	AAQ75734	Reverse transcript
c1835	17.4	0.6	21	1	AAQ75649	Reverse transcript
c1836	17.4	0.6	21	1	AAQ75701	Reverse transcript
c1837	17.4	0.6	21	1	AAF24290	Complementary nucl
c1838	17.4	0.6	21	1	ABX79794	EST polymorphic DN
1839	17.4	0.6	21	1	AAQ75752	Reverse transcript
c1840	17.4	0.6	21	1	AAQ75719	Reverse transcript
c1841	17.4	0.6	21	1	AAQ75722	Reverse transcript
1842	17.4	0.6	21	1	AAQ75751	Reverse transcript
1843	17.4	0.6	21	1	AAQ75759	Reverse transcript
c1844	17.4	0.6	21	1	AAQ75720	Reverse transcript
1845	17.4	0.6	21	1	AAQ75651	Reverse transcript
c1846	17.4	0.6	21	1	AAQ75702	Reverse transcript
c1847	17.4	0.6	21	1	AAQ75675	Reverse transcript
c1848	17.4	0.6	21	1	AAQ75643	Reverse transcript
c1849	17.4	0.6	21	1	AAQ75695	Reverse transcript
c1850	17.4	0.6	21	1	AAQ75646	Reverse transcript
c1851	17.4	0.6	21	1	AAQ75678	Reverse transcript
1852	17.4	0.6	21	1	AAQ75779	Reverse transcript
c1853	17.4	0.6	21	1	AAQ75698	Reverse transcript
c1854	17.4	0.6	21	1	AAQ75699	Reverse transcript
c1855	17.4	0.6	21	1	AAQ75635	Reverse transcript
1856	17.4	0.6	21	1	AAQ75782	Reverse transcript
c1857	17.4	0.6	21	1	AAQ75679	Reverse transcript
c1858	17.4	0.6	21	1	AAQ75638	Reverse transcript

c1859	17.4	0.6	21	1	AAQ75647	Reverse transcript
1860	17.4	0.6	21	1	AAQ75654	Reverse transcript
c1861	17.4	0.6	21	1	AAQ75671	Reverse transcript
c1862	17.4	0.6	21	1	AAQ75674	Reverse transcript
c1863	17.4	0.6	21	1	AAQ75687	Reverse transcript
c1864	17.4	0.6	21	1	AAQ75690	Reverse transcript
1865	17.4	0.6	21	1	AAQ75767	Reverse transcript
c1866	17.4	0.6	21	1	AAQ75689	Reverse transcript
c1867	17.4	0.6	21	1	AAQ75673	Reverse transcript
1868	17.4	0.6	21	1	AAQ75770	Reverse transcript
c1869	17.4	0.6	21	1	AAQ75626	Reverse transcript
c1870	17.4	0.6	21	1	AAQ75669	Reverse transcript
c1871	17.4	0.6	21	1	AAQ75634	Reverse transcript
c1872	17.4	0.6	21	1	AAQ75665	Reverse transcript
c1873	17.4	0.6	21	1	AAQ75641	Reverse transcript
c1874	17.4	0.6	21	1	AAQ75632	Reverse transcript
c1875	17.4	0.6	21	1	AAQ75670	Reverse transcript
c1876	17.4	0.6	21	1	AAQ75657	Reverse transcript
1877	17.4	0.6	21	1	AAQ75631	Reverse transcript
c1878	17.4	0.6	21	1	AAQ75631	Reverse transcript
1879	17.4	0.6	21	1	AAQ75639	Reverse transcript
c1880	17.4	0.6	21	1	AAQ75639	Reverse transcript
c1881	17.4	0.6	21	1	AAQ75667	Reverse transcript
1882	17.4	0.6	21	1	AAQ75642	Reverse transcript
c1883	17.4	0.6	21	1	AAQ75642	Reverse transcript
c1884	17.4	0.6	21	1	AAQ75655	Reverse transcript
c1885	17.4	0.6	21	1	AAQ75663	Reverse transcript
1886	17.4	0.6	21	1	AAQ75624	Reverse transcript
c1887	17.4	0.6	21	1	AAQ75624	Reverse transcript
c1888	17.4	0.6	21	1	AAQ75666	Reverse transcript
1889	17.4	0.6	21	1	AAQ75623	Reverse transcript
c1890	17.4	0.6	21	1	AAQ75623	Reverse transcript
c1891	17.4	0.6	21	1	AAQ75658	Reverse transcript
1892	17.4	0.6	21	1	ADE80976	Human papillomavir
1893	17.4	0.6	23	1	AAT33702	Primer #2 for tiss
c1894	17.4	0.6	23	1	AAT33702	Primer #2 for tiss
1895	17.4	0.6	23	1	AAV61555	Double-anchored ol
c1896	17.4	0.6	23	1	AAA07787	Structure of a fra
1897	17.4	0.6	23	1	AAA07786	Structure of a fra
1898	17.4	0.6	23	1	AAA08408	Oligonucleotide pr
c1899	17.4	0.6	23	1	AAA08408	Oligonucleotide pr
c1900	17.4	0.6	24	1	AAH24266	Human phosphatase
c1901	17.4	0.6	24	1	AAH44623	Human FD 17 PCR pr
c1902	17.4	0.6	24	1	ABK13715	RT-PCR primer #2 f
c1903	17.4	0.6	24	1	AAL47515	Human cyclophilin-
c1904	17.4	0.6	24	1	AAH76998	Human amyloid prec
c1905	17.4	0.6	25	1	AAC96267	HLA DPA1 gene PCR
1906	17.4	0.6	25	1	AAF74925	CD40L poly-A tract
1907	17.4	0.6	25	1	AAF74930	CD40L poly-A tract
c1908	17.4	0.6	25	1	AAH38315	SNP specific SNPE
1909	17.4	0.6	25	1	AAC95727	HLA DQA1 gene PCR
c1910	17.4	0.6	25	1	AAC96201	16s rRNA gene PCR
1911	17.4	0.6	25	1	AAC96718	HLA HLA-A gene PCR
1912	17.4	0.6	25	1	AAH39903	SNP specific SNPE
c1913	17.4	0.6	25	1	AAH39903	SNP specific SNPE
c1914	17.4	0.6	25	1	AAC90736	Human secretory pr
1915	17.4	0.6	25	1	ADB04567	Human MDZ7 scannin
c1916	17.4	0.6	25	1	ADB04567	Human MDZ7 scannin
1917	17.4	0.6	25	1	ADB04568	Human MDZ7 scannin
c1918	17.4	0.6	25	1	ADB04568	Human MDZ7 scannin
1919	17.4	0.6	26	1	AAF16616	Gastric acid produ
1920	17.4	0.6	26	1	AAF74913	CD40L poly-A tract
1921	17.4	0.6	27	1	AAF74926	CD40L poly-A tract
1922	17.4	0.6	27	1	AAF74932	CD40L poly-A tract
1923	17.4	0.6	27	1	AAF74931	CD40L poly-A tract
1924	17.4	0.6	27	1	AAF74934	CD40L poly-A tract
c1925	17.4	0.6	27	1	AAQ05023	Sequence binding t
c1926	17.4	0.6	27	1	AAQ36361	GL6par, targetted
1927	17.4	0.6	28	1	AAF74920	CD40L poly-A tract
1928	17.4	0.6	28	1	AAF74906	CD40L poly-A tract
1929	17.4	0.6	28	1	AAF74916	CD40L poly-A tract
1930	17.4	0.6	28	1	AAF74927	CD40L poly-A tract
c1931	17.4	0.6	28	1	AAQ52308	FKBP12C PCR primer
c1932	17.4	0.6	28	1	AAQ36362	GL6anti, targetted
1933	17.4	0.6	28	1	AAT70113	PolyAB primer 2.
c1934	17.4	0.6	30	1	ADA26181	Rice semi-dwarf (s
c1935	17.4	0.6	30	1	ABL56893	Synthetic deoxyrib
c1936	17.4	0.6	30	1	ABA97617	Poly f nucleotide
c1937	17.4	0.6	30	1	ABL95890	Probe poly f for a
c1938	17.4	0.6	30	1	ABL56894	Synthetic deoxyrib
c1939	17.4	0.6	30	1	ABL56895	Synthetic deoxyrib
c1940	17.4	0.6	30	1	ABA97619	Poly h nucleotide
c1941	17.4	0.6	30	1	ABA97618	Poly g nucleotide
c1942	17.4	0.6	30	1	ABL95891	Probe poly g for a
c1943	17.4	0.6	30	1	ABL95892	Probe poly h for a
c1944	17.4	0.6	30	1	ABL56888	Synthetic deoxyrib
c1945	17.4	0.6	30	1	ABA97612	Poly a nucleotide
c1946	17.4	0.6	30	1	ABL95885	Probe poly a for a
c1947	17.4	0.6	30	1	ABL56892	Synthetic deoxyrib
c1948	17.4	0.6	30	1	ABL56896	Synthetic deoxyrib
c1949	17.4	0.6	30	1	ABL56890	Synthetic deoxyrib
c1950	17.4	0.6	30	1	ABL56891	Synthetic deoxyrib
c1951	17.4	0.6	30	1	ABL56897	Synthetic deoxyrib
c1952	17.4	0.6	30	1	ABL56889	Poly b nucleotide
c1953	17.4	0.6	30	1	ABA97613	Poly i nucleotide
c1954	17.4	0.6	30	1	ABA97620	Poly c nucleotide
c1955	17.4	0.6	30	1	ABA97614	Poly d nucleotide
c1956	17.4	0.6	30	1	ABA97615	Poly e nucleotide
c1957	17.4	0.6	30	1	ABA97616	Probe poly b for a
c1958	17.4	0.6	30	1	ABL95886	Probe poly c for a
c1959	17.4	0.6	30	1	ABL95887	Probe poly j for a
c1960	17.4	0.6	30	1	ABL95894	Probe poly d for a
c1961	17.4	0.6	30	1	ABL95888	Probe poly e for a
c1962	17.4	0.6	30	1	ABL95889	Probe poly I for a
c1963	17.4	0.6	30	1	ABL95893	Template mRNA poly
1964	17.2	0.6	19	1	AAT94431	Template mRNA poly
c1965	17.2	0.6	19	1	AAT94431	RT-PCR primer of t
1966	17.2	0.6	19	1	AAX18390	RT-PCR primer of t
c1967	17.2	0.6	19	1	AAX18390	Oligonucleotide us
1968	17.2	0.6	22	1	ABV74140	Primer #3 for tiss
1969	17.2	0.6	23	1	AAT33703	Double-anchored ol
1970	17.2	0.6	23	1	AAV61556	Oligonucleotide pr
1971	17.2	0.6	23	1	AAA08409	Neurofibromatosis
c1972	17.2	0.6	23	1	AAS04989	5' End of cDNA lib
c1973	17.2	0.6	23	1	ABV74138	Oligonucleotide us
1974	17.2	0.6	23	1	ABV74139	Human CCR4 related
c1975	17.2	0.6	24	1	AAH75510	Primer used to ide
1976	17.2	0.6	24	1	AAV82670	Human neuropeptide
c1977	17.2	0.6	24	1	AAI69702	Human DNA-PK inter
c1978	17.2	0.6	24	1	ABV77761	Human zinc finger
1979	17.2	0.6	24	1	ABQ78896	16s rRNA gene PCR
c1980	17.2	0.6	25	1	AAC96060	16s rRNA gene PCR
1981	17.2	0.6	25	1	AAC96204	16s rRNA gene PCR
1982	17.2	0.6	25	1	AAC96129	HLA HLA-B gene PCR
c1983	17.2	0.6	25	1	AAC95960	16s rRNA gene PCR
c1984	17.2	0.6	25	1	AAC96115	16s rRNA gene PCR
1985	17.2	0.6	25	1	AAC96175	Human microarray D
c1986	17.2	0.6	25	1	ACI84885	Human microarray D
c1987	17.2	0.6	25	1	ACI81786	Primer Mt-2. Synt
c1988	17.2	0.6	26	1	AAT61049	Helicobacter pylor
1989	17.2	0.6	26	1	AAV07974	Human MLT gene int
c1990	17.2	0.6	26	1	AAC92118	E. spinifera fumon
c1991	17.2	0.6	28	1	AAT13977	A. phoenices APOXD
c1992	17.2	0.6	28	1	AAV65735	E. spinifera fumon
c1993	17.2	0.6	28	1	AAX05727	5' RACE primer Bam
c1994	17.2	0.6	28	1	ABZ70568	Breast cancer spec
c1995	17.2	0.6	35	1	AAQ52157	Human flt1 VEGF re
1996	17	0.6	17	1	AAX69800	Human flt1 VEGF re
c1997	17	0.6	17	1	AAX69801	RT-PCR primer of t
1998	17	0.6	17	1	AAX18370	Oestrogen receptor
1999	17	0.6	17	1	AAA25450	Oestrogen receptor
c2000	17	0.6	17	1	AAA25450	Human retrovirus H
2001	17	0.6	17	1	AAA98232	Human retrovirus H
c2002	17	0.6	17	1	AAA98232	2'-Methoxyethoxy-m
2003	17	0.6	17	1	AAA50197	2'-Methoxyethoxy-m
c2004	17	0.6	17	1	AAA50197	

2005	17	0.6	17	1	AAS06654	Human cDNA synthes
c2006	17	0.6	17	1	ABK13941	5'-PCR primer used
2007	17	0.6	17	1	ADB04271	Human MDZ7 scannin
2008	17	0.6	17	1	AAD56441	Antisense oligo #2
c2009	17	0.6	17	1	AAD56441	Antisense oligo #2
2010	17	0.6	17	1	AAD56448	2'F-ANA antisense
c2011	17	0.6	17	1	AAD56448	2'F-ANA antisense
2012	17	0.6	17	1	AAD56449	2'F-ANA antisense
c2013	17	0.6	17	1	AAD56449	2'F-ANA antisense
2014	17	0.6	17	1	AAD56447	2'F-ANA antisense
c2015	17	0.6	17	1	AAD56447	2'F-ANA antisense
2016	17	0.6	17	1	AAD56450	2'F-ANA antisense
c2017	17	0.6	17	1	AAD56450	2'F-ANA antisense
c2018	17	0.6	17	1	ACF36345	Nucleotide sequenc
c2019	17	0.6	17	1	ACF36370	Nucleotide sequenc
2020	17	0.6	17	1	ADB45110	Tumour suppression
c2021	17	0.6	18	1	AAT94667	Anchored poly(T) o
2022	17	0.6	18	1	AAT94668	Anchored poly(T) o
c2023	17	0.6	18	1	AAV37712	Human protein AQ2_
c2024	17	0.6	18	1	AAA40563	Human adult ovary_
2025	17	0.6	18	1	AAT94669	Anchored poly(T) o
c2026	17	0.6	18	1	AAT94669	Anchored poly(T) o
2027	17	0.6	18	1	AAV54164	Nucleotide sequenc
c2028	17	0.6	18	1	AAV54166	Nucleotide sequenc
2029	17	0.6	18	1	AAV07750	Phosphorothioate o
c2030	17	0.6	18	1	AAV07750	Phosphorothioate o
2031	17	0.6	18	1	AAX18373	RT-PCR primer of t
c2032	17	0.6	18	1	AAZ90648	Human adipose tiss
2033	17	0.6	18	1	AAZ90646	Human adipose tiss
2034	17	0.6	18	1	AAD20091	mRNA fragment used
c2035	17	0.6	18	1	AAD20091	mRNA fragment used
c2036	17	0.6	18	1	ABK13935	5'-PCR primer used
c2037	17	0.6	18	1	ACF36339	Nucleotide sequenc
c2038	17	0.6	18	1	ACF36364	Nucleotide sequenc
2039	17	0.6	19	1	AAQ75558	Reverse transcript
c2040	17	0.6	19	1	AAQ75551	Reverse transcript
2041	17	0.6	19	1	AAQ75555	Reverse transcript
2042	17	0.6	19	1	AAQ75550	Reverse transcript
2043	17	0.6	19	1	AAQ75547	Reverse transcript
c2044	17	0.6	19	1	AAQ75547	Reverse transcript
c2045	17	0.6	20	1	AAQ49436	Cytochrome P450 se
2046	17	0.6	20	1	AAQ75572	Reverse transcript
2047	17	0.6	20	1	AAQ75604	Reverse transcript
c2048	17	0.6	20	1	AAQ75578	Reverse transcript
2049	17	0.6	20	1	AAQ75592	Reverse transcript
2050	17	0.6	20	1	ABZ88266	Human oligonucleot
2051	17	0.6	20	1	AAQ75591	Reverse transcript
2052	17	0.6	20	1	AAQ75605	Reverse transcript
c2053	17	0.6	20	1	AAQ75575	Reverse transcript
c2054	17	0.6	20	1	AAQ75577	Reverse transcript
2055	17	0.6	20	1	AAQ75593	Reverse transcript
2056	17	0.6	20	1	AAQ75594	Reverse transcript
2057	17	0.6	20	1	AAQ75606	Reverse transcript
2058	17	0.6	20	1	AAQ75603	Reverse transcript
c2059	17	0.6	20	1	AAQ75576	Reverse transcript
c2060	17	0.6	20	1	ABZ89896	Human oligonucleot
2061	17	0.6	20	1	ABZ89719	Human oligonucleot
2062	17	0.6	20	1	AAQ75574	Reverse transcript
2063	17	0.6	20	1	AAQ75573	Reverse transcript
2064	17	0.6	20	1	AAQ75571	Reverse transcript
2065	17	0.6	20	1	AAQ75559	Reverse transcript
c2066	17	0.6	20	1	AAQ75559	Reverse transcript
2067	17	0.6	20	1	AAQ75560	Reverse transcript
c2068	17	0.6	20	1	AAQ75560	Reverse transcript
2069	17	0.6	20	1	AAQ75561	Reverse transcript
c2070	17	0.6	20	1	AAQ75561	Reverse transcript
2071	17	0.6	20	1	AAQ75562	Reverse transcript
c2072	17	0.6	20	1	AAQ75562	Reverse transcript
2073	17	0.6	20	1	ABQ79871	Nucleotide sequenc
c2074	17	0.6	20	1	ABQ79871	Nucleotide sequenc
c2075	17	0.6	20	1	ABZ91658	Human oligonucleot
c2076	17	0.6	20	1	ABZ89872	Human oligonucleot
2077	17	0.6	21	1	AAQ75741	Reverse transcript
c2078	17	0.6	21	1	AAQ75717	Reverse transcript
2079	17	0.6	21	1	AAQ75789	Reverse transcript
2080	17	0.6	21	1	AAQ75661	Reverse transcript
2081	17	0.6	21	1	AAQ75739	Reverse transcript
2082	17	0.6	21	1	AAQ75787	Reverse transcript
c2083	17	0.6	21	1	AAQ75718	Reverse transcript
2084	17	0.6	21	1	AAQ75659	Reverse transcript
c2085	17	0.6	21	1	AAQ75715	Reverse transcript
2086	17	0.6	21	1	AAQ75735	Reverse transcript
2087	17	0.6	21	1	AAQ75738	Reverse transcript
2088	17	0.6	21	1	AAQ75748	Reverse transcript
2089	17	0.6	21	1	AAQ75795	Reverse transcript
2090	17	0.6	21	1	AAQ75736	Reverse transcript
2091	17	0.6	21	1	AAQ75798	Reverse transcript
2092	17	0.6	21	1	AAQ75794	Reverse transcript
2093	17	0.6	21	1	AAQ75747	Reverse transcript
2094	17	0.6	21	1	AAQ75786	Reverse transcript
2095	17	0.6	21	1	AAQ75791	Reverse transcript
2096	17	0.6	21	1	AAQ75743	Reverse transcript
2097	17	0.6	21	1	AAQ75796	Reverse transcript
c2098	17	0.6	21	1	AAQ75703	Reverse transcript
c2099	17	0.6	21	1	AAQ75714	Reverse transcript
c2100	17	0.6	21	1	AAQ75705	Reverse transcript
c2101	17	0.6	21	1	AAQ75712	Reverse transcript
2102	17	0.6	21	1	AAQ75737	Reverse transcript
c2103	17	0.6	21	1	AAQ75706	Reverse transcript
2104	17	0.6	21	1	AAQ75746	Reverse transcript
2105	17	0.6	21	1	AAQ75784	Reverse transcript
2106	17	0.6	21	1	AAQ75785	Reverse transcript
c2107	17	0.6	21	1	AAQ75704	Reverse transcript
c2108	17	0.6	21	1	AAQ75707	Reverse transcript
2109	17	0.6	21	1	AAQ75750	Reverse transcript
c2110	17	0.6	21	1	AAQ75710	Reverse transcript
c2111	17	0.6	21	1	AAQ75711	Reverse transcript
2112	17	0.6	21	1	AAQ75783	Reverse transcript
2113	17	0.6	21	1	AAQ75620	Reverse transcript
2114	17	0.6	21	1	AAQ75668	Reverse transcript
c2115	17	0.6	21	1	AAQ75614	Reverse transcript
c2116	17	0.6	21	1	AAQ75621	Reverse transcript
2117	17	0.6	21	1	AAQ75656	Reverse transcript
c2118	17	0.6	21	1	AAQ75617	Reverse transcript
2119	17	0.6	21	1	AAQ75613	Reverse transcript
c2120	17	0.6	21	1	AAQ75616	Reverse transcript
2121	17	0.6	21	1	AAQ75670	Reverse transcript
2122	17	0.6	21	1	AAQ75657	Reverse transcript
2123	17	0.6	21	1	AAQ75667	Reverse transcript
2124	17	0.6	21	1	AAQ75655	Reverse transcript
2125	17	0.6	21	1	AAQ75663	Reverse transcript
2126	17	0.6	21	1	AAQ75666	Reverse transcript
2127	17	0.6	21	1	AAQ75658	Reverse transcript
2128	17	0.6	21	1	AAQ75611	Reverse transcript
c2129	17	0.6	21	1	AAQ75611	Reverse transcript
2130	17	0.6	21	1	AAQ75622	Reverse transcript
c2131	17	0.6	21	1	AAQ75622	Reverse transcript
2132	17	0.6	21	1	AAQ75609	Reverse transcript
c2133	17	0.6	21	1	AAQ75609	Reverse transcript
2134	17	0.6	21	1	AAQ75607	Reverse transcript
c2135	17	0.6	21	1	AAQ75607	Reverse transcript
2136	17	0.6	21	1	AAQ75618	Reverse transcript
c2137	17	0.6	21	1	AAQ75618	Reverse transcript
2138	17	0.6	21	1	AAQ75608	Reverse transcript
c2139	17	0.6	21	1	AAQ75608	Reverse transcript
2140	17	0.6	21	1	AAQ75615	Reverse transcript
c2141	17	0.6	21	1	AAQ75615	Reverse transcript
2142	17	0.6	21	1	AAQ75610	Reverse transcript
c2143	17	0.6	21	1	AAQ75610	Reverse transcript
2144	17	0.6	21	1	AAQ75619	Reverse transcript
c2145	17	0.6	21	1	AAQ75619	Reverse transcript
c2146	17	0.6	21	1	AAZ26584	Human polymorphic
c2147	17	0.6	22	1	AAT92356	Amino modified oli
c2148	17	0.6	22	1	AAA98276	Human mismatch rep
c2149	17	0.6	23	1	AAA29753	Synthetic oligonuc
c2150	17	0.6	23	1	AAQ45360	Human protein-tyro

c2151	17	0.6	23	1	AAT37316	RT-PCR Primer for
c2152	17	0.6	23	1	ABA97431	Glycosyltransferas
c2153	17	0.6	23	1	AAF85497	PCR primer for DNA
2154	17	0.6	23	1	ABL95973	Probe #48 for assa
2155	17	0.6	23	1	ABQ96219	Tumour suppression
c2156	17	0.6	23	1	ABQ96219	Tumour suppression
c2157	17	0.6	24	1	AAV48089	Oligonucleotide 25
2158	17	0.6	24	1	AAT76905	S. glaucescens dTD
2159	17	0.6	24	1	AAA63459	dNDP-glucose 4,6-d
2160	17	0.6	24	1	AAH75424	Human homo laminin
2161	17	0.6	24	1	AAD03811	S. galilaeus aclac
2162	17	0.6	24	1	ABQ73254	Human macro protei
c2163	17	0.6	24	1	ABQ73254	Human macro protei
2164	17	0.6	24	1	ABL40114	Human natriuretic
c2165	17	0.6	25	1	AAZ99741	Primer used to rev
c2166	17	0.6	25	1	AAC96419	HLA DQA1 gene PCR
2167	17	0.6	25	1	AAC96289	HLA DPB1 gene PCR
2168	17	0.6	25	1	AAT38116	NotI-oligo primer.
2169	17	0.6	25	1	AAV06660	Unlabeled oligonuc
c2170	17	0.6	25	1	AAX40404	Seq ID No:2 of WO9
c2171	17	0.6	25	1	AAC95828	HLA HLA-A gene PCR
c2172	17	0.6	25	1	AAC96374	HLA DPB1 gene PCR
2173	17	0.6	25	1	AAC96624	HLA HLA-A gene PCR
c2174	17	0.6	25	1	AAC96817	HLA HLA-C gene PCR
2175	17	0.6	25	1	AAC96343	HLA DPB1 gene PCR
2176	17	0.6	25	1	AAC95821	HLA HLA-A gene PCR
c2177	17	0.6	25	1	AAC96433	HLA DQA1 gene PCR
2178	17	0.6	25	1	AAC96784	HLA HLA-A gene PCR
2179	17	0.6	25	1	AAC96788	HLA HLA-A gene PCR
c2180	17	0.6	25	1	AAC96788	HLA HLA-A gene PCR
2181	17	0.6	25	1	AAC95789	HLA DRB1 gene PCR
2182	17	0.6	25	1	AAC96182	16s rRNA gene PCR
2183	17	0.6	25	1	AAC96830	HLA HLA-C gene PCR
2184	17	0.6	25	1	AAC96172	16s rRNA gene PCR
c2185	17	0.6	25	1	AAC96172	16s rRNA gene PCR
2186	17	0.6	25	1	AAC96171	16s rRNA gene PCR
c2187	17	0.6	25	1	AAC96171	16s rRNA gene PCR
c2188	17	0.6	25	1	AAC96219	16s rRNA gene PCR
c2189	17	0.6	25	1	AAC96598	HLA DRB345 gene PC
2190	17	0.6	25	1	AAC96121	16s rRNA gene PCR
2191	17	0.6	25	1	AAC96156	16s rRNA gene PCR
c2192	17	0.6	25	1	AAC95962	HLA HLA-B gene PCR
2193	17	0.6	25	1	AAC96197	16s rRNA gene PCR
c2194	17	0.6	25	1	AAC95728	HLA DQA1 gene PCR
c2195	17	0.6	25	1	AAC96429	HLA DQA1 gene PCR
2196	17	0.6	25	1	AAC95855	HLA HLA-A gene PCR
c2197	17	0.6	25	1	AAC95855	HLA HLA-A gene PCR
2198	17	0.6	25	1	AAC96075	16s rRNA gene PCR
c2199	17	0.6	25	1	AAS06803	Protein kinase cDN
2200	17	0.6	25	1	AAF99738	Immunostimulatory
c2201	17	0.6	25	1	AAF99738	Immunostimulatory
c2202	17	0.6	25	1	AAH39959	SNP specific SNPE
2203	17	0.6	25	1	ABS78459	Angiogenesis inhib
c2204	17	0.6	25	1	ABS78459	Angiogenesis inhib
2205	17	0.6	25	1	ABQ94378	Tumour suppression
2206	17	0.6	25	1	ABQ94374	Tumour suppression
2207	17	0.6	25	1	ABQ94375	Tumour suppression
2208	17	0.6	25	1	ABS76278	Human PAPP-E exon
c2209	17	0.6	25	1	ABS75770	Human PAPP-Ea asso
2210	17	0.6	25	1	ABS76277	Human PAPP-E exon
2211	17	0.6	25	1	ADB04575	Human MDZ7 scannin
2212	17	0.6	25	1	ADB04574	Human MDZ7 scannin
2213	17	0.6	25	1	ABV76902	Inverse-PCR primer
c2214	17	0.6	25	1	ACI00609	Human microarray D
c2215	17	0.6	25	1	ACI03338	Human microarray D
c2216	17	0.6	25	1	ACI61004	Human microarray D
c2217	17	0.6	25	1	ACI89380	Human microarray D
2218	17	0.6	25	1	ACI62001	Human microarray D
c2219	17	0.6	25	1	ACI30406	Human microarray D
2220	17	0.6	25	1	ACK15478	Human microarray D
c2221	17	0.6	25	1	ACI02702	Human microarray D
c2222	17	0.6	25	1	ACI83696	Human microarray D
c2223	17	0.6	25	1	ACK11064	Immunostimulatory
2224	17	0.6	25	1	ACH03276	Immunostimulatory
c2225	17	0.6	25	1	ACH03276	Immunostimulatory
2226	17	0.6	25	1	ADB37240	Immunostimulatory
c2227	17	0.6	25	1	ADB37240	Human PUR-alpha ge
c2228	17	0.6	26	1	AAT99265	Nucleotide sequenc
c2229	17	0.6	26	1	AAV31721	PUR-alpha RACE rea
c2230	17	0.6	26	1	AAX04087	Human CACNA1G R6 3
c2231	17	0.6	26	1	AAS01630	Human MLT gene int
2232	17	0.6	26	1	AAC92118	cDNA primer. Synt
2233	17	0.6	26	1	AAT13051	Cotton fibre cDNA
2234	17	0.6	26	1	AAT39393	Cotton fibre first
2235	17	0.6	26	1	AAT43363	Primer for cotton
2236	17	0.6	26	1	AAT62627	Primer for cotton
2237	17	0.6	26	1	AAT63663	Primer for cotton
2238	17	0.6	26	1	AAT70058	Oligonucleotide #1
c2239	17	0.6	26	1	AAZ59153	SNP specific upper
c2240	17	0.6	26	1	AAH40741	GPCR protein BG37
c2241	17	0.6	26	1	ABL54492	Minority genome me
2242	17	0.6	27	1	ABK52620	PolyTV primer 1.
c2243	17	0.6	28	1	AAT70106	PolyTV primer 2.
c2244	17	0.6	28	1	AAT70107	Minority genome me
c2245	17	0.6	28	1	ABK52626	Oligo-dT primer "n
c2246	17	0.6	29	1	AAQ49467	CD40L poly-A tract
2247	17	0.6	29	1	AAF74917	CD40L poly-A tract
2248	17	0.6	29	1	AAF74929	Human oligonucleot
2249	16.8	0.6	20	1	ABZ92865	Human oligonucleot
2250	16.8	0.6	20	1	ABZ85669	Ribonucleotide red
c2251	16.8	0.6	20	1	AAV12302	Antisense oligonuc
2252	16.8	0.6	20	1	AAV22586	PCR primer for tel
2253	16.8	0.6	20	1	AAX18300	Antisense oligonuc
2254	16.8	0.6	20	1	AAA94537	Ribonucleotide red
2255	16.8	0.6	20	1	AAA90815	Polypyrimidine Cri
2256	16.8	0.6	20	1	AAS05713	BAP28 gene fragmen
2257	16.8	0.6	20	1	AAF83959	DNA oligonucleotid
c2258	16.8	0.6	20	1	ABA91535	Human C/EBP beta p
2259	16.8	0.6	20	1	ABL94271	Human oligonucleot
c2260	16.8	0.6	20	1	ABZ89487	Human oligonucleot
2261	16.8	0.6	20	1	ABZ88564	Human oligonucleot
c2262	16.8	0.6	20	1	ABZ85532	Human oligonucleot
c2263	16.8	0.6	20	1	ABZ85535	DEN-2 cloning/sequ
c2264	16.8	0.6	21	1	AAT76021	Human biallelic po
2265	16.8	0.6	21	1	AAX09559	Human polymorphic
2266	16.8	0.6	21	1	AAZ26235	Human inflammatory
2267	16.8	0.6	21	1	AAH91826	Human Huntington's
2268	16.8	0.6	22	1	AAT78996	SNP specific upper
2269	16.8	0.6	23	1	AAH37805	SNP specific upper
c2270	16.8	0.6	23	1	AAH37805	Human macroprotein
c2271	16.8	0.6	24	1	ABN86902	Forward primer for
2272	16.8	0.6	24	1	ABQ79564	Human translation
c2273	16.8	0.6	24	1	ABN85224	PCR primer #1 for
2274	16.8	0.6	24	1	ABL56666	PCR primer #1 for
c2275	16.8	0.6	24	1	ABL56666	Salmo salar SNP OL
2276	16.8	0.6	24	1	ADD19369	Human MDZ7 scannin
c2277	16.8	0.6	25	1	ADB04574	Hind III primer/ad
2278	16.8	0.6	25	1	AAQ98161	PCR primer EcoR1-d
2279	16.8	0.6	25	1	AAC66194	16s rRNA gene PCR
2280	16.8	0.6	25	1	AAC96039	HLA DPB1 gene PCR
2281	16.8	0.6	25	1	AAC95680	16s rRNA gene PCR
2282	16.8	0.6	25	1	AAC96070	HLA DQA1 gene PCR
2283	16.8	0.6	25	1	AAC96447	HLA DPA1 gene PCR
2284	16.8	0.6	25	1	AAC96249	HLA DPA1 gene PCR
2285	16.8	0.6	25	1	AAC95664	HLA DQB1 gene PCR
2286	16.8	0.6	25	1	AAC96455	HLA DQA1 gene PCR
2287	16.8	0.6	25	1	AAC96434	HLA DQA1 gene PCR
c2288	16.8	0.6	25	1	AAC96421	HLA DPA1 gene PCR
c2289	16.8	0.6	25	1	AAC96251	HLA DQA1 gene PCR
2290	16.8	0.6	25	1	AAC96448	HLA DQA1 gene PCR
c2291	16.8	0.6	25	1	AAC95706	HLA HLA-B gene PCR
c2292	16.8	0.6	25	1	AAC95968	HLA DPB1 gene PCR
2293	16.8	0.6	25	1	AAC96355	HLA DQA1 gene PCR
c2294	16.8	0.6	25	1	AAC96432	HLA DRB345 gene PC
c2295	16.8	0.6	25	1	AAC96550	HLA DPA1 gene PCR
2296	16.8	0.6	25	1	AAC96256	

2297	16.8	0.6	25	1	ABS76271	Human PAPP-E exon
2298	16.8	0.6	25	1	ACD00129	G-protein coupled
2299	16.8	0.6	25	1	ACD00135	G-protein coupled
2300	16.6	0.6	23	1	AAA07787	Structure of a fra
c2301	16.6	0.6	23	1	AAA07786	Structure of a fra
c2302	16.6	0.6	23	1	AAX23577	Deletion sequence
2303	16.6	0.6	24	1	ABN85224	Human translation
2304	16.6	0.6	24	1	AAT03687	Homopyrimidine pro
2305	16.6	0.6	24	1	AAX09351	Human biallelic po
2306	16.6	0.6	24	1	AAF84874	Sequence of the ac
c2307	16.6	0.6	24	1	ABA95669	Human zinc finger
2308	16.6	0.6	24	1	AAL42406	Human ORC413-64 PC
2309	16.6	0.6	24	1	ABV76657	Human EGF receptor
c2310	16.6	0.6	24	1	AAS18179	Human proliferatin
2311	16.6	0.6	24	1	ABN86867	Human macroprotein
c2312	16.6	0.6	24	1	ABL55230	Pax protein 11 RT-
2313	16.6	0.6	24	1	AAL51806	Short chain dehydr
c2314	16.6	0.6	24	1	ABQ79142	Primer #2 related
c2315	16.6	0.6	24	1	ABS56172	PCR primer #4 for
2316	16.6	0.6	25	1	AAC96201	16s rRNA gene PCR
2317	16.6	0.6	25	1	AAC96219	16s rRNA gene PCR
2318	16.6	0.6	25	1	AAC95968	HLA HLA-B gene PCR
2319	16.6	0.6	25	1	AAQ55856	Fragile X probe.
2320	16.6	0.6	25	1	AAQ85271	Probe for Fragile
c2321	16.6	0.6	25	1	AAV81177	Antisense fragment
2322	16.6	0.6	25	1	AAX07505	Synthetic IDDMK1.2
2323	16.6	0.6	25	1	AAX07482	Synthetic IDDMK1.2
2324	16.6	0.6	25	1	AAX05267	Fragile X chromoso
2325	16.6	0.6	25	1	AAX07199	IDDM-associated re
2326	16.6	0.6	25	1	AAX07220	Retroviral R-poly(
2327	16.6	0.6	25	1	AAZ49618	PCR primer-2 for s
c2328	16.6	0.6	25	1	AAC96779	HLA HLA-A gene PCR
c2329	16.6	0.6	25	1	AAC96092	16s rRNA gene PCR
2330	16.6	0.6	25	1	AAC96449	HLA DQB1 gene PCR
2331	16.6	0.6	25	1	AAC95730	HLA DQB1 gene PCR
2332	16.6	0.6	25	1	AAC96753	HLA HLA-A gene PCR
2333	16.6	0.6	25	1	AAC96394	HLA DPB1 gene PCR
c2334	16.6	0.6	25	1	AAC96353	HLA DPB1 gene PCR
2335	16.6	0.6	25	1	AAC96041	16s rRNA gene PCR
2336	16.6	0.6	25	1	AAC96099	16s rRNA gene PCR
c2337	16.6	0.6	25	1	AAC96245	HLA DPA1 gene PCR
c2338	16.6	0.6	25	1	AAC96396	HLA DPB1 gene PCR
c2339	16.6	0.6	25	1	AAC96089	16s rRNA gene PCR
2340	16.6	0.6	25	1	AAC96423	HLA DQA1 gene PCR
2341	16.6	0.6	25	1	AAD03602	Human IAP-like pro
2342	16.6	0.6	25	1	AAH28308	3' untranslated re
2343	16.6	0.6	25	1	AAS20313	Human Cgamma gene
2344	16.6	0.6	25	1	ABN15565	Human GDMLP-1 25-m
2345	16.6	0.6	25	1	ABN15567	Human GDMLP-1 25-m
2346	16.6	0.6	25	1	ABN15566	Human GDMLP-1 25-m
c2347	16.6	0.6	25	1	ABL43221	Human chromosome 1
2348	16.6	0.6	25	1	ABS75946	Human PAPP-Ea asso
2349	16.6	0.6	25	1	ABS75944	Human PAPP-Ea asso
2350	16.6	0.6	25	1	ABS75945	Human PAPP-Ea asso
2351	16.6	0.6	25	1	ABK90953	PCR primer, 25657,
c2352	16.6	0.6	25	1	ABZ83992	Toxicologically re
2353	16.6	0.6	25	1	AAD53331	Probe used in huma
c2354	16.6	0.6	25	1	AAL61680	Oligonucleotide #3
c2355	16.6	0.6	25	1	ACI99045	Human microarray D
c2356	16.6	0.6	25	1	ACI22395	Human microarray D
c2357	16.6	0.6	25	1	ACK13084	Human microarray D
c2358	16.6	0.6	25	1	ACI81508	Human microarray D
2359	16.6	0.6	25	1	ACI27529	Human microarray D
c2360	16.6	0.6	27	1	ADC75076	Biosensor related
c2361	16.4	0.6	18	1	AAX18372	RT-PCR primer of t
2362	16.4	0.6	18	1	AAF75598	Binary encoded seq
c2363	16.4	0.6	18	1	AAX18373	RT-PCR primer of t
2364	16.4	0.6	18	1	AAN30173	Sequence derived f
2365	16.4	0.6	18	1	AAN92257	SS probe #300. Sy
c2366	16.4	0.6	18	1	AAQ20109	Cross-linking olig
c2367	16.4	0.6	18	1	AAQ20108	Cross-linking olig
2368	16.4	0.6	18	1	AAQ30446	Oligomer TNFR941 f
c2369	16.4	0.6	18	1	AAQ25501	Purine rich HUMNFR
c2370	16.4	0.6	18	1	AAQ30448	Oligomer TNFR943 f
c2371	16.4	0.6	18	1	AAQ30447	Oligomer TNFR942 f
c2372	16.4	0.6	18	1	AAF75596	Binary encoded seq
2373	16.4	0.6	18	1	AAF75597	Binary encoded seq
c2374	16.4	0.6	18	1	AAF75597	Binary encoded seq
2375	16.4	0.6	20	1	AAF99943	Synthetic oligonuc
2376	16.4	0.6	20	1	ABZ91658	Human oligonucleot
2377	16.4	0.6	20	1	ABZ89872	Human oligonucleot
2378	16.4	0.6	20	1	AAV12302	Ribonucleotide red
2379	16.4	0.6	20	1	AAX32010	MSH2 gene specific
2380	16.4	0.6	20	1	AAC82913	Human beta-actin d
2381	16.4	0.6	20	1	ABZ72190	Gene 216 SSCP sequ
2382	16.4	0.6	20	1	ABA05916	Hepatitis B virus
c2383	16.4	0.6	20	1	ABA05916	Hepatitis B virus
2384	16.4	0.6	20	1	ABZ87902	Human oligonucleot
2385	16.4	0.6	20	1	ABX75043	Human gene 216 pol
2386	16.4	0.6	20	1	ADA45251	Human MSH2 gene PC
2387	16.4	0.6	21	1	AAZ26563	Human polymorphic
2388	16.4	0.6	21	1	AAZ26584	Human polymorphic
2389	16.4	0.6	21	1	AAZ26142	Human polymorphic
c2390	16.4	0.6	21	1	AAZ26142	Human polymorphic
2391	16.4	0.6	21	1	AAZ26268	Human polymorphic
c2392	16.4	0.6	21	1	AAZ26268	Human polymorphic
2393	16.4	0.6	21	1	AAZ26141	Human polymorphic
c2394	16.4	0.6	21	1	AAZ26141	Human polymorphic
2395	16.4	0.6	21	1	ABK15655	Anchored oligo-dt
c2396	16.4	0.6	21	1	ABK99283	Hepatitis C virus
2397	16.4	0.6	21	1	ADE80960	Human papillomavir
2398	16.4	0.6	22	1	AAT28053	3'-primer K for hu
2399	16.4	0.6	22	1	AAT58493	First primer #10 f
2400	16.4	0.6	22	1	AAZ47351	PCR primer K used
2401	16.4	0.6	22	1	AAH22194	Human hepatocyte a
c2402	16.4	0.6	23	1	AAV61555	Double-anchored ol
2403	16.4	0.6	23	1	AAX23577	Deletion sequence
2404	16.4	0.6	23	1	AAV35580	STS probe GV10 gen
2405	16.4	0.6	23	1	AAZ87324	Maize cytochrome P
c2406	16.4	0.6	23	1	AAZ87324	Maize cytochrome P
c2407	16.4	0.6	23	1	AAA10767	Primer CaYOR110D u
2408	16.4	0.6	23	1	AAZ50028	Oligo dT primer 3'
c2409	16.4	0.6	23	1	AAZ50028	Oligo dT primer 3'
c2410	16.4	0.6	24	1	ABA01048	Human sodium pump
2411	16.4	0.6	24	1	AAC96428	HLA DQA1 gene PCR
c2412	16.4	0.6	24	1	AAA94317	RNA-protein fusion
c2413	16.4	0.6	24	1	ABL57074	Molecular beacon o
2414	16.4	0.6	24	1	ABX92831	Borrelia burgdofer
2415	16.4	0.6	24	1	ADC51227	Brassica defensin
2416	16.4	0.6	25	1	AAC96214	16s rRNA gene PCR
c2417	16.4	0.6	25	1	AAC96549	HLA DRB345 gene PC
c2418	16.4	0.6	25	1	AAC96718	HLA HLA-A gene PCR
c2419	16.4	0.6	25	1	AAC96830	HLA HLA-C gene PCR
c2420	16.4	0.6	25	1	AAC96121	16s rRNA gene PCR
c2421	16.4	0.6	25	1	ADB04575	Human MDZ7 scannin
2422	16.4	0.6	25	1	AAC96251	HLA DPA1 gene PCR
c2423	16.4	0.6	25	1	AAC95851	HLA HLA-A gene PCR
2424	16.4	0.6	25	1	AAC96884	HLA HLA-C gene PCR
c2425	16.4	0.6	25	1	AAC95722	HLA DQA1 gene PCR
2426	16.4	0.6	25	1	AAC96511	HLA DQB1 gene PCR
2427	16.4	0.6	25	1	AAC95684	HLA DPB1 gene PCR
c2428	16.4	0.6	25	1	AAC96213	16s rRNA gene PCR
2429	16.4	0.6	25	1	AAC96504	HLA DQB1 gene PCR
2430	16.4	0.6	25	1	AAC96618	HLA DRB345 gene PC
2431	16.4	0.6	25	1	AAC96321	HLA DPB1 gene PCR
2432	16.4	0.6	25	1	AAC95753	HLA DQB1 gene PCR
c2433	16.4	0.6	25	1	AAC95751	HLA DQB1 gene PCR
2434	16.4	0.6	25	1	AAC96028	HLA HLA-C gene PCR
c2435	16.4	0.6	25	1	AAC96424	HLA DQA1 gene PCR
c2436	16.4	0.6	25	1	ABL57069	Molecular beacon o
c2437	16.4	0.6	25	1	ABL57077	Molecular beacon o
c2438	16.4	0.6	25	1	ADE64628	Recombinant blood
2439	16.4	0.6	25	1	ADB04566	Human MDZ7 scannin
c2440	16.4	0.6	25	1	ADB04566	Human MDZ7 scannin
2441	16.4	0.6	25	1	ADB04576	Human MDZ7 scannin
c2442	16.4	0.6	25	1	ADB04576	Human MDZ7 scannin

c2443	16.4	0.6	25	1	ACI83927	Human microarray D
c2444	16.4	0.6	25	1	ADA14835	Hairpin oligonucle
c2445	16.4	0.6	25	1	AAD57902	Oligonucleotide us
2446	16.4	0.6	25	1	AAD57848	Oligonucleotide re
c2447	16.4	0.6	25	1	AAD57848	Oligonucleotide re
2448	16.4	0.6	25	1	ACF04465	Real time PCR targ
c2449	16.4	0.6	26	1	AAT93819	Antitumoural phosp
2450	16.4	0.6	27	1	AAX23568	Deletion sequence
2451	16.4	0.6	30	1	ABL35101	Phosphorothioate s
c2452	16.4	0.6	35	1	AAT93816	Antitumoural phosp
2453	16.2	0.6	18	1	AAX18389	RT-PCR primer of t
c2454	16.2	0.6	18	1	AAX18389	RT-PCR primer of t
2455	16.2	0.6	21	1	AAZ26249	Human polymorphic
2456	16.2	0.6	21	1	AAZ09196	Oligonucleotide 8
2457	16.2	0.6	21	1	AAZ73804	Human biallelic ma
2458	16.2	0.6	21	1	AAA62856	PCR primer used fo
c2459	16.2	0.6	21	1	AAH89080	Human polymorphic
c2460	16.2	0.6	21	1	ABX79739	EST polymorphic DN
2461	16.2	0.6	22	1	AAA26585	Human HPC1 mutatio
c2462	16.2	0.6	22	1	AAC86203	Primer #3 used to
2463	16.2	0.6	23	1	AAT08689	CRH related G-prot
c2464	16.2	0.6	23	1	AAH45458	PCR primer specifi
2465	16.2	0.6	23	1	AAL46192	Human liver cancer
2466	16.2	0.6	24	1	ABK91269	Leukaemia related
c2467	16.2	0.6	24	1	ABA98547	Insulin-like growt
2468	16.2	0.6	24	1	ABV77761	Human DNA-PK inter
2469	16.2	0.6	24	1	AAV48089	Oligonucleotide 25
c2470	16.2	0.6	24	1	AAL51806	Short chain dehydr
c2471	16.2	0.6	24	1	AAZ07017	Murine alpha-L-idu
2472	16.2	0.6	24	1	AAF70467	Human DRD2 exon 5
2473	16.2	0.6	24	1	ABS57731	Human zinc finger
c2474	16.2	0.6	24	1	ABS57731	Human zinc finger
c2475	16.2	0.6	24	1	ABV74853	Protein 16.17 PCR
2476	16.2	0.6	24	1	ABK67211	Human gene specifi
c2477	16.2	0.6	24	1	ABQ77631	Human Hsmar1 prote
2478	16.2	0.6	24	1	ABL56411	PCR primer F used
2479	16.2	0.6	24	1	AAK99651	Human alpha 2, 3-s
2480	16.2	0.6	24	1	ABZ21302	DNA binding protei
2481	16.2	0.6	24	1	ABQ77543	Human red blood ce
c2482	16.2	0.6	24	1	ABQ77543	Human red blood ce
c2483	16.2	0.6	24	1	AAS19218	Kringle protein 14
c2484	16.2	0.6	24	1	ABL58652	Human development
2485	16.2	0.6	24	1	ABZ25620	Human zinc finger
c2486	16.2	0.6	24	1	AAL57131	RT-PCR primer 2 re
c2487	16.2	0.6	24	1	ADC10360	Human NOVX polypep
c2488	16.2	0.6	25	1	AAV57477	Cytochrome P450ox
c2489	16.2	0.6	25	1	ABA03917	Human connexin 9 P
c2490	16.2	0.6	25	1	AAC96118	16s rRNA gene PCR
2491	16.2	0.6	25	1	AAH38027	SNP specific SNPE
2492	16.2	0.6	25	1	AAC95728	HLA DQA1 gene PCR
2493	16.2	0.6	25	1	AAC96429	HLA DQA1 gene PCR
c2494	16.2	0.6	25	1	AAC96256	HLA DPA1 gene PCR
2495	16.2	0.6	25	1	AAC96779	HLA HLA-A gene PCR
2496	16	0.6	16	1	AAT75139	Arbitrary anchor p
2497	16	0.6	16	1	AAV36965	Rat pituitary-tumo
2498	16	0.6	16	1	AAX57361	P. obesus beacon P
2499	16	0.6	16	1	AAX24309	Differential displ
2500	16	0.6	16	1	AAX19462	Human senescence f
c2501	16	0.6	16	1	AAX18362	RT-PCR primer of t
2502	16	0.6	16	1	AAX07568	Homo sapiens fetal
c2503	16	0.6	16	1	AAX07568	Homo sapiens fetal
2504	16	0.6	16	1	AAC66068	DNA chip primer #4
c2505	16	0.6	16	1	AAC66068	DNA chip primer #4
2506	16	0.6	16	1	AAC87710	MMLV reverse trans
2507	16	0.6	16	1	AAA94101	Fruit-associated b
2508	16	0.6	16	1	ABA04585	Oligonucleotide #5
c2509	16	0.6	16	1	ABA04585	Oligonucleotide #5
2510	16	0.6	16	1	AAF83580	B. gymnorrhiza sal
2511	16	0.6	16	1	AAS06651	Human cDNA synthes
2512	16	0.6	16	1	AAF30895	Oligonucleotide-mi
c2513	16	0.6	16	1	AAF30895	Oligonucleotide-mi
2514	16	0.6	16	1	AAF30880	Oligonucleotide po
c2515	16	0.6	16	1	AAF30880	Oligonucleotide po
2516	16	0.6	16	1	AAH42481	Oligonucleotide us
c2517	16	0.6	16	1	AAH42481	Oligonucleotide us
2518	16	0.6	16	1	ABA02556	HCCS-1 differentia
2519	16	0.6	16	1	ABK87148	Scarlet runner bea
2520	16	0.6	16	1	AAD34285	Mouse E2 cDNA ampl
2521	16	0.6	16	1	ABL57075	Molecular beacon t
2522	16	0.6	16	1	ABA97402	Nucleotide sequenc
c2523	16	0.6	16	1	ABA97402	Nucleotide sequenc
2524	16	0.6	16	1	ABK90584	Target cDNA PCR pr
2525	16	0.6	16	1	AAD32157	H-T11-G PCR primer
2526	16	0.6	16	1	ABK12623	Mouse E4 protein,
2527	16	0.6	16	1	AAD30090	PTTG cDNA isolatin
2528	16	0.6	16	1	AAD30914	Rat PTTG1 cDNA amp
2529	16	0.6	16	1	ABZ21814	Anti-cancer drug r
2530	16	0.6	16	1	ABN87395	PTTG isolation rel
2531	16	0.6	16	1	ABA98029	Human PTTG2 cDNA c
2532	16	0.6	16	1	ACC58340	MMLV-RT PCR; prime
2533	16	0.6	16	1	ABX16054	RNA differential d
2534	16	0.6	16	1	ABZ58394	H-T11G anchored ol
2535	16	0.6	16	1	AAD56451	2'F-ANA antisense
c2536	16	0.6	16	1	AAD56451	2'F-ANA antisense
2537	16	0.6	16	1	AAL54078	Oligo-homodeoxyrib
c2538	16	0.6	16	1	AAL54078	Oligo-homodeoxyrib
2539	16	0.6	16	1	AAD57845	Target oligonucleo
2540	16	0.6	16	1	ADB68519	DNA hybridisation
c2541	16	0.6	16	1	ADB68519	DNA hybridisation
c2542	16	0.6	17	1	AAX69800	Human flt1 VEGF re
2543	16	0.6	17	1	AAX69801	Human flt1 VEGF re
2544	16	0.6	17	1	ABK13941	5'-PCR primer used
c2545	16	0.6	17	1	ADB04271	Human MDZ7 scannin
2546	16	0.6	17	1	ACF36345	Nucleotide sequenc
2547	16	0.6	17	1	ACF36370	Nucleotide sequenc
2548	16	0.6	17	1	AAX69799	Human flt1 VEGF re
c2549	16	0.6	17	1	AAX69802	Human flt1 VEGF re
c2550	16	0.6	17	1	AAV37934	Primer of the spec
2551	16	0.6	17	1	AAV49503	Human eosinophil c
2552	16	0.6	17	1	AAX18371	RT-PCR primer of t
2553	16	0.6	17	1	AAA30179	PCR primer GT15A u
c2554	16	0.6	17	1	AAA30180	PCR primer GT15C u
c2555	16	0.6	17	1	AAX82722	Human IgA nephropa
2556	16	0.6	17	1	AAX82720	Human IgA nephropa
2557	16	0.6	17	1	AAZ36739	Anchored oligo(dT)
2558	16	0.6	17	1	AAA25449	Oestrogen receptor
c2559	16	0.6	17	1	AAA25449	Oestrogen receptor
2560	16	0.6	17	1	AAA25451	Oestrogen receptor
c2561	16	0.6	17	1	AAA25451	Oestrogen receptor
2562	16	0.6	17	1	AAC64202	PCR anchor primer,
c2563	16	0.6	17	1	AAC64203	PCR anchor primer,
2564	16	0.6	17	1	AAC64181	PCR anchor primer,
c2565	16	0.6	17	1	AAC64182	PCR anchor primer,
2566	16	0.6	17	1	AAC64171	PCR anchor primer,
c2567	16	0.6	17	1	AAC64172	PCR anchor primer,
2568	16	0.6	17	1	AAC64161	PCR anchor primer,
c2569	16	0.6	17	1	AAC64162	PCR anchor primer,
2570	16	0.6	17	1	AAC64213	PCR anchor primer,
c2571	16	0.6	17	1	AAC64214	PCR anchor primer,
c2572	16	0.6	17	1	AAC64231	PCR anchor primer,
2573	16	0.6	17	1	AAC64230	PCR anchor primer,
2574	16	0.6	17	1	AAC92292	Human pollinosis-a
c2575	16	0.6	17	1	AAC92293	Human pollinosis-a
2576	16	0.6	17	1	AAS06655	Human cDNA synthes
c2577	16	0.6	17	1	AAC91720	PCR anchor primer,
2578	16	0.6	17	1	AAC91719	PCR anchor primer,
c2579	16	0.6	17	1	AAC82875	Human pollinosis-a
2580	16	0.6	17	1	AAC82874	Human pollinosis-a
c2581	16	0.6	17	1	AAH47127	Nucleotide sequenc
2582	16	0.6	17	1	AAH47126	Nucleotide sequenc
2583	16	0.6	17	1	ABK49634	Human Acetyltransf
c2584	16	0.6	17	1	ABK49635	Human Acetyltransf
2585	16	0.6	17	1	ABL59038	Nucleotide sequenc
c2586	16	0.6	17	1	ABL59039	Nucleotide sequenc
2587	16	0.6	17	1	ABN99829	Human allergic dis
c2588	16	0.6	17	1	ABN99830	Human allergic dis

2589	16	0.6	17	1	AAL49948	Human B1153 expres
c2590	16	0.6	17	1	AAL49949	Human B1153 expres
2591	16	0.6	17	1	AAL47234	Allergic disease e
c2592	16	0.6	17	1	AAL47235	Allergic disease e
c2593	16	0.6	17	1	ABK49757	Human atopic derma
2594	16	0.6	17	1	ABK49756	Human atopic derma
c2595	16	0.6	17	1	ABX79793	EST polymorphic DN
2596	16	0.6	17	1	ADB04270	Human MDZ7 scannin
2597	16	0.6	17	1	ADB04272	Human MDZ7 scannin
c2598	16	0.6	17	1	ADB04272	Human MDZ7 scannin
2599	16	0.6	17	1	ACC64866	Murine oligonucleo
2600	16	0.6	17	1	ABZ70578	Primer. Synthetic
c2601	16	0.6	17	1	ABZ70578	Primer. Synthetic
c2602	16	0.6	17	1	ADC84469	PCR primer for amp
2603	16	0.6	17	1	ADC84468	PCR primer for amp
c2604	16	0.6	17	1	ADE77745	DNA oligo (SeqID 5
2605	16	0.6	18	1	ABK13935	5'-PCR primer used
2606	16	0.6	18	1	ACF36339	Nucleotide sequenc
2607	16	0.6	18	1	ACF36364	Nucleotide sequenc
c2608	16	0.6	18	1	AAN30173	Sequence derived f
2609	16	0.6	18	1	AAF75596	Binary encoded seq
2610	16	0.6	18	1	AAV54170	Nucleotide sequenc
c2611	16	0.6	18	1	AAV54175	Nucleotide sequenc
2612	16	0.6	18	1	AAV54173	Nucleotide sequenc
c2613	16	0.6	18	1	AAV54169	Nucleotide sequenc
c2614	16	0.6	18	1	AAV54172	Nucleotide sequenc
2615	16	0.6	18	1	AAV54167	Nucleotide sequenc
2616	16	0.6	18	1	AAV35391	HIV-1 gag protein
2617	16	0.6	18	1	AAZ90649	Human adipose tiss
c2618	16	0.6	18	1	AAZ90642	Human adipose tiss
2619	16	0.6	18	1	AAZ90640	Human adipose tiss
c2620	16	0.6	18	1	AAZ90645	Human adipose tiss
2621	16	0.6	18	1	AAZ90643	Human adipose tiss
c2622	16	0.6	18	1	AAZ90651	Human adipose tiss
2623	16	0.6	18	1	AAA58385	Polynucleotide # 1
2624	16	0.6	18	1	ABK51158	Human cytomegalovi
c2625	16	0.6	18	1	ABK51158	Human cytomegalovi
2626	16	0.6	18	1	AAD52799	Primer used to pre
c2627	16	0.6	18	1	AAD52799	Primer used to pre
2628	16	0.6	20	1	ABZ89487	Human oligonucleot
2629	16	0.6	20	1	ABZ85532	Human oligonucleot
c2630	16	0.6	20	1	AAT73293	Primer for pUC19 D
2631	16	0.6	20	1	AAX93567	PCR primer used to
c2632	16	0.6	20	1	AAD15533	Human C-Raf protei
c2633	16	0.6	20	1	AAC82924	Human S-9 derived
2634	16	0.6	20	1	AAC82922	Human S-9 derived
2635	16	0.6	20	1	AAD33499	T7T18Apad_PS27-20-
c2636	16	0.6	20	1	AAD33499	T7T18Apad_PS27-20-
2637	16	0.6	20	1	AAD35095	HT15-C downstream
c2638	16	0.6	20	1	AAD35095	HT15-C downstream
c2639	16	0.6	20	1	ABZ89873	Human oligonucleot
c2640	16	0.6	20	1	ABZ89014	Human oligonucleot
c2641	16	0.6	21	1	AAZ09196	Oligonucleotide 8
2642	16	0.6	21	1	ABL57071	Molecular beacon t
c2643	16	0.6	21	1	ABS97317	Aryl hydrocarbon n
2644	16	0.6	21	1	AAD33500	T7T18Apad_PS26-21-
c2645	16	0.6	21	1	AAD33500	T7T18Apad_PS26-21-
2646	16	0.6	22	1	AAD33501	T7T18Apad_PS25-22-
c2647	16	0.6	22	1	AAD33501	T7T18Apad_PS25-22-
c2648	16	0.6	23	1	AAT33701	Primer #1 for tiss
c2649	16	0.6	23	1	AAV61554	Double-anchored ol
c2650	16	0.6	23	1	AAA08407	Oligonucleotide pr
c2651	16	0.6	23	1	ABA99682	Murine osteoporosi
c2652	16	0.6	23	1	AAT33703	Primer #3 for tiss
c2653	16	0.6	23	1	AAV61556	Double-anchored ol
c2654	16	0.6	23	1	AAA08409	Oligonucleotide pr
2655	16	0.6	23	1	AAZ99839	Nucleotide sequenc
2656	16	0.6	23	1	AAD33502	T7T18Apad_PS24-23-
c2657	16	0.6	23	1	AAD33502	T7T18Apad_PS24-23-
c2658	16	0.6	24	1	AAI65187	Human gap connexin
c2659	16	0.6	24	1	ABK11020	Gamma-COP13 polype
c2660	16	0.6	24	1	AAV82670	Primer used to ide
c2661	16	0.6	24	1	ABL40114	Human natriuretic
2662	16	0.6	24	1	ABQ79142	Primer #2 related
2663	16	0.6	24	1	AAQ43999	HIV-1 LTR region a
c2664	16	0.6	24	1	AAX26962	PCR primer used to
2665	16	0.6	24	1	AAZ49466	Gene specific sens
c2666	16	0.6	24	1	AAC70288	Single nucleotide
c2667	16	0.6	24	1	AAC67230	Fibrosis modulator
2668	16	0.6	24	1	AAH44680	Human Kazal type i
c2669	16	0.6	24	1	AAF30562	Human Factor V gen
2670	16	0.6	24	1	AAL47095	Human proliferatin
2671	16	0.6	24	1	ABV74361	Signalase 10.01 PC
c2672	16	0.6	24	1	ABV74361	Signalase 10.01 PC
2673	16	0.6	24	1	ABL56688	PCR primer #2 for
2674	16	0.6	24	1	AAD26271	Human caspase-12 c
2675	16	0.6	24	1	AAD33504	T7T18Apad_PS23-24-
c2676	16	0.6	24	1	AAD33504	T7T18Apad_PS23-24-
2677	16	0.6	24	1	ABN86391	Basophilic nucleop
c2678	16	0.6	24	1	ABZ57032	Human kinesin ligh
c2679	16	0.6	24	1	ABZ23085	Human GPCR 10823 P
2680	16	0.6	24	1	ACD27468	Human LTBP 1 bindi
2681	16	0.6	24	1	ADE86193	Ret gene chair gua
c2682	16	0.6	25	1	AAC95686	HLA DPB1 gene PCR
c2683	16	0.6	25	1	AAC96367	HLA DPB1 gene PCR
c2684	16	0.6	25	1	ABK87632	BamT15C PCR primer
2685	16	0.6	25	1	AAC96038	16s rRNA gene PCR
c2686	16	0.6	25	1	AAC96204	16s rRNA gene PCR
2687	16	0.6	25	1	AAC95828	HLA HLA-A gene PCR
2688	16	0.6	25	1	AAH39959	SNP specific SNPE
c2689	16	0.6	25	1	AAC96753	HLA HLA-A gene PCR
c2690	16	0.6	25	1	AAC96423	HLA DQA1 gene PCR
2691	16	0.6	25	1	AAC95851	HLA HLA-A gene PCR
c2692	16	0.6	25	1	AAC96884	HLA HLA-C gene PCR
2693	16	0.6	25	1	AAC96213	16s rRNA gene PCR
c2694	16	0.6	25	1	AAC96028	HLA HLA-C gene PCR
c2695	16	0.6	26	1	AAA62140	A. auricaliformis
c2696	16	0.6	26	1	AAZ25387	Infectious pancrea
2697	16	0.6	27	1	AAX23572	Deletion sequence
2698	16	0.6	27	1	AAD49491	Oligonucleotide #2
2699	16	0.6	28	1	AAD33514	T7T18Apad_PS19-28-
2700	16	0.6	29	1	AAD33516	T7T18Apad_PS18-29-
c2701	16	0.6	34	1	ADC65905	DNA oligonucleotid
2702	15.8	0.6	19	1	ADE27346	Stearoyl-CoA desat
c2703	15.8	0.6	19	1	ADE27636	Stearoyl-CoA desat
c2704	15.8	0.6	20	1	AAS05713	Polypyrimidine Cri
c2705	15.8	0.6	20	1	AAF83959	BAP28 gene fragmen
c2706	15.8	0.6	20	1	ABZ88564	Human oligonucleot
2707	15.8	0.6	20	1	ABZ85535	Human oligonucleot
c2708	15.8	0.6	20	1	AAQ37797	Antisense oligonuc
2709	15.8	0.6	20	1	AAQ48269	Glucocerebrosidase
c2710	15.8	0.6	20	1	AAQ68872	Oligonucleotide (S
c2711	15.8	0.6	20	1	AAT44565	Antisense oligo OL
c2712	15.8	0.6	20	1	AAT93630	Human p53 oncogene
c2713	15.8	0.6	20	1	AAT88465	Phosphorothioate l
2714	15.8	0.6	20	1	AAV47686	Unmethylated CpG d
c2715	15.8	0.6	20	1	AAV18923	Phosphorothioate o
2716	15.8	0.6	20	1	AAV22438	Antisense oligonuc
2717	15.8	0.6	20	1	AAV74243	CpG-N motif O-ODN
c2718	15.8	0.6	20	1	AAX27854	PCR primer for mut
c2719	15.8	0.6	20	1	AAA39400	Human p53 antisens
2720	15.8	0.6	20	1	AAA94536	Antisense oligonuc
c2721	15.8	0.6	20	1	AAZ77398	Human biallelic ma
2722	15.8	0.6	20	1	AAA91253	Antisense IGFBP-5
2723	15.8	0.6	20	1	AAK95041	Human cDNA clone-s
2724	15.8	0.6	20	1	AAK95078	Human cDNA clone-s
2725	15.8	0.6	20	1	AAF99116	Immunostimulatory
c2726	15.8	0.6	20	1	AAH91454	Human inflammatory
c2727	15.8	0.6	20	1	AAH44608	20-mer p53 phospho
c2728	15.8	0.6	20	1	ABK90841	p53 antisense olig
c2729	15.8	0.6	20	1	ABN84654	p53 antisense olig
2730	15.8	0.6	20	1	ABS77759	Angiogenesis inhib
c2731	15.8	0.6	20	1	ABT07490	Rat protein phosph
2732	15.8	0.6	20	1	ABL39008	Immunostimulatory
c2733	15.8	0.6	20	1	AAL42562	Humulus lupulus fa
c2734	15.8	0.6	20	1	ABQ96037	Tumour suppression

c2735	15.8	0.6	20	1	ABA97643	probe n. Unidenti
c2736	15.8	0.6	20	1	ABZ91981	Human oligonucleot
2737	15.8	0.6	20	1	ABZ85436	Human oligonucleot
2738	15.8	0.6	20	1	ABZ85668	Human oligonucleot
2739	15.8	0.6	20	1	ABZ92287	Human oligonucleot
c2740	15.8	0.6	20	1	ABZ89545	Human oligonucleot
c2741	15.8	0.6	20	1	ABZ22859	Clonal T cell rece
2742	15.8	0.6	20	1	ACD99549	Immunostimulatory
c2743	15.8	0.6	20	1	ADA24235	Human p53 oncogene
2744	15.8	0.6	20	1	ADB36618	Immunostimulatory
2745	15.8	0.6	21	1	ABS97317	Aryl hydrocarbon n
c2746	15.8	0.6	21	1	AAT80586	Anti-p53 phosphoro
c2747	15.8	0.6	21	1	AAV67330	Nucleotide fragmen
c2748	15.8	0.6	21	1	AAZ18450	Polymorphic fragme
c2749	15.8	0.6	21	1	AAZ58827	Human MUC12 gene s
2750	15.8	0.6	21	1	AAZ44349	Protein kinase inh
2751	15.8	0.6	21	1	AAF95374	Human gene single
2752	15.8	0.6	21	1	AAH91825	Human inflammatory
c2753	15.8	0.6	21	1	AAF75035	Primer #7. Homo s
c2754	15.8	0.6	21	1	ABK99279	Hepatitis C virus
2755	15.8	0.6	21	1	ABS98381	Human multidrug re
2756	15.8	0.6	21	1	ABS66998	Human MRP-1 polymo
c2757	15.8	0.6	21	1	ABS66997	Human MRP-1 polymo
c2758	15.8	0.6	22	1	AAF98936	Immunostimulatory
c2759	15.8	0.6	22	1	ABS77577	Angiogenesis inhib
c2760	15.8	0.6	22	1	ACD99369	Immunostimulatory
c2761	15.8	0.6	22	1	ADB36438	Immunostimulatory
c2762	15.8	0.6	22	1	ABV74140	Oligonucleotide us
2763	15.8	0.6	22	1	AAA66932	Dog genomic marker
2764	15.8	0.6	22	1	ABL35690	Immunostimulatory
2765	15.8	0.6	23	1	ABV74138	5' End of cDNA lib
c2766	15.8	0.6	23	1	ABV74139	Oligonucleotide us
2767	15.8	0.6	23	1	AAT60786	Subtelomeric prime
c2768	15.8	0.6	23	1	AAT60790	Subtelomeric prime
c2769	15.8	0.6	23	1	AAV62118	Telomere length an
2770	15.8	0.6	23	1	AAV62114	Telomere length an
2771	15.8	0.6	23	1	AAF60331	Human liver RNA re
2772	15.8	0.6	23	1	ABQ81205	Human endostatin c
c2773	15.8	0.6	23	1	ABT16546	Ethylene insensiti
c2774	15.8	0.6	24	1	AAF98935	Immunostimulatory
c2775	15.8	0.6	24	1	ABS77576	Angiogenesis inhib
c2776	15.8	0.6	24	1	ACD99368	Immunostimulatory
c2777	15.8	0.6	24	1	ADB36437	Immunostimulatory
2778	15.8	0.6	24	1	ABV74853	Protein 16.17 PCR
c2779	15.8	0.6	24	1	AAX75929	Human interleukin
2780	15.8	0.6	24	1	AAZ24999	Sense probe to Fra
c2781	15.8	0.6	24	1	AAZ24998	Antisense probe to
c2782	15.8	0.6	24	1	AAZ95163	Forward primer #9
2783	15.8	0.6	24	1	AAC96274	HLA DPB1 gene PCR
2784	15.8	0.6	24	1	AAC61624	Reporter probe for
2785	15.8	0.6	24	1	ABA04964	Human FD14 PCR pri
c2786	15.8	0.6	24	1	AAD46030	Human UGT2B7 DNA s
c2787	15.8	0.6	24	1	ABK53197	Bacillus subtilis
c2788	15.8	0.6	24	1	ABL60935	Human nucleotide r
2789	15.8	0.6	24	1	ABQ76045	Human actin simila
c2790	15.8	0.6	24	1	ABQ76045	Human actin simila
2791	15.8	0.6	25	1	ABL45245	Human chromosome 1
c2792	15.8	0.6	25	1	AAC96268	HLA DPA1 gene PCR
c2793	15.8	0.6	25	1	AAH38199	SNP specific SNPE
c2794	15.8	0.6	25	1	AAC95727	HLA DQA1 gene PCR
c2795	15.8	0.6	25	1	AAC96129	16s rRNA gene PCR
c2796	15.8	0.6	25	1	AAQ98161	Hind III primer/ad
c2797	15.8	0.6	25	1	AAC96249	HLA DPA1 gene PCR
c2798	15.8	0.6	25	1	AAC95664	HLA DPA1 gene PCR
2799	15.8	0.6	25	1	AAC96421	HLA DQA1 gene PCR
2800	15.8	0.6	25	1	AAC95706	HLA DQA1 gene PCR
2801	15.8	0.6	25	1	AAC96550	HLA DRB345 gene PC
c2802	15.8	0.6	26	1	AAQ47178	MHC DR A intron bi
2803	15.8	0.6	27	1	AAF74933	CD40L poly-A tract
c2804	15.8	0.6	29	1	AAQ85070	Oligonucleotide cl
c2805	15.8	0.6	29	1	AAQ83933	Oligonucleotide cl
c2806	15.8	0.6	34	1	AAV12929	Oligonucleotide SE
c2807	15.8	0.6	34	1	AAV59243	Small synthetic DN
c2808	15.6	0.6	17	1	AAV19118	Anchored oligo(T)
2809	15.6	0.6	17	1	AAZ89372	RNA detecting prim
c2810	15.6	0.6	17	1	AAZ89372	RNA detecting prim
2811	15.6	0.6	22	1	AAX19021	Calravirus PCR pri
c2812	15.6	0.6	22	1	AAI67259	B533S forward prim
2813	15.6	0.6	22	1	AAF55172	Probe used to iden
c2814	15.6	0.6	22	1	AAS21990	Human COL1A1 PCR p
2815	15.6	0.6	22	1	ADA45284	Human MLH1 gene PC
c2816	15.6	0.6	22	1	ADD21919	Protein translatio
2817	15.6	0.6	23	1	AAT28017	Primer (B5LFr4) fo
c2818	15.6	0.6	23	1	AAT76235	Human IL6 antisens
c2819	15.6	0.6	23	1	AAX54065	Human IL-6 antisen
c2820	15.6	0.6	23	1	AAX81611	PCR primer used to
c2821	15.6	0.6	23	1	AAA33509	Low adenosine anti
c2822	15.6	0.6	23	1	AAF19631	Human IL6 polynucl
c2823	15.6	0.6	23	1	ABZ95325	Human IL-6 antisen
2824	15.6	0.6	24	1	AAA94317	RNA-protein fusion
2825	15.6	0.6	24	1	ABQ77631	Human Hsmar1 prote
2826	15.6	0.6	24	1	ABL58652	Human development
2827	15.6	0.6	24	1	AAT39969	Minimal motif codi
c2828	15.6	0.6	24	1	AAD12863	Human CASB765 cDNA
2829	15.6	0.6	24	1	AAC91733	Human pollinosis-a
2830	15.6	0.6	24	1	AAC91993	T-box binding site
2831	15.6	0.6	24	1	ABL40063	DNA-cysteine methy
2832	15.6	0.6	24	1	ABK13945	RT-PCR primer #2 f
c2833	15.6	0.6	24	1	ABQ78172	Plant related PCR
2834	15.6	0.6	24	1	AAD35583	Human hSCD5 cDNA a
2835	15.6	0.6	24	1	ABV74368	Ubiquitin specific
2836	15.6	0.6	24	1	AAD38971	Human GDD DNA ampl
2837	15.6	0.6	24	1	ABS62457	Analyte sorting ta
2838	15.6	0.6	24	1	ABS61625	Analyte sorting ta
2839	15.6	0.6	24	1	ABI89286	Capture oligonucle
c2840	15.6	0.6	24	1	ABI89287	Capture oligonucle
2841	15.6	0.6	24	1	ABA97546	Cancer cell discri
2842	15.6	0.6	24	1	ABS55785	Human Sailor trans
2843	15.6	0.6	24	1	ABV93494	Bacillus thuringie
2844	15.6	0.6	24	1	ABV93779	B. thuringiensis t
2845	15.6	0.6	25	1	AAC96427	HLA DQA1 gene PCR
2846	15.6	0.6	25	1	AAC95726	HLA DQA1 gene PCR
c2847	15.6	0.6	25	1	AAC96039	16s rRNA gene PCR
2848	15.6	0.6	25	1	AAC96245	HLA DPA1 gene PCR
2849	15.6	0.6	26	1	AAZ59153	Oligonucleotide #1
2850	15.6	0.6	26	1	AAH40741	SNP specific upper
c2851	15.4	0.5	17	1	AAX18370	RT-PCR primer of t
c2852	15.4	0.5	17	1	AAX18371	RT-PCR primer of t
c2853	15.4	0.5	17	1	ADB04270	Human MDZ7 scannin
2854	15.4	0.5	17	1	AAX69798	Human flt1 VEGF re
c2855	15.4	0.5	17	1	AAX69804	Human flt1 VEGF re
c2856	15.4	0.5	17	1	AAX69803	Human flt1 VEGF re
2857	15.4	0.5	17	1	AAX69796	Human flt1 VEGF re
2858	15.4	0.5	17	1	AAX69797	Human flt1 VEGF re
2859	15.4	0.5	17	1	AAA25453	Oestrogen receptor
2860	15.4	0.5	17	1	AAA25452	Oestrogen receptor
c2861	15.4	0.5	17	1	AAA25452	Oestrogen receptor
2862	15.4	0.5	17	1	ABA91530	DNA-RNA-DNA oligon
c2863	15.4	0.5	17	1	ABA91530	DNA-RNA-DNA oligon
2864	15.4	0.5	17	1	AAD44151	Oligo-AT PCR prime
c2865	15.4	0.5	17	1	AAD44151	Oligo-AT PCR prime
2866	15.4	0.5	17	1	ABT38816	Tumour suppression
2867	15.4	0.5	17	1	ABT34888	Tumour suppression
2868	15.4	0.5	17	1	ADB04269	Human MDZ7 scannin
c2869	15.4	0.5	17	1	ADB04269	Human MDZ7 scannin
2870	15.4	0.5	17	1	ADB04273	Human MDZ7 scannin
c2871	15.4	0.5	17	1	ADB04273	Human MDZ7 scannin
2872	15.4	0.5	17	1	ADB43022	Tumour suppression
c2873	15.4	0.5	18	1	AAV54164	Nucleotide sequenc
2874	15.4	0.5	18	1	AAV54166	Nucleotide sequenc
2875	15.4	0.5	18	1	AAZ90648	Human adipose tiss
c2876	15.4	0.5	18	1	AAZ90646	Human adipose tiss
2877	15.4	0.5	18	1	AAQ20109	Cross-linking olig
2878	15.4	0.5	18	1	AAQ20108	Cross-linking olig
c2879	15.4	0.5	18	1	AAQ30446	Oligomer TNFR941 f
2880	15.4	0.5	18	1	AAQ25501	Purine rich HUMNFR

2881	15.4	0.5	18	1	AAQ30448	Oligomer TNFR943 f
2882	15.4	0.5	18	1	AAQ30447	Oligomer TNFR942 f
c2883	15.4	0.5	18	1	AAV54173	Nucleotide sequenc
2884	15.4	0.5	18	1	AAV54169	Nucleotide sequenc
c2885	15.4	0.5	18	1	AAV54167	Nucleotide sequenc
c2886	15.4	0.5	18	1	AAZ90649	Human adipose tiss
2887	15.4	0.5	18	1	AAZ90645	Human adipose tiss
c2888	15.4	0.5	18	1	AAZ90643	Human adipose tiss
2889	15.4	0.5	18	1	AAV54168	Nucleotide sequenc
c2890	15.4	0.5	18	1	AAV54168	Nucleotide sequenc
c2891	15.4	0.5	18	1	AAV54174	Nucleotide sequenc
2892	15.4	0.5	18	1	AAV54165	Nucleotide sequenc
c2893	15.4	0.5	18	1	AAV54165	Nucleotide sequenc
2894	15.4	0.5	18	1	AAV16014	PCR primer G-R use
2895	15.4	0.5	18	1	AAZ90644	Human adipose tiss
c2896	15.4	0.5	18	1	AAZ90644	Human adipose tiss
c2897	15.4	0.5	18	1	AAZ90650	Human adipose tiss
2898	15.4	0.5	18	1	AAZ90647	Human adipose tiss
c2899	15.4	0.5	18	1	AAZ90647	Human adipose tiss
2900	15.4	0.5	18	1	AAZ43273	Murine Sox3 gene P
2901	15.4	0.5	18	1	AAA05258	PCR primer G-R use
c2902	15.4	0.5	18	1	AAF56305	Human mGluR1alpha
2903	15.4	0.5	18	1	ACF36862	Human lactoferrin
2904	15.4	0.5	18	1	ADA27361	Human microsatelli
c2905	15.4	0.5	18	1	ADD20088	Oreochromis niloti
2906	15.4	0.5	19	1	AAV44628	Human uncoupling p
c2907	15.4	0.5	20	1	ABZ85436	Human oligonucleot
c2908	15.4	0.5	20	1	AAT73291	Primer 1 for pUC19
c2909	15.4	0.5	20	1	AAT73292	Primer 2 for pUC19
c2910	15.4	0.5	20	1	AAT76100	Human histidine de
2911	15.4	0.5	20	1	AAV44626	Human uncoupling p
c2912	15.4	0.5	20	1	AAX53905	Histidine decarbox
c2913	15.4	0.5	20	1	AAA33348	Low adenosine anti
c2914	15.4	0.5	20	1	AAF19470	Human histidine de
2915	15.4	0.5	20	1	AAF99302	Immunostimulatory
2916	15.4	0.5	20	1	AAL40102	Pathogenic microor
2917	15.4	0.5	20	1	ABS77947	Angiogenesis inhib
2918	15.4	0.5	20	1	ABL39308	Immunostimulatory
c2919	15.4	0.5	20	1	ABK99977	Human CADPKL DNA P
c2920	15.4	0.5	20	1	ABA05915	Hepatitis B virus
c2921	15.4	0.5	20	1	ABI94179	Capture oligonucle
2922	15.4	0.5	20	1	ABT23594	Stabilising reagen
2923	15.4	0.5	20	1	ABZ89676	Human oligonucleot
c2924	15.4	0.5	20	1	ABZ89676	Human oligonucleot
c2925	15.4	0.5	20	1	ABZ89720	Human oligonucleot
c2926	15.4	0.5	20	1	ABZ89440	Human oligonucleot
2927	15.4	0.5	20	1	ABZ89119	Human oligonucleot
c2928	15.4	0.5	20	1	ABZ95164	Human histidine de
c2929	15.4	0.5	20	1	ABZ90649	Human oligonucleot
2930	15.4	0.5	20	1	ACC47638	Human IGFBP5 phosp
2931	15.4	0.5	20	1	ACD99727	Immunostimulatory
2932	15.4	0.5	20	1	ADB36804	Immunostimulatory
2933	15.4	0.5	21	1	ABK99283	Hepatitis C virus
c2934	15.4	0.5	21	1	AAQ71626	Primer to amplify
2935	15.4	0.5	21	1	AAZ26573	Human polymorphic
2936	15.4	0.5	21	1	AAZ26500	Human polymorphic
c2937	15.4	0.5	21	1	AAZ26500	Human polymorphic
c2938	15.4	0.5	21	1	AAZ57386	Factor VII mutagen
2939	15.4	0.5	21	1	AAC59861	Oligonucleotide pr
c2940	15.4	0.5	21	1	AAC80381	Forward primer #15
c2941	15.4	0.5	21	1	AAF57100	Human Factor VII m
c2942	15.4	0.5	21	1	ABS97681	Histamine N-methyl
c2943	15.4	0.5	21	1	ABS97669	Histamine N-methyl
2944	15.4	0.5	21	1	ABT06086	Human IgM heavy ch
2945	15.4	0.5	21	1	ABT23595	Stabilising reagen
2946	15.4	0.5	22	1	AAT28050	3'-primer G for hu
2947	15.4	0.5	22	1	AAT28051	3'-primer H for hu
2948	15.4	0.5	22	1	AAT28052	3'-primer J for hu
2949	15.4	0.5	22	1	AAT58492	First primer #9 fo
2950	15.4	0.5	22	1	AAT58490	First primer #7 fo
2951	15.4	0.5	22	1	AAT58491	First primer #8 fo
2952	15.4	0.5	22	1	AAZ47348	PCR primer G used
2953	15.4	0.5	22	1	AAZ47349	PCR primer H used
2954	15.4	0.5	22	1	AAZ47350	PCR primer I used
c2955	15.4	0.5	22	1	AAA90070	Bovine lysosomal t
c2956	15.4	0.5	22	1	AAA88330	Bovine lysosomal t
c2957	15.4	0.5	22	1	AAC80382	Forward primer #15
2958	15.4	0.5	22	1	AAH22191	Human hepatocyte a
2959	15.4	0.5	22	1	AAH22192	Human hepatocyte a
2960	15.4	0.5	22	1	AAH22193	Human hepatocyte a
c2961	15.4	0.5	22	1	ADC10242	Human NOVX polypep
c2962	15.4	0.5	23	1	AAC80383	Forward primer #15
2963	15.4	0.5	23	1	ABL51554	Human NSAID regula
2964	15.4	0.5	23	1	ADC66134	Human CFTR exon 21
2965	15.4	0.5	24	1	ABL57074	Molecular beacon o
c2966	15.4	0.5	24	1	ADC51227	Brassica defensin
c2967	15.4	0.5	24	1	AAH44680	Human Kazal type i
2968	15.4	0.5	24	1	AAZ95163	Forward primer #9
2969	15.4	0.5	24	1	AAD46030	Human UGT2B7 DNA s
c2970	15.4	0.5	25	1	AAC96418	HLA DQA1 gene PCR
2971	15.4	0.5	25	1	AAC96237	16s rRNA gene PCR
c2972	15.4	0.5	25	1	AAC96175	16s rRNA gene PCR
c2973	15.4	0.5	25	1	AAC96624	HLA HLA-A gene PCR
c2974	15.4	0.5	25	1	AAC95821	HLA HLA-A gene PCR
2975	15.4	0.5	25	1	AAC95722	HLA DQA1 gene PCR
2976	15.4	0.5	25	1	AAC96424	HLA DQA1 gene PCR
2977	15.4	0.5	25	1	ABL57069	Molecular beacon o
2978	15.4	0.5	25	1	ABL57077	Molecular beacon o
2979	15.4	0.5	25	1	ADA14835	Hairpin oligonucle
2980	15.4	0.5	25	1	AAD57902	Oligonucleotide us
c2981	15.4	0.5	29	1	AAH28298	3' untranslated re
c2982	15.4	0.5	29	1	ADA26182	Rice semi-dwarf (s
c2983	15.4	0.5	33	1	AAV06769	Oligonucleotide co
2984	15.2	0.5	16	1	AAF82119	Human TSA7005 gene
c2985	15.2	0.5	16	1	AAF82119	Human TSA7005 gene
2986	15.2	0.5	16	1	AAH27758	Primer used in hum
c2987	15.2	0.5	16	1	AAH27758	Primer used in hum
2988	15.2	0.5	16	1	AAD44145	Oligo-dT PCR prime
2989	15.2	0.5	17	1	AAX18388	RT-PCR primer of t
c2990	15.2	0.5	17	1	AAX18388	RT-PCR primer of t
2991	15.2	0.5	17	1	AAS06666	Human differential
2992	15.2	0.5	17	1	AAS14174	Modified Poly-T Pr
c2993	15.2	0.5	17	1	AAS14174	Modified Poly-T Pr
c2994	15.2	0.5	20	1	ABA05917	Hepatitis B virus
2995	15.2	0.5	20	1	ABZ88879	Human oligonucleot
c2996	15.2	0.5	20	1	AAC82913	Human beta-actin d
2997	15.2	0.5	20	1	AAQ95389	Primer A (Group 2,
c2998	15.2	0.5	20	1	AAT10129	Sequence #1 used i
c2999	15.2	0.5	20	1	AAT50899	Probe #13 for inte
3000	15.2	0.5	20	1	AAT91100	Bovine lysosomal a
c3001	15.2	0.5	20	1	AAV47995	Human B7-1 targett
3002	15.2	0.5	20	1	AAZ37559	Human mdm2 phospho
3003	15.2	0.5	20	1	AAX36657	PCR primer for mar
3004	15.2	0.5	20	1	AAZ06095	PCR primer used to
3005	15.2	0.5	20	1	AAZ04917	PCR primer used to
c3006	15.2	0.5	20	1	AAX96826	PCR primer used to
c3007	15.2	0.5	20	1	AAF32837	Human B7-1 mRNA an
c3008	15.2	0.5	20	1	AAF32944	Human B7-1 antisen
3009	15.2	0.5	20	1	AAF80713	Human mdm2 phospho
c3010	15.2	0.5	20	1	AAC84794	Human TLR4 gene ex
c3011	15.2	0.5	20	1	AAC82910	Human beta-actin d
3012	15.2	0.5	20	1	AAC82909	Human beta-actin d
3013	15.2	0.5	20	1	AAC82914	Human beta-actin d
3014	15.2	0.5	20	1	AAF99949	Synthetic oligonuc
3015	15.2	0.5	20	1	AAS29328	Human mdm2 antisen
3016	15.2	0.5	20	1	AAH80594	Oligonucleotide hy
c3017	15.2	0.5	20	1	ABA91532	DNA oligonucleotid
c3018	15.2	0.5	20	1	ABA91537	DNA oligonucleotid
c3019	15.2	0.5	20	1	ABA91534	DNA oligonucleotid
c3020	15.2	0.5	20	1	ABA02210	Human/mouse C/EBP
c3021	15.2	0.5	20	1	ABL45622	Human chromosome 2
c3022	15.2	0.5	20	1	ABL94262	Human C/EBP beta p
3023	15.2	0.5	20	1	ABX04655	Human endogenous r
c3024	15.2	0.5	20	1	ABZ85316	Human oligonucleot
c3025	15.2	0.5	20	1	ABZ90374	Human oligonucleot
3026	15.2	0.5	20	1	ABZ85667	Human oligonucleot

3027	15.2	0.5	20	1	ABZ85670	Human oligonucleot
3028	15.2	0.5	20	1	ABZ88438	Human oligonucleot
c3029	15.2	0.5	20	1	ABZ90373	Human oligonucleot
3030	15.2	0.5	20	1	ABZ91225	Human oligonucleot
3031	15.2	0.5	20	1	ABX12581	Human cytochrome P
3032	15.2	0.5	20	1	ACC49194	Human ribonuclease
c3033	15.2	0.5	20	1	AAL53968	DNA mutation detec
3034	15.2	0.5	20	1	AAL61401	Human FXR antisens
3035	15.2	0.5	20	1	ADC98404	ITGA12 polymorphis
3036	15.2	0.5	20	1	ADD21524	Human mdm2 antisen
3037	15.2	0.5	20	1	ADD81485	HIV PRT antisense
c3038	15.2	0.5	20	1	ADE27772	Human B7-1 mRNA ta
c3039	15.2	0.5	20	1	ADE27879	Human B7-1 targete
c3040	15.2	0.5	21	1	AAZ26235	Human polymorphic
c3041	15.2	0.5	21	1	ABK15655	Anchored oligo-dt
c3042	15.2	0.5	21	1	AAZ25989	Human polymorphic
c3043	15.2	0.5	21	1	AAX25672	Human endogenous r
3044	15.2	0.5	21	1	AAX14731	Triple helix third
c3045	15.2	0.5	21	1	AAA11484	Human dysferlin PC
c3046	15.2	0.5	21	1	AAA11497	Human dysferlin PC
c3047	15.2	0.5	21	1	AAA36939	Human dysferlin ex
c3048	15.2	0.5	21	1	AAA36952	Human dysferlin ex
3049	15.2	0.5	21	1	AAZ52058	5'PCR primer L1-5
c3050	15.2	0.5	21	1	AAZ75737	Human biallelic ma
3051	15.2	0.5	21	1	AAZ75372	Human biallelic ma
3052	15.2	0.5	21	1	AAC72800	Single nucleotide
3053	15.2	0.5	21	1	AAC72803	Single nucleotide
c3054	15.2	0.5	21	1	AAA80353	Human ASTH1I 5' re
3055	15.2	0.5	21	1	AAF29175	DNA encoding an E-
3056	15.2	0.5	21	1	AAH88904	Human polymorphic
c3057	15.2	0.5	21	1	AAF81140	Primer used for se
3058	15.2	0.5	21	1	ABK37488	Packaged vector pl
3059	15.2	0.5	21	1	ABK37472	Packaging signal a
3060	15.2	0.5	21	1	ABL44934	Human chromosome 1
3061	15.2	0.5	21	1	ABS97218	Human CYP4502E1 pr
3062	15.2	0.5	21	1	ABK89936	Virus like particl
3063	15.2	0.5	21	1	ABZ69339	Human SLC11A3 codi
3064	15.2	0.5	21	1	ADC16521	Short interfering
3065	15.2	0.5	22	1	AAT78995	Mouse Huntington's
c3066	15.2	0.5	22	1	AAV81783	Rat ALK-7 PCR prim
3067	15.2	0.5	22	1	AAC61618	Probe specific for
c3068	15.2	0.5	22	1	AAD14545	Arabidopsis thalia
c3069	15.2	0.5	22	1	AAS03330	ABRE binding facto
3070	15.2	0.5	22	1	AAS01584	Human fibrillin-1
c3071	15.2	0.5	22	1	AAS01637	Human fibrillin-1
c3072	15.2	0.5	22	1	AAS07849	Abscisic acid resp
c3073	15.2	0.5	22	1	AAD08919	Arabidopsis thalia
c3074	15.2	0.5	22	1	AAS00383	5' PCR primer #2 u
3075	15.2	0.5	22	1	ABL44301	Human chromosome 1
3076	15.2	0.5	22	1	ABX97353	Human NOV-associat
c3077	15.2	0.5	22	1	ACF42669	Human ALMS1 PCR pr
c3078	15.2	0.5	22	1	ABZ58799	Cinnamycin cinA ge
3079	15.2	0.5	22	1	ABT33591	NOV reverse PCR pr
3080	15.2	0.5	23	1	AAQ10627	HLA Class I locus-
c3081	15.2	0.5	23	1	AAV27967	Ataxia telangiecta
c3082	15.2	0.5	23	1	AAA39504	Human Factor V sta
3083	15.2	0.5	23	1	AAA28111	Human androgen shu
3084	15.2	0.5	23	1	AAH56004	Human SCN2A PCR-SS
3085	15.2	0.5	23	1	AAF70491	Human DRD2 fragmen
c3086	15.2	0.5	23	1	ABK90968	PCR primer, 22164,
3087	15.2	0.5	23	1	ACC47485	PCR primer for det
c3088	15.2	0.5	23	1	ADC42610	Human FANCD2 PCR p
3089	15.2	0.5	23	1	ADD28129	HIV-1 LTR region D
3090	15.2	0.5	24	1	AAS18179	Human proliferatin
3091	15.2	0.5	24	1	AAL57131	RT-PCR primer 2 re
c3092	15.2	0.5	25	1	AAT27193	Stem loop oligonuc
3093	15.2	0.5	25	1	AAC96817	HLA HLA-C gene PCR
c3094	15.2	0.5	25	1	AAC96075	16s rRNA gene PCR
c3095	15.2	0.5	25	1	AAC96447	HLA DQA1 gene PCR
c3096	15.2	0.5	25	1	AAC96434	HLA DQA1 gene PCR
c3097	15.2	0.5	25	1	AAC96448	HLA DQA1 gene PCR
c3098	15.2	0.5	25	1	AAC96449	HLA DQB1 gene PCR
c3099	15.2	0.5	25	1	AAC95730	HLA DQB1 gene PCR
c3100	15.2	0.5	26	1	AAX89364	Chromosomal bindin
c3101	15.2	0.5	26	1	ABS54659	Human p53 protein
3102	15	0.5	15	1	AAQ79185	Nuclease resistant
c3103	15	0.5	15	1	AAQ79185	Nuclease resistant
3104	15	0.5	15	1	AAQ79184	Nuclease resistant
c3105	15	0.5	15	1	AAQ79184	Nuclease resistant
3106	15	0.5	15	1	AAT52136	Human ICAM hammerh
c3107	15	0.5	15	1	AAT52136	Human ICAM hammerh
3108	15	0.5	15	1	AAT52138	Human ICAM hammerh
c3109	15	0.5	15	1	AAT52138	Human ICAM hammerh
c3110	15	0.5	15	1	AAT52140	Human ICAM hammerh
c3111	15	0.5	15	1	AAT52142	Human ICAM hammerh
3112	15	0.5	15	1	AAV01604	Oligonucleotide co
c3113	15	0.5	15	1	AAV01604	Oligonucleotide co
3114	15	0.5	15	1	AAV01603	Oligonucleotide co
c3115	15	0.5	15	1	AAV01603	Oligonucleotide co
3116	15	0.5	15	1	AAV07431	Synthetic peptide-
c3117	15	0.5	15	1	AAV07431	Synthetic peptide-
3118	15	0.5	15	1	AAT86675	Oligonucleotide li
c3119	15	0.5	15	1	AAT86675	Oligonucleotide li
3120	15	0.5	15	1	AAT86605	Oligonucleotide se
c3121	15	0.5	15	1	AAT86605	Oligonucleotide se
3122	15	0.5	15	1	AAX00787	N3-P5 phosphoramid
c3123	15	0.5	15	1	AAX00787	N3-P5 phosphoramid
3124	15	0.5	15	1	AAX00788	N3-P5 phosphoramid
c3125	15	0.5	15	1	AAX00788	N3-P5 phosphoramid
3126	15	0.5	15	1	AAX55056	C/EBP-beta antisen
3127	15	0.5	15	1	AAA34503	Human adenosine re
3128	15	0.5	15	1	AAZ61854	HCV 3' non core re
c3129	15	0.5	15	1	AAZ61854	HCV 3' non core re
3130	15	0.5	15	1	AAZ64910	Substrate for HH r
c3131	15	0.5	15	1	AAZ64910	Substrate for HH r
3132	15	0.5	15	1	AAA46502	PCR primer used to
c3133	15	0.5	15	1	AAA46502	PCR primer used to
3134	15	0.5	15	1	AAA75048	Primer used to rev
c3135	15	0.5	15	1	AAA75048	Primer used to rev
3136	15	0.5	15	1	AAA07792	Nucleic acid seque
c3137	15	0.5	15	1	AAA07792	Nucleic acid seque
3138	15	0.5	15	1	AAA07794	Nucleic acid seque
c3139	15	0.5	15	1	AAA07794	Nucleic acid seque
3140	15	0.5	15	1	AAA07828	Nucleic acid seque
c3141	15	0.5	15	1	AAA07828	Nucleic acid seque
3142	15	0.5	15	1	AAA07790	Nucleic acid seque
c3143	15	0.5	15	1	AAA07790	Nucleic acid seque
3144	15	0.5	15	1	AAA07789	Nucleic acid seque
c3145	15	0.5	15	1	AAA07789	Nucleic acid seque
3146	15	0.5	15	1	AAA07795	Nucleic acid seque
c3147	15	0.5	15	1	AAA07795	Nucleic acid seque
3148	15	0.5	15	1	AAA07797	Nucleic acid seque
c3149	15	0.5	15	1	AAA07797	Nucleic acid seque
3150	15	0.5	15	1	AAA07799	Nucleic acid seque
c3151	15	0.5	15	1	AAA07799	Nucleic acid seque
3152	15	0.5	15	1	AAA07802	Nucleic acid seque
c3153	15	0.5	15	1	AAA07802	Nucleic acid seque
3154	15	0.5	15	1	AAA07825	Nucleic acid seque
c3155	15	0.5	15	1	AAA07825	Nucleic acid seque
3156	15	0.5	15	1	AAA07831	Nucleic acid seque
c3157	15	0.5	15	1	AAA07831	Nucleic acid seque
3158	15	0.5	15	1	AAA07803	Nucleic acid seque
c3159	15	0.5	15	1	AAA07803	Nucleic acid seque
3160	15	0.5	15	1	AAA07834	Nucleic acid seque
c3161	15	0.5	15	1	AAA07834	Nucleic acid seque
3162	15	0.5	15	1	AAA07796	Nucleic acid seque
c3163	15	0.5	15	1	AAA07796	Nucleic acid seque
3164	15	0.5	15	1	AAA07800	Nucleic acid seque
c3165	15	0.5	15	1	AAA07800	Nucleic acid seque
3166	15	0.5	15	1	AAA07793	Nucleic acid seque
c3167	15	0.5	15	1	AAA07793	Nucleic acid seque
3168	15	0.5	15	1	AAA07798	Nucleic acid seque
c3169	15	0.5	15	1	AAA07798	Nucleic acid seque
3170	15	0.5	15	1	AAA07788	Nucleic acid seque
c3171	15	0.5	15	1	AAA07788	Nucleic acid seque
3172	15	0.5	15	1	AAA07791	Nucleic acid seque

c3173	15	0.5	15	1	AAA07791	Nucleic acid seque
3174	15	0.5	15	1	AAA07801	Nucleic acid seque
c3175	15	0.5	15	1	AAA07801	Nucleic acid seque
3176	15	0.5	15	1	AAF20625	Human C/EBP polynu
3177	15	0.5	15	1	AAA62350	Oligonucleotide #2
c3178	15	0.5	15	1	AAA62350	Oligonucleotide #2
3179	15	0.5	15	1	AAA62347	Oligonucleotide #3
c3180	15	0.5	15	1	AAA62347	Oligonucleotide #3
3181	15	0.5	15	1	AAA62348	Oligonucleotide #4
c3182	15	0.5	15	1	AAA62348	Oligonucleotide #4
3183	15	0.5	15	1	AAH20308	Oligo dT15 EDTA la
c3184	15	0.5	15	1	AAH20308	Oligo dT15 EDTA la
3185	15	0.5	15	1	AAF30882	Oligonucleotide po
c3186	15	0.5	15	1	AAF30882	Oligonucleotide po
3187	15	0.5	15	1	AAH20511	Oligonucleotide b)
c3188	15	0.5	15	1	AAH20511	Oligonucleotide b)
c3189	15	0.5	15	1	AAF16603	Gastric acid produ
3190	15	0.5	15	1	AAH49243	PNA-forming oligon
c3191	15	0.5	15	1	AAH49243	PNA-forming oligon
3192	15	0.5	15	1	ABL40743	Chicken heparanase
c3193	15	0.5	15	1	ABL40743	Chicken heparanase
3194	15	0.5	15	1	ABA97403	Nucleotide sequenc
c3195	15	0.5	15	1	ABA97403	Nucleotide sequenc
3196	15	0.5	15	1	AAL49453	Mutation detection
c3197	15	0.5	15	1	AAL49453	Mutation detection
3198	15	0.5	15	1	AAL49455	Mutation detection
c3199	15	0.5	15	1	AAL49455	Mutation detection
3200	15	0.5	15	1	AAD29506	Primer used for th
c3201	15	0.5	15	1	AAD29506	Primer used for th
3202	15	0.5	15	1	AAD22531	Retroviral reverse
c3203	15	0.5	15	1	AAD22531	Retroviral reverse
3204	15	0.5	15	1	ABQ82140	Acceptor vector pH
c3205	15	0.5	15	1	ABQ82140	Acceptor vector pH
3206	15	0.5	15	1	ABX00240	Hepatitis C virus
c3207	15	0.5	15	1	ABX00240	Hepatitis C virus
3208	15	0.5	15	1	ABX03406	Hepatitis C virus
c3209	15	0.5	15	1	ABX03406	Hepatitis C virus
3210	15	0.5	15	1	ABL57064	Hydrazide precurso
c3211	15	0.5	15	1	ABL57064	Hydrazide precurso
3212	15	0.5	15	1	ABL57054	Hydrazide phosphor
c3213	15	0.5	15	1	ABL57054	Hydrazide phosphor
3214	15	0.5	15	1	ABL57063	Hydrazide precurso
c3215	15	0.5	15	1	ABL57063	Hydrazide precurso
3216	15	0.5	15	1	ABL57066	Amino-C6-modified
c3217	15	0.5	15	1	ABL57066	Amino-C6-modified
3218	15	0.5	15	1	ABL57059	Hydrazide precurso
c3219	15	0.5	15	1	ABL57059	Hydrazide precurso
3220	15	0.5	15	1	ABL57061	Hydrazide precurso
c3221	15	0.5	15	1	ABL57061	Hydrazide precurso
3222	15	0.5	15	1	ABL57056	Hydrazide phosphor
c3223	15	0.5	15	1	ABL57056	Hydrazide phosphor
3224	15	0.5	15	1	ABL57060	Hydrazide precurso
c3225	15	0.5	15	1	ABL57060	Hydrazide precurso
3226	15	0.5	15	1	ABK98141	Triple helix formi
c3227	15	0.5	15	1	ABK98141	Triple helix formi
3228	15	0.5	15	1	ABK98184	Triple helix formi
c3229	15	0.5	15	1	ABK98184	Triple helix formi
3230	15	0.5	15	1	ABZ96319	Human C/EBP antise
3231	15	0.5	15	1	ABZ37501	Oligonucleotide SE
c3232	15	0.5	15	1	ABZ37501	Oligonucleotide SE
3233	15	0.5	15	1	ABV74142	5' End of cDNA lib
c3234	15	0.5	15	1	ABV74142	5' End of cDNA lib
3235	15	0.5	15	1	ABV74141	Oligonucleotide us
c3236	15	0.5	15	1	ABV74141	Oligonucleotide us
3237	15	0.5	15	1	ABV75865	Oligonucleotide T1
c3238	15	0.5	15	1	ABV75865	Oligonucleotide T1
3239	15	0.5	15	1	ADA14836	Hairpin target seq
c3240	15	0.5	15	1	ADA14836	Hairpin target seq
3241	15	0.5	15	1	ADB68520	Single-base mismat
c3242	15	0.5	15	1	ADB68520	Single-base mismat
3243	15	0.5	15	1	ADC18592	Annealing control
c3244	15	0.5	15	1	ADC18592	Annealing control
c3245	15	0.5	16	1	ABL57075	Molecular beacon t
c3246	15	0.5	16	1	AAD57845	Target oligonucleo
3247	15	0.5	16	1	AAT75138	Arbitrary anchor p
3248	15	0.5	16	1	AAX89227	PCR primer H-T11A.
3249	15	0.5	16	1	AAX55055	C/EBP-beta antisen
3250	15	0.5	16	1	AAX19464	Human senescence f
3251	15	0.5	16	1	AAX19463	Human senescence f
c3252	15	0.5	16	1	AAX18360	RT-PCR primer of t
3253	15	0.5	16	1	AAX18369	RT-PCR primer of t
3254	15	0.5	16	1	AAX18368	RT-PCR primer of t
c3255	15	0.5	16	1	AAX18363	RT-PCR primer of t
3256	15	0.5	16	1	AAA99205	Human apoptosis re
3257	15	0.5	16	1	AAA99206	Human apoptosis re
3258	15	0.5	16	1	AAA34502	Human adenosine re
3259	15	0.5	16	1	AAA97561	Reverse transcript
3260	15	0.5	16	1	AAA60992	Rapid analysis of
3261	15	0.5	16	1	AAA29747	Rabbit KKIAMRE kin
3262	15	0.5	16	1	AAF20624	Human C/EBP polynu
3263	15	0.5	16	1	AAA94103	Fruit-associated b
3264	15	0.5	16	1	AAA94102	Fruit-associated b
3265	15	0.5	16	1	AAF82230	Human SFRP-1 gene
3266	15	0.5	16	1	AAF83581	B. gymnorrhiza sal
3267	15	0.5	16	1	AAF83582	B. gymnorrhiza sal
3268	15	0.5	16	1	AAS06650	Human cDNA synthes
3269	15	0.5	16	1	AAS06649	Human cDNA synthes
3270	15	0.5	16	1	ABK87149	Scarlet runner bea
3271	15	0.5	16	1	AAD34283	Mouse E2 cDNA ampl
3272	15	0.5	16	1	AAD34284	Mouse E2 cDNA ampl
3273	15	0.5	16	1	AAD32156	H-T11-C PCR primer
3274	15	0.5	16	1	AAD32155	H-T11-A PCR primer
3275	15	0.5	16	1	ABK12621	Mouse E4 protein,
3276	15	0.5	16	1	ABK12622	Mouse E4 protein,
3277	15	0.5	16	1	ABK87933	Anchored oligo-dT
3278	15	0.5	16	1	ABK87932	Anchored oligo-dT
3279	15	0.5	16	1	AAD30092	PTTG cDNA isolatin
3280	15	0.5	16	1	AAD30916	Rat PTTG1 cDNA amp
3281	15	0.5	16	1	ABZ21815	Anti-cancer drug r
3282	15	0.5	16	1	ABZ21816	Anti-cancer drug r
3283	15	0.5	16	1	ABN87397	PTTG isolation rel
3284	15	0.5	16	1	ABA98031	Human PTTG4 encodi
3285	15	0.5	16	1	ABZ96318	Human C/EBP antise
3286	15	0.5	16	1	ACC69782	Human cervical can
3287	15	0.5	16	1	ABZ70966	Human cervical can
3288	15	0.5	16	1	ADB68508	PNA-HypNA hybridis
c3289	15	0.5	16	1	ADB68508	PNA-HypNA hybridis
3290	15	0.5	16	1	ADD26193	Primer relating to
3291	15	0.5	16	1	ADD26194	Primer relating to
3292	15	0.5	16	1	ADE48126	Oligo-dT primer of
c3293	15	0.5	16	1	ADE86353	Human PTPN11 PCR p
c3294	15	0.5	17	1	AAX69799	Human flt1 VEGF re
3295	15	0.5	17	1	AAX69802	Human flt1 VEGF re
3296	15	0.5	17	1	AAV37934	Primer of the spec
c3297	15	0.5	17	1	AAV49503	Human eosinophil c
c3298	15	0.5	17	1	AAA30179	PCR primer GT15A u
3299	15	0.5	17	1	AAA30180	PCR primer GT15C u
3300	15	0.5	17	1	AAX82722	Human IgA nephropa
c3301	15	0.5	17	1	AAX82720	Human IgA nephropa
c3302	15	0.5	17	1	AAZ36739	Anchored oligo(dT)
c3303	15	0.5	17	1	AAC64202	PCR anchor primer,
3304	15	0.5	17	1	AAC64203	PCR anchor primer,
c3305	15	0.5	17	1	AAC64181	PCR anchor primer,
3306	15	0.5	17	1	AAC64182	PCR anchor primer,
c3307	15	0.5	17	1	AAC64171	PCR anchor primer,
3308	15	0.5	17	1	AAC64172	PCR anchor primer,
c3309	15	0.5	17	1	AAC64161	PCR anchor primer,
3310	15	0.5	17	1	AAC64162	PCR anchor primer,
c3311	15	0.5	17	1	AAC64213	PCR anchor primer,
3312	15	0.5	17	1	AAC64214	PCR anchor primer,
3313	15	0.5	17	1	AAC64231	PCR anchor primer,
c3314	15	0.5	17	1	AAC64230	PCR anchor primer,
c3315	15	0.5	17	1	AAC92292	Human pollinosis-a
3316	15	0.5	17	1	AAC92293	Human pollinosis-a
3317	15	0.5	17	1	AAC91720	PCR anchor primer,
c3318	15	0.5	17	1	AAC91719	PCR anchor primer,

3319	15	0.5	17	1	AAC82875	Human pollinosis-a
c3320	15	0.5	17	1	AAC82874	Human pollinosis-a
3321	15	0.5	17	1	AAH47127	Nucleotide sequenc
c3322	15	0.5	17	1	AAH47126	Nucleotide sequenc
c3323	15	0.5	17	1	ABK49634	Human Acetyltransf
3324	15	0.5	17	1	ABK49635	Human Acetyltransf
c3325	15	0.5	17	1	ABL59038	Nucleotide sequenc
3326	15	0.5	17	1	ABL59039	Nucleotide sequenc
c3327	15	0.5	17	1	ABN99829	Human allergic dis
3328	15	0.5	17	1	ABN99830	Human allergic dis
c3329	15	0.5	17	1	AAL49948	Human B1153 expres
3330	15	0.5	17	1	AAL49949	Human B1153 expres
c3331	15	0.5	17	1	AAL47234	Allergic disease e
3332	15	0.5	17	1	AAL47235	Allergic disease e
3333	15	0.5	17	1	ABK49757	Human atopic derma
c3334	15	0.5	17	1	ABK49756	Human atopic derma
3335	15	0.5	17	1	ABX79793	EST polymorphic DN
3336	15	0.5	17	1	ADC84469	PCR primer for amp
c3337	15	0.5	17	1	ADC84468	PCR primer for amp
3338	15	0.5	17	1	ADE77745	DNA oligo (SeqID 5
3339	15	0.5	17	1	AAV19118	Anchored oligo(T)
3340	15	0.5	17	1	AAX69437	Human flt1 VEGF re
3341	15	0.5	17	1	AAX69436	Human flt1 VEGF re
3342	15	0.5	17	1	AAX69435	Human flt1 VEGF re
3343	15	0.5	17	1	AAX55054	C/EBP-beta antisen
3344	15	0.5	17	1	AAA30181	PCR primer GT15G u
c3345	15	0.5	17	1	AAA30181	PCR primer GT15G u
3346	15	0.5	17	1	AAA34501	Human adenosine re
3347	15	0.5	17	1	AAZ35714	Murine gene anchor
c3348	15	0.5	17	1	AAZ35714	Murine gene anchor
3349	15	0.5	17	1	AAX82721	Human IgA nephropa
c3350	15	0.5	17	1	AAX82721	Human IgA nephropa
3351	15	0.5	17	1	AAZ36740	Anchored oligo(dT)
c3352	15	0.5	17	1	AAZ36740	Anchored oligo(dT)
3353	15	0.5	17	1	AAF20623	Human C/EBP polynu
3354	15	0.5	17	1	AAA25448	Oestrogen receptor
c3355	15	0.5	17	1	AAA25448	Oestrogen receptor
3356	15	0.5	17	1	AAC64204	PCR anchor primer,
c3357	15	0.5	17	1	AAC64204	PCR anchor primer,
3358	15	0.5	17	1	AAC64183	PCR anchor primer,
c3359	15	0.5	17	1	AAC64183	PCR anchor primer,
3360	15	0.5	17	1	AAC64173	PCR anchor primer,
c3361	15	0.5	17	1	AAC64173	PCR anchor primer,
3362	15	0.5	17	1	AAC64163	PCR anchor primer,
c3363	15	0.5	17	1	AAC64163	PCR anchor primer,
3364	15	0.5	17	1	AAC64215	PCR anchor primer,
c3365	15	0.5	17	1	AAC64215	PCR anchor primer,
3366	15	0.5	17	1	AAC64232	PCR anchor primer,
c3367	15	0.5	17	1	AAC64232	PCR anchor primer,
3368	15	0.5	17	1	AAC92294	Human pollinosis-a
c3369	15	0.5	17	1	AAC92294	Human pollinosis-a
3370	15	0.5	17	1	AAS06653	Human cDNA synthes
3371	15	0.5	17	1	AAS06656	Human cDNA synthes
3372	15	0.5	17	1	AAS06657	Human cDNA synthes
3373	15	0.5	17	1	AAS06652	Human cDNA synthes
3374	15	0.5	17	1	AAC91721	PCR anchor primer,
c3375	15	0.5	17	1	AAC91721	PCR anchor primer,
3376	15	0.5	17	1	AAC82876	Human pollinosis-a
c3377	15	0.5	17	1	AAC82876	Human pollinosis-a
3378	15	0.5	17	1	AAH47128	Nucleotide sequenc
c3379	15	0.5	17	1	AAH47128	Nucleotide sequenc
3380	15	0.5	17	1	ABK49636	Human Acetyltransf
c3381	15	0.5	17	1	ABK49636	Human Acetyltransf
c3382	15	0.5	17	1	ABQ64253	Human KTOM1a porti
c3383	15	0.5	17	1	ABQ64255	Human KTOM1a porti
c3384	15	0.5	17	1	ABQ64254	Human KTOM1a porti
3385	15	0.5	17	1	ABL59040	Nucleotide sequenc
c3386	15	0.5	17	1	ABL59040	Nucleotide sequenc
3387	15	0.5	17	1	ABN99831	Human allergic dis
c3388	15	0.5	17	1	ABN99831	Human allergic dis
3389	15	0.5	17	1	AAL49950	Human B1153 expres
c3390	15	0.5	17	1	AAL49950	Human B1153 expres
3391	15	0.5	17	1	AAL47236	Allergic disease e
c3392	15	0.5	17	1	AAL47236	Allergic disease e
3393	15	0.5	17	1	ABK49758	Human atopic derma
c3394	15	0.5	17	1	ABK49758	Human atopic derma
3395	15	0.5	17	1	ABZ96317	Human C/EBP antise
3396	15	0.5	17	1	ACC64290	Murine oligonucleo
3397	15	0.5	17	1	ADC84470	PCR primer for amp
c3398	15	0.5	17	1	ADC84470	PCR primer for amp
c3399	15	0.5	18	1	AAV54170	Nucleotide sequenc
3400	15	0.5	18	1	AAV54175	Nucleotide sequenc
3401	15	0.5	18	1	AAV54172	Nucleotide sequenc
c3402	15	0.5	18	1	AAV35391	HIV-1 gag protein
3403	15	0.5	18	1	AAZ90642	Human adipose tiss
c3404	15	0.5	18	1	AAZ90640	Human adipose tiss
3405	15	0.5	18	1	AAZ90651	Human adipose tiss
c3406	15	0.5	18	1	AAA58385	Polynucleotide # 1
3407	15	0.5	18	1	AAV54174	Nucleotide sequenc
3408	15	0.5	18	1	AAZ90650	Human adipose tiss
3409	15	0.5	18	1	AAV54171	Nucleotide sequenc
c3410	15	0.5	18	1	AAV54171	Nucleotide sequenc
3411	15	0.5	18	1	AAX55053	C/EBP-beta antisen
3412	15	0.5	18	1	AAX87332	Reverse transcript
3413	15	0.5	18	1	AAA34500	Human adenosine re
3414	15	0.5	18	1	AAZ90641	Human adipose tiss
c3415	15	0.5	18	1	AAZ90641	Human adipose tiss
3416	15	0.5	18	1	AAA58386	Polynucleotide # 2
c3417	15	0.5	18	1	AAA58386	Polynucleotide # 2
3418	15	0.5	18	1	AAZ71127	Human biallelic ma
3419	15	0.5	18	1	AAF20622	Human C/EBP polynu
3420	15	0.5	18	1	AAH74930	DNA sequence of ca
c3421	15	0.5	18	1	ABA91525	Rifampicin resista
3422	15	0.5	18	1	ABZ96316	Human C/EBP antise
c3423	15	0.5	18	1	AAL53956	DNA mutation detec
3424	15	0.5	18	1	ADC64943	Camellia sinensis
3425	15	0.5	18	1	ADC64942	Camellia sinensis
3426	15	0.5	18	1	ADC64941	Camellia sinensis
3427	15	0.5	19	1	AAX55052	C/EBP-beta antisen
3428	15	0.5	19	1	AAA34499	Human adenosine re
3429	15	0.5	19	1	AAF20621	Human C/EBP polynu
3430	15	0.5	19	1	ABK94423	Human MLH1 DNA mis
3431	15	0.5	19	1	ABZ96315	Human C/EBP antise
3432	15	0.5	20	1	AAT73293	Primer for pUC19 D
3433	15	0.5	20	1	ABZ89014	Human oligonucleot
3434	15	0.5	20	1	ABA05915	Hepatitis B virus
c3435	15	0.5	20	1	ABZ89119	Human oligonucleot
3436	15	0.5	20	1	AAC82910	Human beta-actin d
3437	15	0.5	20	1	AAZ09195	Oligonucleotide 7
c3438	15	0.5	20	1	AAZ09195	Oligonucleotide 7
3439	15	0.5	20	1	AAX55051	C/EBP-beta antisen
3440	15	0.5	20	1	AAX32003	MSH2 gene specific
3441	15	0.5	20	1	AAA34498	Human adenosine re
3442	15	0.5	20	1	AAF20620	Human C/EBP polynu
c3443	15	0.5	20	1	AAC80380	Forward primer #14
3444	15	0.5	20	1	AAC82923	Human S-9 derived
3445	15	0.5	20	1	AAC82917	Human S-9 derived
3446	15	0.5	20	1	AAC82918	Human S-9 derived
3447	15	0.5	20	1	AAC82911	Human beta-actin d
3448	15	0.5	20	1	AAC82912	Human beta-actin d
3449	15	0.5	20	1	AAC82919	Human S-9 derived
3450	15	0.5	20	1	AAC82908	Human beta-actin d
3451	15	0.5	20	1	AAC82920	Human S-9 derived
3452	15	0.5	20	1	AAC82921	Human S-9 derived
3453	15	0.5	20	1	AAF87713	Human glutathione
3454	15	0.5	20	1	ABL57070	Molecular beacon t
c3455	15	0.5	20	1	ABL57070	Molecular beacon t
c3456	15	0.5	20	1	ABZ87682	Human oligonucleot
3457	15	0.5	20	1	ABZ96314	Human C/EBP antise
c3458	15	0.5	20	1	ABZ85313	Human oligonucleot
c3459	15	0.5	20	1	ABZ89178	Human oligonucleot
3460	15	0.5	20	1	ADA45244	Human MSH2 gene PC
3461	15	0.5	20	1	AAD57844	Target oligonucleo
c3462	15	0.5	20	1	AAD57844	Target oligonucleo
c3463	15	0.5	21	1	ABL57071	Molecular beacon t
3464	15	0.5	21	1	ABS97681	Histamine N-methyl

3465	15	0.5	21	1	ABS97669	Histamine N-methyl
3466	15	0.5	21	1	AAZ26619	Human polymorphic
3467	15	0.5	21	1	AAZ26366	Human polymorphic
3468	15	0.5	21	1	AAX55050	C/EBP-beta antisen
3469	15	0.5	21	1	AAA34497	Human adenosine re
3470	15	0.5	21	1	AAF20619	Human C/EBP polynu
c3471	15	0.5	21	1	AAH62016	IL8 hairpin/hammer
3472	15	0.5	21	1	ABZ96313	Human C/EBP antise
c3473	15	0.5	21	1	ADB88602	Frizzled-4 (FZD4)
3474	15	0.5	22	1	AAT28045	3'-primer B for hu
3475	15	0.5	22	1	AAT28046	3'-primer C for hu
3476	15	0.5	22	1	AAT28048	3'-primer E for hu
3477	15	0.5	22	1	AAT28049	3'-primer F for hu
3478	15	0.5	22	1	AAT28054	3'-primer L for hu
3479	15	0.5	22	1	AAT28055	3'-primer M for hu
3480	15	0.5	22	1	AAT28047	3'-primer D for hu
3481	15	0.5	22	1	AAT28044	3'-primer A for hu
3482	15	0.5	22	1	AAT58488	First primer #5 fo
3483	15	0.5	22	1	AAT58494	First primer #11 f
3484	15	0.5	22	1	AAT58489	First primer #6 fo
3485	15	0.5	22	1	AAT58487	First primer #4 fo
3486	15	0.5	22	1	AAT58495	First primer #12 f
3487	15	0.5	22	1	AAT58484	First primer #1 fo
3488	15	0.5	22	1	AAT58485	First primer #2 fo
3489	15	0.5	22	1	AAT58486	First primer #3 fo
3490	15	0.5	22	1	AAV58375	Biotinylated prime
3491	15	0.5	22	1	AAV03675	Oligo dT primer.
3492	15	0.5	22	1	AAX55049	C/EBP-beta antisen
3493	15	0.5	22	1	AAX77101	GC6 gene 3' primer
3494	15	0.5	22	1	AAA34496	Human adenosine re
3495	15	0.5	22	1	AAZ47353	PCR primer M used
3496	15	0.5	22	1	AAZ47347	PCR primer F used
3497	15	0.5	22	1	AAZ47346	PCR primer E used
3498	15	0.5	22	1	AAZ47352	PCR primer L used
3499	15	0.5	22	1	AAZ47342	PCR primer A used
3500	15	0.5	22	1	AAZ47344	PCR primer C used
3501	15	0.5	22	1	AAZ47343	PCR primer B used
3502	15	0.5	22	1	AAZ47345	PCR primer D used
3503	15	0.5	22	1	AAA99617	(T)-primer for fir
3504	15	0.5	22	1	AAF20618	Human C/EBP polynu
3505	15	0.5	22	1	AAH22185	Human hepatocyte a
3506	15	0.5	22	1	AAH22189	Human hepatocyte a
3507	15	0.5	22	1	AAH22188	Human hepatocyte a
3508	15	0.5	22	1	AAH22187	Human hepatocyte a
3509	15	0.5	22	1	AAH22190	Human hepatocyte a
3510	15	0.5	22	1	AAH22195	Human hepatocyte a
3511	15	0.5	22	1	AAH22186	Human hepatocyte a
3512	15	0.5	22	1	ABZ96312	Human C/EBP antise
3513	15	0.5	22	1	AAL56810	T(13) bio-primer o
c3514	15	0.5	23	1	AAZ99839	Nucleotide sequenc
c3515	15	0.5	23	1	AAQ36059	HIV-2 detection se
c3516	15	0.5	23	1	AAV30513	Sunflower ORF522 p
3517	15	0.5	23	1	AAX55048	C/EBP-beta antisen
3518	15	0.5	23	1	AAA34495	Human adenosine re
c3519	15	0.5	23	1	AAZ47417	Probe 1 used to co
3520	15	0.5	23	1	AAZ49423	Human Galectin 11
3521	15	0.5	23	1	AAZ55321	Neisseria species
3522	15	0.5	23	1	AAA10628	PCR primer #2 used
3523	15	0.5	23	1	AAF20617	Human C/EBP polynu
c3524	15	0.5	23	1	AAA53817	Primer BTU1-75 hyb
3525	15	0.5	23	1	AAC66214	Galectin 11 PCR pr
c3526	15	0.5	23	1	AAC83568	Human FMR1 gene 5'
c3527	15	0.5	23	1	AAC92334	Human hTMPT27 PCR
3528	15	0.5	23	1	AAH28300	3' untranslated re
3529	15	0.5	23	1	AAS13613	Forward PCR primer
c3530	15	0.5	23	1	ABT05505	NOVX related probe
3531	15	0.5	23	1	ABZ96311	Human C/EBP antise
3532	15	0.5	23	1	ABV74137	Oligonucleotide us
c3533	15	0.5	23	1	ABV74137	Oligonucleotide us
c3534	15	0.5	24	1	AAH75424	Human homo laminin
3535	15	0.5	24	1	ABL60935	Human nucleotide r
c3536	15	0.5	24	1	ABV93494	Bacillus thuringie
c3537	15	0.5	24	1	ABV93779	B. thuringiensis t
c3538	15	0.5	25	1	ABK87633	BamT15G PCR primer
c3539	15	0.5	25	1	ABK87631	BamT15A PCR primer
3540	15	0.5	25	1	AAC96446	HLA DQA1 gene PCR
c3541	15	0.5	25	1	AAT38116	NotI-oligo primer.
3542	15	0.5	25	1	AAX40404	Seq ID No:2 of WO9
c3543	15	0.5	25	1	AAC96343	HLA DPB1 gene PCR
3544	15	0.5	25	1	AAC96433	HLA DQA1 gene PCR
c3545	15	0.5	25	1	AAC66194	PCR primer EcoR1-d
c3546	15	0.5	25	1	AAC96099	16s rRNA gene PCR
c3547	15	0.5	26	1	AAT13051	cDNA primer. Synt
c3548	15	0.5	26	1	AAT39393	Cotton fibre cDNA
c3549	15	0.5	26	1	AAT43363	Cotton fibre first
c3550	15	0.5	26	1	AAT62627	Primer for cotton
c3551	15	0.5	26	1	AAT63663	Primer for cotton
c3552	15	0.5	26	1	AAT70058	Primer for cotton
c3553	15	0.5	30	1	AAI65862	Nucleotide sequenc
c3554	14.8	0.5	18	1	AAN60096	Sequence of probe
c3555	14.8	0.5	18	1	AAX32947	Duplex target sequ
c3556	14.8	0.5	18	1	AAZ31863	Human G-alpha-13 a
c3557	14.8	0.5	18	1	AAZ46099	PCR primer used to
c3558	14.8	0.5	18	1	AAA55497	TRAF1 antisense ol
3559	14.8	0.5	18	1	AAA51250	Primer 4 for casei
c3560	14.8	0.5	18	1	AAA63121	Antisense oligonuc
3561	14.8	0.5	18	1	AAF85699	Multiple repeated
3562	14.8	0.5	18	1	ABA91529	DNA-RNA-DNA oligon
c3563	14.8	0.5	18	1	ABA91529	DNA-RNA-DNA oligon
c3564	14.8	0.5	19	1	ADE27346	Stearoyl-CoA desat
3565	14.8	0.5	19	1	ADE27636	Stearoyl-CoA desat
c3566	14.8	0.5	19	1	ABK94423	Human MLH1 DNA mis
3567	14.8	0.5	19	1	AAQ20030	Cross-linking olig
3568	14.8	0.5	19	1	AAQ30373	Oligomer HUM beta
3569	14.8	0.5	19	1	AAQ30376	Oligomer HUM beta
3570	14.8	0.5	19	1	AAT32774	Triple helix-formi
c3571	14.8	0.5	19	1	AAT43004	Rat type L pyruvat
3572	14.8	0.5	19	1	AAV05816	Oligonucleotide #4
3573	14.8	0.5	19	1	AAZ59024	Oligonucleotide GA
3574	14.8	0.5	19	1	AAZ59016	Triple helix formi
c3575	14.8	0.5	19	1	AAX09077	Tumour necrosis fa
3576	14.8	0.5	19	1	AAA83538	cdk-we-hu ribozyme
3577	14.8	0.5	19	1	AAF76366	Mutant E. coli J g
3578	14.8	0.5	19	1	AAH58700	Cdk-we-hu ribozyme
3579	14.8	0.5	19	1	AAS01754	5' end of endochit
3580	14.8	0.5	19	1	AAS19331	Triple helix formi
3581	14.8	0.5	19	1	AAD27678	RNA/DNA hybrid com
3582	14.8	0.5	19	1	ADD00279	HCV coding region-
3583	14.8	0.5	19	1	ADD00127	HCV coding region-
3584	14.8	0.5	19	1	ADE65640	Human c-fos transc
c3585	14.8	0.5	19	1	ADE65756	Human c-fos siNA 1
3586	14.8	0.5	20	1	AAQ68872	Oligonucleotide (S
c3587	14.8	0.5	20	1	AAA94536	Antisense oligonuc
3588	14.8	0.5	20	1	AAH91454	Human inflammatory
3589	14.8	0.5	20	1	ABQ96037	Tumour suppression
c3590	14.8	0.5	20	1	ABZ85668	Human oligonucleot
3591	14.8	0.5	20	1	ABZ89545	Human oligonucleot
3592	14.8	0.5	20	1	ABZ90649	Human oligonucleot
c3593	14.8	0.5	20	1	AAC82909	Human beta-actin d
c3594	14.8	0.5	20	1	AAC82923	Human S-9 derived
c3595	14.8	0.5	20	1	AAC82911	Human beta-actin d
c3596	14.8	0.5	20	1	AAC82908	Human beta-actin d
c3597	14.8	0.5	20	1	AAQ20027	Cross-linking olig
c3598	14.8	0.5	20	1	AAQ30371	Oligomer HUM beta
c3599	14.8	0.5	20	1	AAQ30372	Oligomer HUM beta
3600	14.8	0.5	20	1	AAQ54136	Multiplex vector 1
c3601	14.8	0.5	20	1	AAQ68869	Self paired oligon
3602	14.8	0.5	20	1	AAT44460	5' primer for lami
3603	14.8	0.5	20	1	AAT13503	PCR primer (TSK8B)
c3604	14.8	0.5	20	1	AAX32946	Seq ID No: 13 of U
3605	14.8	0.5	20	1	AAT73396	S. pneumoniae HSP7
c3606	14.8	0.5	20	1	AAX80654	Primer2 for mutant
c3607	14.8	0.5	20	1	AAZ46525	Mouse CACNA1F exon
3608	14.8	0.5	20	1	AAA55739	TRAF1 antisense ol
c3609	14.8	0.5	20	1	AAA60337	Human HPC2 cDNA ex
c3610	14.8	0.5	20	1	AAA60341	Human HPC2 cDNA ex

c3611	14.8	0.5	20	1	AAA94534	Antisense oligonuc
3612	14.8	0.5	20	1	AAA94535	Antisense oligonuc
c3613	14.8	0.5	20	1	AAA94535	Antisense oligonuc
3614	14.8	0.5	20	1	AAA11308	Human TRPC7 gene i
c3615	14.8	0.5	20	1	AAZ60521	PCR primer CATATGN
c3616	14.8	0.5	20	1	AAA50702	Sense strand encod
c3617	14.8	0.5	20	1	AAA80354	Human ASTH1I 5' re
c3618	14.8	0.5	20	1	AAF81969	Escherichia coli F
3619	14.8	0.5	20	1	AAH02131	C. difficile cdtA
3620	14.8	0.5	20	1	AAH25642	Antisense oligonuc
3621	14.8	0.5	20	1	AAS10558	Human caspase 3 an
c3622	14.8	0.5	20	1	AAH42680	Primer and probe f
3623	14.8	0.5	20	1	ABN84466	Alpha-amylase-2A f
3624	14.8	0.5	20	1	ABA83519	Human MP-1 antisen
3625	14.8	0.5	20	1	AAD31950	Human microtubule
3626	14.8	0.5	20	1	AAD31912	Borrelia burgdorfe
c3627	14.8	0.5	20	1	ABS53426	Human Jun-B PCR pr
c3628	14.8	0.5	20	1	AAS99076	Human prostate can
c3629	14.8	0.5	20	1	AAS99072	Human prostate can
3630	14.8	0.5	20	1	ABN81300	Ancyclobacter form
c3631	14.8	0.5	20	1	ABZ30368	Candida albicans G
3632	14.8	0.5	20	1	AAD44835	Human raf kinase r
3633	14.8	0.5	20	1	ABI93269	Capture oligonucle
3634	14.8	0.5	20	1	ABI96918	Capture oligonucle
c3635	14.8	0.5	20	1	ABK47115	Mouse R1-OS-B1-B2
c3636	14.8	0.5	20	1	ABZ93604	Human oligonucleot
3637	14.8	0.5	20	1	ABZ89084	Human oligonucleot
c3638	14.8	0.5	20	1	ABZ90035	Human oligonucleot
3639	14.8	0.5	20	1	ABZ90375	Human oligonucleot
c3640	14.8	0.5	20	1	ABZ90375	Human oligonucleot
3641	14.8	0.5	20	1	ABZ99051	Human PDE4C oligon
c3642	14.8	0.5	20	1	ABZ99051	Human PDE4C oligon
3643	14.8	0.5	20	1	ABZ86258	Human oligonucleot
c3644	14.8	0.5	20	1	ADA66499	Transforming growt
c3645	14.8	0.5	20	1	ABV72400	PCR primer used to
3646	14.8	0.5	20	1	ACD42151	Human raf-associat
3647	14.8	0.5	20	1	ABT34147	Human short hetero
3648	14.8	0.5	20	1	ABZ68360	Primer XpYpB2 used
3649	14.8	0.5	20	1	ACC70832	Thiobacillus halog
c3650	14.8	0.5	20	1	ACC47022	Mouse phospholipas
c3651	14.8	0.5	20	1	AAD47544	Human Artemis exon
c3652	14.8	0.5	20	1	AAD55496	Human FGFR-3 antis
c3653	14.8	0.5	20	1	AAL53965	DNA mutation detec
3654	14.8	0.5	20	1	ACF57337	Human atlastin exo
3655	14.8	0.5	20	1	ACF04230	Murine embryonic c
3656	14.8	0.5	20	1	ACH66496	Sense PCR primer u
c3657	14.8	0.5	20	1	ADC65824	Mouse TGF-beta rec
3658	14.8	0.5	21	1	AAQ65146	Antisense oligonuc
3659	14.8	0.5	21	1	AAT05742	Plant consensus sp
c3660	14.8	0.5	21	1	AAT76513	Endothelial nitric
c3661	14.8	0.5	21	1	AAZ26632	Human polymorphic
c3662	14.8	0.5	21	1	AAZ26714	Human polymorphic
c3663	14.8	0.5	21	1	AAX56816	WO9922023 probe 52
c3664	14.8	0.5	21	1	AAX54304	Endothelial nitric
c3665	14.8	0.5	21	1	AAA33748	Low adenosine anti
c3666	14.8	0.5	21	1	AAF19870	Human endothelial
c3667	14.8	0.5	21	1	AAC86173	Tyr300 primer #1.
3668	14.8	0.5	21	1	ABK65637	Human single nucle
c3669	14.8	0.5	21	1	ABZ95564	Human endothelial
3670	14.8	0.5	21	1	ACC79539	Human TCH169 PCR p
c3671	14.8	0.5	22	1	AAV26091	Mandarin mb2ch1 ge
3672	14.8	0.5	22	1	AAV82676	5' PCR primer F2 u
c3673	14.8	0.5	22	1	ABZ10343	Haematopoietic cel
c3674	14.8	0.5	22	1	ACC80022	Human HDAC9 exon 2
c3675	14.8	0.5	22	1	ADE84289	Human lymphoid cel
c3676	14.8	0.5	23	1	AAH91823	Human inflammatory
c3677	14.8	0.5	24	1	AAC96428	HLA DQA1 gene PCR
3678	14.8	0.5	24	1	AAZ07017	Murine alpha-L-idu
3679	14.8	0.5	24	1	AAS19218	Kringle protein 14
c3680	14.8	0.5	25	1	AAC96784	HLA HLA-A gene PCR
c3681	14.8	0.5	25	1	AAC96182	16s rRNA gene PCR
3682	14.8	0.5	25	1	AAC96089	16s rRNA gene PCR
c3683	14.8	0.5	25	1	AAH28308	3' untranslated re
c3684	14.8	0.5	25	1	AAC96511	HLA DQB1 gene PCR
c3685	14.8	0.5	25	1	AAC96618	HLA DRB345 gene PC
3686	14.6	0.5	15	1	ABN87920	Human GSR allele s
3687	14.6	0.5	21	1	ADB88602	Frizzled-4 (FZD4)
3688	14.6	0.5	21	1	AAZ26632	Human polymorphic
3689	14.6	0.5	21	1	AAQ61989	HIV replication in
3690	14.6	0.5	21	1	AAQ99590	Human TPO anti-sen
3691	14.6	0.5	21	1	AAT35001	HIV inhibitor #4.
3692	14.6	0.5	21	1	AAT10482	Anti-HIV TAR regio
3693	14.6	0.5	21	1	AAZ26823	Human polymorphic
3694	14.6	0.5	21	1	AAZ26499	Human polymorphic
c3695	14.6	0.5	21	1	AAZ26499	Human polymorphic
3696	14.6	0.5	21	1	AAZ26114	Human polymorphic
c3697	14.6	0.5	21	1	AAV99170	Antisense primer f
3698	14.6	0.5	21	1	AAX33038	Human BRCA2 gene P
3699	14.6	0.5	21	1	AAZ59327	Human STP2 exon 7
c3700	14.6	0.5	21	1	AAZ58833	Human beta2-microg
3701	14.6	0.5	21	1	AAZ99642	Nucleotide sequenc
c3702	14.6	0.5	21	1	AAZ74861	Human biallelic ma
3703	14.6	0.5	21	1	AAF97598	Human gene single
3704	14.6	0.5	21	1	AAF96163	Human gene single
c3705	14.6	0.5	21	1	AAF95716	Human gene single
c3706	14.6	0.5	21	1	AAF30891	Mismatched target
c3707	14.6	0.5	21	1	AAH62490	PTK2 polymorphism
c3708	14.6	0.5	21	1	AAH62659	Glucosidase alpha
3709	14.6	0.5	21	1	ABA04384	AtERF4 PCR primer
3710	14.6	0.5	21	1	ABK70498	In-situ analysis s
c3711	14.6	0.5	21	1	ABA03336	S chrysomallus act
3712	14.6	0.5	21	1	ABS97903	Human UDP-glucuron
c3713	14.6	0.5	21	1	ABS97903	Human UDP-glucuron
c3714	14.6	0.5	21	1	ABS98297	Human lactoferrin
3715	14.6	0.5	21	1	ABS66996	Human MRP-1 polymo
c3716	14.6	0.5	21	1	ABS66995	Human MRP-1 polymo
3717	14.6	0.5	21	1	ABV73012	Murine cPLA2/B mut
c3718	14.6	0.5	21	1	ABX70767	Human RTQ-PCR prim
c3719	14.6	0.5	21	1	ABQ83354	Beta-2-microglobul
c3720	14.6	0.5	21	1	ABQ83360	Beta-2-microglobul
c3721	14.6	0.5	21	1	ACF04379	Respiratory syncyt
c3722	14.6	0.5	21	1	ACF04375	Respiratory syncyt
c3723	14.6	0.5	21	1	ACF04377	Respiratory syncyt
3724	14.6	0.5	21	1	AAL56640	S36 primer to ampl
3725	14.6	0.5	21	1	ADC16469	Short interfering
c3726	14.6	0.5	21	1	ADC16522	Short interfering
3727	14.6	0.5	21	1	ADD56745	Human gene express
c3728	14.6	0.5	22	1	AAQ42237	PCR primer Gelo-19
3729	14.6	0.5	22	1	AAQ87318	PCR primer of micr
c3730	14.6	0.5	22	1	AAT37086	DNA primer to ampl
c3731	14.6	0.5	22	1	AAT12804	E. coli ilvGMEDA o
c3732	14.6	0.5	22	1	AAT62748	Primer for Escheri
3733	14.6	0.5	22	1	AAT93818	Antitumoural phosp
3734	14.6	0.5	22	1	AAV47448	Antisense oligonuc
3735	14.6	0.5	22	1	AAX14678	Triple helix formi
3736	14.6	0.5	22	1	AAV74151	Human thyroid gene
c3737	14.6	0.5	22	1	AAA35437	Myrtaceae microsat
c3738	14.6	0.5	22	1	AAA12754	5' PCR primer for
3739	14.6	0.5	22	1	AAD00662	Synthetic oligonuc
c3740	14.6	0.5	22	1	AAA06866	Human IgG4 PCR pri
3741	14.6	0.5	22	1	AAA53024	Human beta-1,3-gal
c3742	14.6	0.5	22	1	AAC83021	alpha V integrin p
3743	14.6	0.5	22	1	AAA66933	Dog genomic marker
3744	14.6	0.5	22	1	AAH22316	Brain ankyrin-2 hy
3745	14.6	0.5	22	1	AAH28299	3' untranslated re
3746	14.6	0.5	22	1	AAH28297	3' untranslated re
c3747	14.6	0.5	22	1	AAC85377	Mutagenic primer #
3748	14.6	0.5	22	1	ABQ79748	Human znssp2 cDNA
c3749	14.6	0.5	22	1	ABT06326	Human NOVX coding
3750	14.6	0.5	22	1	ABZ31358	Candida albicans G
3751	14.6	0.5	22	1	AAL47282	Hepatitis C virus
c3752	14.6	0.5	22	1	AAD32695	Escherichia coli M
c3753	14.6	0.5	22	1	ABT21552	Multiplex group PC
c3754	14.6	0.5	22	1	ACC78700	Nucleotide sequenc
3755	14.6	0.5	22	1	ACC90648	Human CYP1A2 PCR p
c3756	14.6	0.5	22	1	ACD06310	Reverse RT-PCR pri

3757	14.6	0.5	22	1	ACC84173	Human butyrylcholi
c3758	14.6	0.5	22	1	ADD21875	Protein translatio
c3759	14.6	0.5	24	1	ABQ78896	Human zinc finger
c3760	14.6	0.5	24	1	ADD19369	Salmo salar SNP OL
c3761	14.6	0.5	24	1	AAK99651	Human alpha 2, 3-s
c3762	14.6	0.5	25	1	AAC96700	HLA HLA-A gene PCR
3763	14.6	0.5	25	1	AAC95708	HLA DQA1 gene PCR
c3764	14.6	0.5	25	1	AAC95789	HLA DRB1 gene PCR
3765	14.6	0.5	25	1	AAC96432	HLA DQA1 gene PCR
3766	14.6	0.5	25	1	AAC96396	HLA DPB1 gene PCR
c3767	14.6	0.5	26	1	AAV07974	Helicobacter pylor
3768	14.4	0.5	16	1	AAX18362	RT-PCR primer of t
c3769	14.4	0.5	16	1	AAX18369	RT-PCR primer of t
3770	14.4	0.5	16	1	AAX18363	RT-PCR primer of t
c3771	14.4	0.5	16	1	AAX18365	RT-PCR primer of t
3772	14.4	0.5	16	1	AAX18366	RT-PCR primer of t
c3773	14.4	0.5	16	1	AAX18366	RT-PCR primer of t
3774	14.4	0.5	16	1	AAX18367	RT-PCR primer of t
c3775	14.4	0.5	16	1	AAX18367	RT-PCR primer of t
c3776	14.4	0.5	16	1	AAC91050	Selection target #
c3777	14.4	0.5	16	1	AAS11434	Selection target #
c3778	14.4	0.5	16	1	AAS11444	Oligonucleotide #2
c3779	14.4	0.5	16	1	AAA89332	DNA ligand modulat
3780	14.4	0.5	16	1	ABL57076	Molecular beacon t
3781	14.4	0.5	16	1	ABK87931	Anchored oligo-dT
3782	14.4	0.5	16	1	AAD44143	Oligo-dT PCR prime
c3783	14.4	0.5	16	1	AAD44143	Oligo-dT PCR prime
3784	14.4	0.5	16	1	AAD57846	Target oligonucleo
c3785	14.4	0.5	17	1	AAA25453	Oestrogen receptor
3786	14.4	0.5	17	1	AAQ30741	DNA/RNA expression
3787	14.4	0.5	17	1	AAX69795	Human flt1 VEGF re
c3788	14.4	0.5	17	1	AAX69805	Human flt1 VEGF re
3789	14.4	0.5	17	1	AAX71230	Human KDR VEGF rec
c3790	14.4	0.5	17	1	AAV97632	Human EGF-R target
3791	14.4	0.5	17	1	AAX14657	Triple helix third
c3792	14.4	0.5	17	1	AAX14656	Triple helix formi
3793	14.4	0.5	17	1	AAA25454	Oestrogen receptor
c3794	14.4	0.5	17	1	AAC72830	Single nucleotide
3795	14.4	0.5	17	1	AAF06381	Hammerhead ribozym
3796	14.4	0.5	17	1	AAF02423	Hammerhead ribozym
3797	14.4	0.5	17	1	AAF06380	Hammerhead ribozym
c3798	14.4	0.5	17	1	AAF02617	Hammerhead ribozym
c3799	14.4	0.5	17	1	AAF06327	Hammerhead ribozym
c3800	14.4	0.5	17	1	ABK02790	Human CD20 Hammerh
3801	14.4	0.5	17	1	ABS76195	Human PAPP-Eb asso
3802	14.4	0.5	17	1	ABS75130	Human PAPP-Ea asso
3803	14.4	0.5	17	1	ABS75129	Human PAPP-Ea asso
3804	14.4	0.5	17	1	ABS76196	Human PAPP-Eb asso
3805	14.4	0.5	17	1	ACA99707	G-protein coupled
3806	14.4	0.5	17	1	ACA99708	G-protein coupled
c3807	14.4	0.5	17	1	ABT35038	Tumour suppression
3808	14.4	0.5	17	1	ADB04268	Human MDZ7 scannin
c3809	14.4	0.5	17	1	ADB04268	Human MDZ7 scannin
3810	14.4	0.5	17	1	ADB04274	Human MDZ7 scannin
c3811	14.4	0.5	17	1	ADB04274	Human MDZ7 scannin
3812	14.4	0.5	17	1	ABZ65389	Human HER2 DNAzyme
3813	14.4	0.5	17	1	ABZ61368	Human H-Ras DNAzym
c3814	14.4	0.5	17	1	ACD58402	HCV DNAzyme substr
3815	14.4	0.5	17	1	ACD64268	HCV minus strand D
c3816	14.4	0.5	17	1	ACC68555	Murine oligonucleo
3817	14.4	0.5	17	1	ADB44223	Tumour suppression
3818	14.4	0.5	18	1	AAQ67045	Polynucleotide dir
3819	14.4	0.5	18	1	AAQ90172	Pollen allergen ge
3820	14.4	0.5	18	1	AAX32945	Seq ID No: 12 of U
c3821	14.4	0.5	18	1	AAX63290	Delta-9 desaturase
c3822	14.4	0.5	18	1	AAZ48497	Human TNFR1 mRNA i
3823	14.4	0.5	18	1	ABL57566	Synthetic deoxyrib
c3824	14.4	0.5	18	1	ABA82471	Zmax1 gene region
c3825	14.4	0.5	18	1	ABT04993	TNFR1 expression m
c3826	14.4	0.5	18	1	AAD40585	HIV-1 LTR lucifera
3827	14.4	0.5	18	1	ABA97651	Poly w nucleotide
c3828	14.4	0.5	18	1	ABK23268	Human Zmax1 cDNA r
3829	14.4	0.5	18	1	ABL95913	Probe poly w for a
c3830	14.4	0.5	18	1	ACA60581	Antisense inhibiti
3831	14.4	0.5	18	1	ACF62964	Human p16 PCR prim
c3832	14.4	0.5	18	1	ACF62962	Human p16 PCR prim
c3833	14.4	0.5	18	1	ABZ10570	Haematopoietic cel
c3834	14.4	0.5	18	1	ACC45851	Human HBM STS mark
c3835	14.4	0.5	18	1	ADB98549	Sequence tagged si
c3836	14.4	0.5	18	1	ADB54572	Hybridisation olig
c3837	14.4	0.5	18	1	ADC70087	Primer oligo used
c3838	14.4	0.5	19	1	AAQ79881	Adrenodoxin-reduct
3839	14.4	0.5	19	1	AAV44620	Human uncoupling p
c3840	14.4	0.5	19	1	AAX79665	Human LKB1 gene pr
3841	14.4	0.5	19	1	AAZ57803	HSV-2 ICP4 gene fo
c3842	14.4	0.5	19	1	AAA27545	Fas ligand promote
c3843	14.4	0.5	19	1	ADC65121	Methylobacillus ep
3844	14.4	0.5	20	1	AAL62328	Human transcriptio
c3845	14.4	0.5	20	1	AAV22586	Antisense oligonuc
c3846	14.4	0.5	20	1	AAA90815	Ribonucleotide red
c3847	14.4	0.5	20	1	AAX32010	MSH2 gene specific
c3848	14.4	0.5	20	1	ADA45251	Human MSH2 gene PC
3849	14.4	0.5	20	1	AAC82924	Human S-9 derived
3850	14.4	0.5	20	1	ABZ89440	Human oligonucleot
c3851	14.4	0.5	20	1	AAC82917	Human S-9 derived
c3852	14.4	0.5	20	1	AAC82918	Human S-9 derived
c3853	14.4	0.5	20	1	AAC82919	Human S-9 derived
c3854	14.4	0.5	20	1	AAC82920	Human S-9 derived
3855	14.4	0.5	20	1	ABZ85313	Human oligonucleot
3856	14.4	0.5	20	1	ABZ89178	Human oligonucleot
3857	14.4	0.5	20	1	AAQ52305	FKBP12C PCR primer
3858	14.4	0.5	20	1	AAQ53303	Probe 5 based on s
3859	14.4	0.5	20	1	AAQ40165	DiGeorge syndrome
3860	14.4	0.5	20	1	AAQ77670	Probe for alcohol
3861	14.4	0.5	20	1	AAT87898	Lower primer for e
3862	14.4	0.5	20	1	AAV41334	Interleukin-9 (IL-
c3863	14.4	0.5	20	1	AAX95502	PCR primer used to
c3864	14.4	0.5	20	1	AAX93519	PCR primer used to
3865	14.4	0.5	20	1	AAX93371	PCR primer used to
3866	14.4	0.5	20	1	AAX96785	PCR primer used to
3867	14.4	0.5	20	1	AAA55978	Human G713 PCR pri
3868	14.4	0.5	20	1	AAZ77152	Human biallelic ma
3869	14.4	0.5	20	1	AAZ70964	Human biallelic ma
c3870	14.4	0.5	20	1	AAD11331	Human cot oncogene
3871	14.4	0.5	20	1	AAF23315	Oligonucleotide fo
3872	14.4	0.5	20	1	AAH80592	Oligonucleotide hy
3873	14.4	0.5	20	1	AAH80591	Oligonucleotide hy
3874	14.4	0.5	20	1	AAH80593	Oligonucleotide hy
3875	14.4	0.5	20	1	AAH80590	Oligonucleotide hy
3876	14.4	0.5	20	1	ABK90289	Bcl-2-targeting an
c3877	14.4	0.5	20	1	AAD33529	Actin specific RT-
c3878	14.4	0.5	20	1	ABQ65350	Human gene methyla
3879	14.4	0.5	20	1	AAD36554	Human Her-1 antise
c3880	14.4	0.5	20	1	ABK34138	Human MHC PCR prim
c3881	14.4	0.5	20	1	ABZ26083	Mitochondrial cyto
3882	14.4	0.5	20	1	AAD24274	Human chromosome 2
3883	14.4	0.5	20	1	ABQ78545	Antisense oligodeo
c3884	14.4	0.5	20	1	ABK28076	Human MHC methylat
3885	14.4	0.5	20	1	ABK69560	Rat phosphorylase
3886	14.4	0.5	20	1	ABL54173	Oligonucleotide.
3887	14.4	0.5	20	1	ABZ85693	Human oligonucleot
c3888	14.4	0.5	20	1	ABZ90754	Human oligonucleot
3889	14.4	0.5	20	1	ABZ88617	Human oligonucleot
c3890	14.4	0.5	20	1	ABZ88617	Human oligonucleot
3891	14.4	0.5	20	1	ABZ90451	Human oligonucleot
c3892	14.4	0.5	20	1	ABZ91600	Human oligonucleot
3893	14.4	0.5	20	1	ABZ88121	Human oligonucleot
c3894	14.4	0.5	20	1	ABZ85508	Human oligonucleot
3895	14.4	0.5	20	1	ABZ93178	Human oligonucleot
3896	14.4	0.5	20	1	ABQ77172	Human ABCC12 intro
c3897	14.4	0.5	20	1	ADA20513	Prostate tumour re
c3898	14.4	0.5	20	1	ADA84316	Human G6E PCR prim
c3899	14.4	0.5	20	1	AAL53963	DNA mutation detec
c3900	14.4	0.5	20	1	ADB89911	Antinsense oligonu
3901	14.4	0.5	20	1	ADC66070	Human CFTR sequenc
3902	14.4	0.5	20	1	ADC66069	Human CFTR sequenc

3903	14.4	0.5	20	1	ADD20414	Oreochromis niloti
3904	14.4	0.5	20	1	ADD81484	HIV PRT antisense
3905	14.4	0.5	20	1	ADD81483	HIV PRT antisense
3906	14.4	0.5	20	1	ADD81482	HIV PRT antisense
3907	14.4	0.5	20	1	ADD81481	HIV PRT antisense
c3908	14.4	0.5	21	1	AAZ26619	Human polymorphic
c3909	14.4	0.5	21	1	AAT94317	Human DPC4 sequenc
3910	14.4	0.5	21	1	AAZ26572	Human polymorphic
c3911	14.4	0.5	21	1	AAA11454	Human dysferlin PC
c3912	14.4	0.5	21	1	AAA36909	Human dysferlin ex
c3913	14.4	0.5	21	1	AAA30231	Human housekeeping
3914	14.4	0.5	21	1	AAF95557	Human gene single
3915	14.4	0.5	21	1	AAF95571	Human gene single
3916	14.4	0.5	21	1	AAF87033	Anchored 3' oligo
c3917	14.4	0.5	21	1	AAF80105	Nucleotide sequenc
3918	14.4	0.5	21	1	ABL57072	Molecular beacon t
3919	14.4	0.5	21	1	ABX11284	Mouse P0 gene 5' U
c3920	14.4	0.5	21	1	ABS58234	Sequence surroundi
3921	14.4	0.5	21	1	ABQ80008	SiRNA duplex antis
3922	14.4	0.5	22	1	AAQ90036	Human SMP30 gene P
c3923	14.4	0.5	22	1	AAQ82287	Chromosome 11 (loc
3924	14.4	0.5	22	1	AAT62686	Primer for human s
c3925	14.4	0.5	22	1	AAV51724	Zea mays genome re
3926	14.4	0.5	22	1	AAA72031	Human cathepsin Y
c3927	14.4	0.5	22	1	ABS52173	Human forward prim
3928	14.4	0.5	22	1	ABV73127	N-acetyltransferas
3929	14.4	0.5	22	1	ABV74921	NAT1*14 allele spe
c3930	14.4	0.5	22	1	ABQ78653	Nucleotide sequenc
3931	14.4	0.5	22	1	ABA00253	NAT1 A560G mutatio
3932	14.4	0.5	22	1	AAD54260	NAT1 mutant allele
3933	14.4	0.5	22	1	ABZ75815	NAT1 allele NAT1*1
3934	14.4	0.5	22	1	AAD50983	NAT1 allele specif
3935	14.4	0.5	22	1	ABZ20529	Human NAT1 genotyp
3936	14.4	0.5	22	1	ABZ23147	PCR primer used to
3937	14.4	0.5	22	1	ABV72580	Primer used to det
3938	14.4	0.5	22	1	AAL53876	Gastroesophageal r
3939	14.4	0.5	22	1	AAD51919	N-acetyl transfera
3940	14.4	0.5	22	1	ABZ23435	Primer used to amp
3941	14.4	0.5	22	1	AAD54568	Human M2-PK gene a
3942	14.4	0.5	22	1	AAD47697	N-acetyltransferss
3943	14.4	0.5	22	1	ABV76236	N-acetyltransferas
3944	14.4	0.5	22	1	ACF05573	N-acetyltransferas
3945	14.4	0.5	22	1	ACC79724	N-acetyltransferas
3946	14.4	0.5	22	1	ACC83560	N-acetyltransferas
3947	14.4	0.5	22	1	ACF04612	Human NAT1 NAT1*14
c3948	14.4	0.5	24	1	ABA05517	Human Tre carcinog
c3949	14.4	0.5	24	1	ABA99264	Human tra oncogene
3950	14.4	0.5	24	1	ABZ57032	Human kinesin ligh
c3951	14.4	0.5	24	1	ADE86193	Ret gene chair qua
c3952	14.4	0.5	25	1	AAC95684	HLA DPB1 gene PCR
c3953	14.4	0.5	25	1	AAC96504	HLA DQB1 gene PCR
c3954	14.4	0.5	25	1	AAC96321	HLA DPB1 gene PCR
c3955	14.4	0.5	25	1	AAC95753	HLA DQB1 gene PCR
3956	14.4	0.5	28	1	ADD41445	Hepatitis C virus
3957	14.2	0.5	15	1	AAA47676	Oligo d(T) primer
c3958	14.2	0.5	15	1	AAA47676	Oligo d(T) primer
3959	14.2	0.5	15	1	AAD44150	Oligo-AT PCR prime
c3960	14.2	0.5	15	1	AAD44150	Oligo-AT PCR prime
3961	14.2	0.5	16	1	AAX18387	RT-PCR primer of t
c3962	14.2	0.5	16	1	AAX18387	RT-PCR primer of t
3963	14.2	0.5	16	1	AAD44147	Oligo-dT PCR prime
3964	14.2	0.5	16	1	AAD44149	Oligo-dT PCR prime
c3965	14.2	0.5	19	1	AAT65892	Primer #1 to ampli
3966	14.2	0.5	19	1	AAZ00090	Primer LCF used fo
c3967	14.2	0.5	19	1	AAZ87035	RBP-7 microsequenc
c3968	14.2	0.5	19	1	AAA86471	PCBA HH ribozyme b
c3969	14.2	0.5	19	1	AAA85728	Cyclin B1 ribozyme
c3970	14.2	0.5	19	1	AAA84722	Cyclin E ribozyme
c3971	14.2	0.5	19	1	AAA86468	PCBA HH ribozyme b
3972	14.2	0.5	19	1	AAC60721	CYP2D1 gene partia
c3973	14.2	0.5	19	1	AAZ71872	Human biallelic ma
3974	14.2	0.5	19	1	AAC67521	Alzheimer's diseas
3975	14.2	0.5	19	1	AAC83562	DNA synthesis meth
c3976	14.2	0.5	19	1	AAH88897	Human polymorphic
c3977	14.2	0.5	19	1	AAH61633	PCNA HH ribozyme b
c3978	14.2	0.5	19	1	AAH59884	Cyclin E ribozyme
c3979	14.2	0.5	19	1	AAH61630	PCNA HH ribozyme b
c3980	14.2	0.5	19	1	AAH60890	Cyclin B1 ribozyme
3981	14.2	0.5	19	1	ABA91528	DNA-RNA-DNA oligon
c3982	14.2	0.5	19	1	ABA91528	DNA-RNA-DNA oligon
3983	14.2	0.5	19	1	ABX13088	Hantavirus gene re
c3984	14.2	0.5	19	1	AAD34425	Barley chymotrypsi
c3985	14.2	0.5	19	1	ABL40490	Nucleotide sequenc
c3986	14.2	0.5	19	1	ABA97625	Probe d. Unidenti
c3987	14.2	0.5	19	1	ABT13058	Human apolipoprote
3988	14.2	0.5	19	1	ADD43444	Human mitochondria
3989	14.2	0.5	19	1	ADE65656	Human c-fos transc
c3990	14.2	0.5	19	1	ADE65772	Human c-fos siNA 1
3991	14.2	0.5	19	1	ADE27175	Stearoyl-CoA desat
c3992	14.2	0.5	19	1	ADE27465	Stearoyl-CoA desat
3993	14.2	0.5	19	1	ADE27307	Stearoyl-CoA desat
c3994	14.2	0.5	19	1	ADE27597	Stearoyl-CoA desat
3995	14.2	0.5	20	1	ABZ89873	Human oligonucleot
3996	14.2	0.5	20	1	AAT10129	Sequence #1 used i
c3997	14.2	0.5	20	1	AAF99949	Synthetic oligonuc
3998	14.2	0.5	20	1	ABA91537	DNA oligonucleotid
c3999	14.2	0.5	20	1	ABX04655	Human endogenous r
4000	14.2	0.5	20	1	ABZ90374	Human oligonucleot
c4001	14.2	0.5	20	1	ABZ85670	Human oligonucleot
c4002	14.2	0.5	20	1	ABZ88438	Human oligonucleot
c4003	14.2	0.5	20	1	ABZ91225	Human oligonucleot
4004	14.2	0.5	20	1	AAL53968	DNA mutation detec
c4005	14.2	0.5	20	1	ADC98404	ITGA12 polymorphis
4006	14.2	0.5	20	1	AAQ22135	Primer G corresp.
c4007	14.2	0.5	20	1	AAQ51661	ADV primer (II)a.
c4008	14.2	0.5	20	1	AAQ62025	Mutant Ki-ras 5'-U
c4009	14.2	0.5	20	1	AAT41033	Human gene signatu
c4010	14.2	0.5	20	1	AAT41311	Human gene signatu
c4011	14.2	0.5	20	1	AAQ79844	K-ras modulating s
c4012	14.2	0.5	20	1	AAT86501	S-adenosylmethioni
4013	14.2	0.5	20	1	AAV37666	Allelic variant M4
4014	14.2	0.5	20	1	AAV69993	Mouse c-jun protei
c4015	14.2	0.5	20	1	AAV11765	Nucleic acid-polym
4016	14.2	0.5	20	1	AAZ11062	PCR primer for clo
4017	14.2	0.5	20	1	AAZ00584	Human glypican seq
c4018	14.2	0.5	20	1	AAV84024	Antisense oligonuc
c4019	14.2	0.5	20	1	AAX21620	Human Ki-ras speci
c4020	14.2	0.5	20	1	AAX56984	Ras gene modulatin
4021	14.2	0.5	20	1	AAZ01454	PCR primer used to
c4022	14.2	0.5	20	1	AAZ05484	PCR primer used to
c4023	14.2	0.5	20	1	AAX21925	Human B-raf kinase
4024	14.2	0.5	20	1	AAX92436	PCR primer used to
c4025	14.2	0.5	20	1	AAX95694	PCR primer used to
4026	14.2	0.5	20	1	AAX29320	JNK1-specific prob
4027	14.2	0.5	20	1	AAZ57332	Human interferon a
c4028	14.2	0.5	20	1	AAA46210	Primer IPM18R for
c4029	14.2	0.5	20	1	AAA95858	Human Ki-ras antis
4030	14.2	0.5	20	1	AAZ47296	Enterohaemorrhagic
c4031	14.2	0.5	20	1	AAZ70845	Human biallelic ma
4032	14.2	0.5	20	1	AAZ71898	Human biallelic ma
4033	14.2	0.5	20	1	AAZ76242	Human biallelic ma
c4034	14.2	0.5	20	1	AAA09679	Human SHP-1 antise
4035	14.2	0.5	20	1	AAA11880	Human MDMX antisen
4036	14.2	0.5	20	1	AAZ59002	Escherichia coli s
c4037	14.2	0.5	20	1	AAC60557	Human fra-1 mRNA a
4038	14.2	0.5	20	1	AAC62863	JNK antisense olig
c4039	14.2	0.5	20	1	AAC65597	Human uteroglobin
4040	14.2	0.5	20	1	AAC66295	Primer P13 used in
4041	14.2	0.5	20	1	AAC60958	Interleukin 2 shor
4042	14.2	0.5	20	1	AAS02211	A. thaliana phosph
c4043	14.2	0.5	20	1	AAD14811	Human glycogen syn
4044	14.2	0.5	20	1	AAS45779	Mouse PARP-2 antis
4045	14.2	0.5	20	1	AAH00614	Staphylococcus det
c4046	14.2	0.5	20	1	AAF62926	Human PEPCK-cytoso
4047	14.2	0.5	20	1	AAS04459	Human DAXX gene pr
4048	14.2	0.5	20	1	AAF28352	DNA oligomer #2.

c4049	14.2	0.5	20	1	AAF28352	DNA oligomer #2.
4050	14.2	0.5	20	1	AAS03670	PCR primer re012,
c4051	14.2	0.5	20	1	AAF27109	Human MEKK1 phosph
4052	14.2	0.5	20	1	AAH45579	Enterohaemorrhagic
4053	14.2	0.5	20	1	AAS23808	Primer B #61 used
4054	14.2	0.5	20	1	AAF91339	Human E2F transcri
c4055	14.2	0.5	20	1	AAS08770	Human PD-ABC form
c4056	14.2	0.5	20	1	AAS08861	Human PD-ABC form
4057	14.2	0.5	20	1	ABL96288	Primer #1 related
4058	14.2	0.5	20	1	AAH80595	Oligonucleotide hy
4059	14.2	0.5	20	1	ABA01567	HLA class I micros
c4060	14.2	0.5	20	1	ABK96703	Interleukin-3 (IL-
c4061	14.2	0.5	20	1	ABQ78576	RT-PCR primer used
4062	14.2	0.5	20	1	AAD41796	Human RECQL2 antis
4063	14.2	0.5	20	1	AAL43954	Polynucleotide sep
4064	14.2	0.5	20	1	ABK99983	Human CADPKL DNA P
4065	14.2	0.5	20	1	ABL45623	Human chromosome 2
c4066	14.2	0.5	20	1	AAL45626	Human serine/threo
c4067	14.2	0.5	20	1	ABK94489	Human BRCA1 gene f
c4068	14.2	0.5	20	1	ABA03194	Human KRGF1 PCR pr
c4069	14.2	0.5	20	1	ABK24613	EIF2AK3 gene seque
4070	14.2	0.5	20	1	ABL58300	Human GLUT 10 SSCP
4071	14.2	0.5	20	1	ABZ30568	Candida albicans G
4072	14.2	0.5	20	1	ABZ30869	Candida albicans G
c4073	14.2	0.5	20	1	ABA97642	probe m. Unidenti
c4074	14.2	0.5	20	1	ABA97644	probe o. Unidenti
4075	14.2	0.5	20	1	ABN80890	Human caspase 7 ph
4076	14.2	0.5	20	1	ABQ74654	STEAP gene sense P
c4077	14.2	0.5	20	1	AAD44809	Human B-raf kinase
4078	14.2	0.5	20	1	ABL30917	Human HLA genotypi
c4079	14.2	0.5	20	1	ABI94721	Capture oligonucle
4080	14.2	0.5	20	1	ABK47121	Mouse OtS2-B9 forw
4081	14.2	0.5	20	1	ABS65064	Human casein kinas
c4082	14.2	0.5	20	1	AAL53492	Signal transducer
c4083	14.2	0.5	20	1	ABX78222	Human bifunctional
4084	14.2	0.5	20	1	ABZ98046	Human MCP4 oligonu
c4085	14.2	0.5	20	1	ABZ90034	Human oligonucleot
c4086	14.2	0.5	20	1	ABZ88602	Human oligonucleot
4087	14.2	0.5	20	1	ABZ98097	Human MCP4 oligonu
c4088	14.2	0.5	20	1	ABZ98729	Human tryptase a o
c4089	14.2	0.5	20	1	ABZ99386	Human PDE4C oligon
c4090	14.2	0.5	20	1	ABZ85859	Human oligonucleot
4091	14.2	0.5	20	1	ABZ87871	Human oligonucleot
c4092	14.2	0.5	20	1	ABZ92871	Human oligonucleot
4093	14.2	0.5	20	1	ABZ88203	Human oligonucleot
4094	14.2	0.5	20	1	ABZ98593	Human tryptase a o
c4095	14.2	0.5	20	1	ABZ91192	Human oligonucleot
4096	14.2	0.5	20	1	ABZ88600	Human oligonucleot
c4097	14.2	0.5	20	1	ABZ90510	Human oligonucleot
c4098	14.2	0.5	20	1	ABZ85536	Human oligonucleot
4099	14.2	0.5	20	1	ABZ88781	Human oligonucleot
c4100	14.2	0.5	20	1	ABZ88781	Human oligonucleot
c4101	14.2	0.5	20	1	ABZ90942	Human oligonucleot
c4102	14.2	0.5	20	1	ABZ85566	Human oligonucleot
4103	14.2	0.5	20	1	ABZ89197	Human oligonucleot
c4104	14.2	0.5	20	1	ABZ86102	Human oligonucleot
4105	14.2	0.5	20	1	ABZ87395	Human oligonucleot
c4106	14.2	0.5	20	1	ABZ87364	Human oligonucleot
4107	14.2	0.5	20	1	ABZ89513	Human oligonucleot
c4108	14.2	0.5	20	1	ABZ91731	Human oligonucleot
c4109	14.2	0.5	20	1	ABZ98830	Human tryptase b o
c4110	14.2	0.5	20	1	ABZ76530	Lactobacillus brev
4111	14.2	0.5	20	1	ADA55771	Human protein-rela
c4112	14.2	0.5	20	1	ABX33988	Human interleukin
c4113	14.2	0.5	20	1	ABX34004	Human interleukin
c4114	14.2	0.5	20	1	ABQ84614	DPP10 related PSQ
4115	14.2	0.5	20	1	ACC82913	Human TRIP6 antise
c4116	14.2	0.5	20	1	ACD42192	Antisense oligonuc
c4117	14.2	0.5	20	1	ACA92581	Human Ki-ras antis
c4118	14.2	0.5	20	1	ADA44763	Antisense oligonuc
c4119	14.2	0.5	20	1	ADA44762	Antisense oligonuc
4120	14.2	0.5	20	1	ACC58274	Vascular endotheli
c4121	14.2	0.5	20	1	ACC49680	Human KSR chimeric
c4122	14.2	0.5	20	1	ABZ76424	PRRSV polymerase p
4123	14.2	0.5	20	1	ABZ74905	Human acyl coenzym
4124	14.2	0.5	20	1	ADA26567	Human Jun N-termin
4125	14.2	0.5	20	1	ABX95044	Human RAK mutagene
4126	14.2	0.5	20	1	ACH66530	Antisense PCR prim
c4127	14.2	0.5	20	1	ADA14704	PCR primer #1 for
4128	14.2	0.5	20	1	ADC20037	Synthetic oligonuc
c4129	14.2	0.5	20	1	AAD61385	Primer #12 used to
4130	14.2	0.5	20	1	ADD81486	HIV PRT antisense
c4131	14.2	0.5	20	1	ADE15814	Human PKR exon 13
c4132	14.2	0.5	20	1	ADE43612	Human KNSL1 sequen
c4133	14.2	0.5	20	1	ADE43690	Human KNSL1 sequen
c4134	14.2	0.5	21	1	AAX14731	Triple helix third
c4135	14.2	0.5	21	1	AAT42561	3' primer #1087-11
c4136	14.2	0.5	21	1	AAT46179	Pyruvate decarboxy
4137	14.2	0.5	21	1	AAT48456	Human beta-globin
c4138	14.2	0.5	21	1	AAT48456	Human beta-globin
4139	14.2	0.5	21	1	AAT48469	Third-strand oligo
c4140	14.2	0.5	21	1	AAV60859	Primer #2 for the
4141	14.2	0.5	21	1	AAV51661	Zea mays genome fo
c4142	14.2	0.5	21	1	AAV05205	Antisense primer u
c4143	14.2	0.5	21	1	AAV40600	Human TSC gene exo
4144	14.2	0.5	21	1	AAZ26264	Human polymorphic
4145	14.2	0.5	21	1	AAZ26012	Human polymorphic
4146	14.2	0.5	21	1	AAZ40513	Human STE20-relate
c4147	14.2	0.5	21	1	AAX27494	Human TFIID gene c
4148	14.2	0.5	21	1	AAX14729	Triple helix third
4149	14.2	0.5	21	1	AAX14730	Triple helix formi
c4150	14.2	0.5	21	1	AAX14730	Triple helix formi
4151	14.2	0.5	21	1	AAZ23796	HSV RNA fragment 1
c4152	14.2	0.5	21	1	AAZ18469	Polymorphic fragme
c4153	14.2	0.5	21	1	AAZ18390	Polymorphic fragme
c4154	14.2	0.5	21	1	AAZ01252	PCR primer for PG1
4155	14.2	0.5	21	1	AAD00468	Human MINT1 clone
4156	14.2	0.5	21	1	AAZ59336	Human STP2 intron
4157	14.2	0.5	21	1	AAA14463	AUUUA RNA target s
c4158	14.2	0.5	21	1	AAZ69623	Human biallelic ma
c4159	14.2	0.5	21	1	AAZ73890	Human biallelic ma
4160	14.2	0.5	21	1	AAZ75985	Human biallelic ma
c4161	14.2	0.5	21	1	AAD00964	Primer PAD4.5 to s
c4162	14.2	0.5	21	1	AAZ46461	Rat opsin gene spe
c4163	14.2	0.5	21	1	AAA80291	Human ASTH1J trans
c4164	14.2	0.5	21	1	AAA80375	Human ASTH1I 5' re
c4165	14.2	0.5	21	1	AAA87655	Rat hepatocyte car
c4166	14.2	0.5	21	1	AAF96485	Human gene single
c4167	14.2	0.5	21	1	AAF97089	Human gene single
4168	14.2	0.5	21	1	AAF96326	Human gene single
c4169	14.2	0.5	21	1	AAC92911	Mouse ISF PCR prim
c4170	14.2	0.5	21	1	AAH62338	Transcription fact
4171	14.2	0.5	21	1	AAH20432	PCR primer used in
4172	14.2	0.5	21	1	AAS23721	Primer A #35 used
c4173	14.2	0.5	21	1	ABS58442	Bovine CVM disease
c4174	14.2	0.5	21	1	AAD33350	TGF-beta type II r
4175	14.2	0.5	21	1	ABK65500	Human single nucle
c4176	14.2	0.5	21	1	ABK65490	Human single nucle
c4177	14.2	0.5	21	1	ABT13236	Fanconi anaemia FA
c4178	14.2	0.5	21	1	ABK41517	Human CTNNA3 exon-
4179	14.2	0.5	21	1	ABS55055	R. obamensis DNA p
4180	14.2	0.5	21	1	ABZ29935	Candida albicans G
4181	14.2	0.5	21	1	ABS98382	Human multidrug re
c4182	14.2	0.5	21	1	ABS98479	Human orphan nucle
4183	14.2	0.5	21	1	ABS56153	Sperm formation re
c4184	14.2	0.5	21	1	ABK14355	Human interleukin-
c4185	14.2	0.5	21	1	ABK37957	Forward RT-PCR pri
4186	14.2	0.5	21	1	AAL40172	Isoprenoid related
4187	14.2	0.5	21	1	ABK94369	Endothelin convert
c4188	14.2	0.5	21	1	ABK94370	Endothelin convert
4189	14.2	0.5	21	1	AAL50228	Human ARE-mRNA seq
c4190	14.2	0.5	21	1	ABZ24198	Humanised R. renif
4191	14.2	0.5	21	1	AAL53707	Adenylate Uridylat
4192	14.2	0.5	21	1	AAD49639	Human adenylate ur
4193	14.2	0.5	21	1	ACC83520	AU rich element (A
c4194	14.2	0.5	21	1	ADC42473	FANCD2 PCR primer

c4195	14.2	0.5	21	1	ADD14366	Human src biomarke
c4196	14.2	0.5	21	1	AAD61847	Mouse MORC exon 1
4197	14.2	0.5	21	1	ADE86000	AU-rich element mo
c4198	14.2	0.5	22	1	ABL35690	Immunostimulatory
c4199	14.2	0.5	22	1	AAT28054	3'-primer L for hu
c4200	14.2	0.5	22	1	AAT58494	First primer #11 f
c4201	14.2	0.5	22	1	AAZ47352	PCR primer L used
c4202	14.2	0.5	22	1	AAH22195	Human hepatocyte a
c4203	14.2	0.5	22	1	AAH28299	3' untranslated re
c4204	14.2	0.5	22	1	AAH28297	3' untranslated re
c4205	14.2	0.5	23	1	ADD28129	HIV-1 LTR region D
c4206	14.2	0.5	24	1	ABQ73262	Human ribosomal pr
4207	14.2	0.5	24	1	ABL55230	Pax protein 11 RT-
c4208	14.2	0.5	24	1	ABZ21302	DNA binding protei
4209	14.2	0.5	25	1	AAC95960	HLA HLA-B gene PCR
c4210	14.2	0.5	25	1	AAV06660	Unlabeled oligonuc
4211	14	0.5	14	1	AAQ33508	Sequence of micros
c4212	14	0.5	14	1	AAQ33508	Sequence of micros
4213	14	0.5	14	1	AAV09230	3' poly(T) primer
c4214	14	0.5	14	1	AAV09234	3' poly(T) primer
4215	14	0.5	14	1	AAV12222	Poly(T) oligonucle
c4216	14	0.5	14	1	AAV12226	Poly(T) oligonucle
c4217	14	0.5	14	1	AAT99552	Oligo-dT primer us
c4218	14	0.5	14	1	AAX02696	Barley HPPD primer
4219	14	0.5	14	1	AAX55057	C/EBP-beta antisen
4220	14	0.5	14	1	AAX14689	Triple helix third
c4221	14	0.5	14	1	AAX14689	Triple helix third
4222	14	0.5	14	1	AAX14688	Triple helix formi
c4223	14	0.5	14	1	AAX14688	Triple helix formi
4224	14	0.5	14	1	AAX57019	WO9923258 oligonuc
c4225	14	0.5	14	1	AAX57019	WO9923258 oligonuc
4226	14	0.5	14	1	AAX19465	Human senescence f
c4227	14	0.5	14	1	AAX19467	Human senescence f
4228	14	0.5	14	1	AAA34504	Human adenosine re
4229	14	0.5	14	1	AAF20626	Human C/EBP polynu
4230	14	0.5	14	1	AAA62349	Oligonucleotide #1
c4231	14	0.5	14	1	AAA62349	Oligonucleotide #1
4232	14	0.5	14	1	AAF84160	Oligonucleotide #2
c4233	14	0.5	14	1	AAF84160	Oligonucleotide #2
4234	14	0.5	14	1	AAC83821	RNA oligonucleotid
c4235	14	0.5	14	1	AAC83821	RNA oligonucleotid
4236	14	0.5	14	1	ABL88471	Oligo dT 3P1 prime
4237	14	0.5	14	1	ABQ83278	EGI cDNA tag relat
c4238	14	0.5	14	1	ABQ83278	EGI cDNA tag relat
c4239	14	0.5	14	1	ABQ83276	EGI cDNA tag relat
4240	14	0.5	14	1	ABQ83275	EGI cDNA tag relat
c4241	14	0.5	14	1	ABQ83271	EGI cDNA tag relat
4242	14	0.5	14	1	ABQ83269	EGI cDNA tag relat
c4243	14	0.5	14	1	ABQ83269	EGI cDNA tag relat
c4244	14	0.5	14	1	AAD24496	Retinoid-regulated
4245	14	0.5	14	1	AAD24492	Retinoid-regulated
4246	14	0.5	14	1	ABA93701	Light responsive o
c4247	14	0.5	14	1	ABA93701	Light responsive o
4248	14	0.5	14	1	ABZ96320	Human C/EBP antise
c4249	14	0.5	14	1	ABX79769	EST polymorphic DN
4250	14	0.5	15	1	AAT52140	Human ICAM hammerh
4251	14	0.5	15	1	AAF16603	Gastric acid produ
c4252	14	0.5	15	1	AAT52144	Human ICAM hammerh
4253	14	0.5	15	1	AAT52134	Human ICAM hammerh
c4254	14	0.5	15	1	AAT52134	Human ICAM hammerh
c4255	14	0.5	15	1	AAX18361	RT-PCR primer of t
c4256	14	0.5	15	1	AAA11718	Human MIF gene D5k
4257	14	0.5	15	1	AAF81549	Dye-labeled molecu
4258	14	0.5	15	1	AAF49041	IGF-I oligonucleot
c4259	14	0.5	15	1	AAF49041	IGF-I oligonucleot
c4260	14	0.5	15	1	AAF60455	Oligonucleotide cl
4261	14	0.5	15	1	AAH23587	Dye-labeled dideox
4262	14	0.5	15	1	AAD30518	Oligonucleotide us
4263	14	0.5	15	1	ABK98169	Triple helix formi
c4264	14	0.5	15	1	ABK98169	Triple helix formi
4265	14	0.5	15	1	ABK98187	Triple helix formi
c4266	14	0.5	15	1	ABK98187	Triple helix formi
4267	14	0.5	15	1	ABK98168	Triple helix formi
c4268	14	0.5	15	1	ABK98168	Triple helix formi
4269	14	0.5	15	1	ABK98167	Triple helix formi
c4270	14	0.5	15	1	ABK98167	Triple helix formi
4271	14	0.5	15	1	ABK98186	Triple helix formi
c4272	14	0.5	15	1	ABK98186	Triple helix formi
4273	14	0.5	15	1	ABX79833	EST polymorphic DN
c4274	14	0.5	15	1	ABX79833	EST polymorphic DN
c4275	14	0.5	16	1	AAD44145	Oligo-dT PCR prime
4276	14	0.5	16	1	AAX18360	RT-PCR primer of t
c4277	14	0.5	16	1	AAX18368	RT-PCR primer of t
4278	14	0.5	16	1	AAX18365	RT-PCR primer of t
c4279	14	0.5	16	1	AAD44147	Oligo-dT PCR prime
c4280	14	0.5	16	1	AAD44149	Oligo-dT PCR prime
4281	14	0.5	16	1	AAV33896	PCR primer #6 for
c4282	14	0.5	17	1	AAX69798	Human flt1 VEGF re
4283	14	0.5	17	1	AAX69803	Human flt1 VEGF re
4284	14	0.5	17	1	AAX70117	Human flt1 VEGF re
4285	14	0.5	17	1	AAX70116	Human flt1 VEGF re
4286	14	0.5	17	1	AAX69438	Human flt1 VEGF re
4287	14	0.5	17	1	AAX69434	Human flt1 VEGF re
4288	14	0.5	17	1	AAA20469	Integrin alpha 6 s
4289	14	0.5	17	1	AAA20470	Integrin alpha 6 s
4290	14	0.5	17	1	AAA25447	Oestrogen receptor
c4291	14	0.5	17	1	AAA25447	Oestrogen receptor
4292	14	0.5	17	1	AAF03225	Hammerhead ribozym
4293	14	0.5	17	1	AAF03223	Hammerhead ribozym
c4294	14	0.5	17	1	AAF07018	Hammerhead ribozym
4295	14	0.5	17	1	AAF03224	Hammerhead ribozym
4296	14	0.5	17	1	AAF03226	Hammerhead ribozym
c4297	14	0.5	17	1	ABK02792	Human CD20 Hammerh
c4298	14	0.5	17	1	ABK02791	Human CD20 Hammerh
c4299	14	0.5	17	1	ABQ64252	Human KTOM1a porti
c4300	14	0.5	17	1	ABQ64256	Human KTOM1a porti
c4301	14	0.5	17	1	ABQ99687	Murine Ikbkap exon
4302	14	0.5	17	1	ABS76198	Human PAPP-Eb asso
4303	14	0.5	17	1	ABS76197	Human PAPP-Eb asso
4304	14	0.5	17	1	ACD55508	HBV amberzyme subs
4305	14	0.5	17	1	ACD50744	HBV hammerhead rib
4306	14	0.5	17	1	ACD55509	HBV amberzyme subs
c4307	14	0.5	17	1	ACD63827	HCV minus strand D
4308	14	0.5	17	1	ACD58843	HCV DNAzyme substr
4309	14	0.5	17	1	ACC63818	Murine oligonucleo
4310	14	0.5	17	1	ADB40646	Tumour suppression
4311	14	0.5	17	1	ADB40890	Tumour suppression
c4312	14	0.5	17	1	ADB45762	Tumour suppression
c4313	14	0.5	18	1	AAH74930	DNA sequence of ca
c4314	14	0.5	18	1	ADC64942	Camellia sinensis
c4315	14	0.5	18	1	AAV48547	p53 gene antisense
c4316	14	0.5	18	1	AAV48548	p53 gene antisense
4317	14	0.5	18	1	AAZ70573	Human biallelic ma
4318	14	0.5	18	1	ABX95294	Human ABCA7 associ
c4319	14	0.5	19	1	ADE27175	Stearoyl-CoA desat
4320	14	0.5	19	1	ADE27465	Stearoyl-CoA desat
c4321	14	0.5	19	1	AAZ59379	Forward PCR primer
c4322	14	0.5	19	1	AAA86064	Cdc 25 hs ribozyme
c4323	14	0.5	19	1	AAA86065	Cdc 25 hs ribozyme
c4324	14	0.5	19	1	AAH61226	Cdc25 hs ribozyme
c4325	14	0.5	19	1	AAH61227	Cdc25 hs ribozyme
4326	14	0.5	20	1	AAT73291	Primer 1 for pUC19
4327	14	0.5	20	1	AAT73292	Primer 2 for pUC19
c4328	14	0.5	20	1	AAF99302	Immunostimulatory
c4329	14	0.5	20	1	ABS77947	Angiogenesis inhib
c4330	14	0.5	20	1	ABL39308	Immunostimulatory
c4331	14	0.5	20	1	ACD99727	Immunostimulatory
c4332	14	0.5	20	1	ADB36804	Immunostimulatory
4333	14	0.5	20	1	AAQ97488	M. sexta alaserpin
c4334	14	0.5	20	1	AAX33317	PEBP2 alpha A gene
c4335	14	0.5	20	1	AAX33251	PEBP2 alpha A gene
c4336	14	0.5	20	1	AAX33257	PEBP2 alpha A gene
c4337	14	0.5	20	1	AAS10630	Human caspase 3 an
c4338	14	0.5	20	1	AAF74765	Human hDPP PCR pri
4339	14	0.5	20	1	AAD11975	Human PTP1B antise
4340	14	0.5	20	1	ABK85050	Human PTP1B antise

4341	14	0.5	20	1	ABK37219	Human PTP1B mRNA 1
4342	14	0.5	20	1	ABI96879	Capture oligonucle
c4343	14	0.5	20	1	ABZ89489	Human oligonucleot
4344	14	0.5	20	1	ABZ90889	Human oligonucleot
4345	14	0.5	20	1	ABZ91792	Human oligonucleot
c4346	14	0.5	20	1	ADC51216	PCR primer #1 for
c4347	14	0.5	21	1	AAZ26249	Human polymorphic
4348	14	0.5	21	1	AAQ71292	Feline zona pelluc
c4349	14	0.5	21	1	AAZ26403	Human polymorphic
c4350	14	0.5	21	1	AAF96504	Human gene single
c4351	14	0.5	22	1	AAH22316	Brain ankyrin-2 hy
4352	14	0.5	23	1	AAX81611	PCR primer used to
c4353	14	0.5	24	1	ABN86867	Human macroprotein
4354	14	0.5	25	1	AAC95962	HLA HLA-B gene PCR
c4355	14	0.5	25	1	AAC95680	HLA DPB1 gene PCR
4356	14	0.5	30	1	ABL35095	RNA/DNA hybrid con
4357	14	0.5	30	1	ABL35096	Phosphorothioate s
4358	14	0.5	30	1	ABL35097	Phosphorothioate s
4359	14	0.5	30	1	ABL35105	RNA/DNA hybrid ass
4360	14	0.5	30	1	ABL35098	Phosphorothioate s
4361	13.8	0.5	17	1	AAX69804	Human flt1 VEGF re
c4362	13.8	0.5	17	1	AAA25454	Oestrogen receptor
c4363	13.8	0.5	17	1	AAQ20006	Oligonucleotide #2
4364	13.8	0.5	17	1	AAQ20005	Oligonucleotide #1
c4365	13.8	0.5	17	1	AAQ25487	Purine rich HUMIL2
4366	13.8	0.5	17	1	AAT32744	Hepatitis C virus
4367	13.8	0.5	17	1	AAX71549	Human KDR VEGF rec
4368	13.8	0.5	17	1	AAX75068	Mouse flt-1 VEGF r
c4369	13.8	0.5	17	1	AAX75068	Mouse flt-1 VEGF r
4370	13.8	0.5	17	1	AAX69794	Human flt1 VEGF re
c4371	13.8	0.5	17	1	AAX69807	Human flt1 VEGF re
4372	13.8	0.5	17	1	AAX75069	Mouse flt-1 VEGF r
c4373	13.8	0.5	17	1	AAX75069	Mouse flt-1 VEGF r
c4374	13.8	0.5	17	1	AAX69806	Human flt1 VEGF re
4375	13.8	0.5	17	1	AAX73109	Mouse flk-1 VEGF r
4376	13.8	0.5	17	1	AAX71548	Human KDR VEGF rec
4377	13.8	0.5	17	1	AAX73108	Mouse flk-1 VEGF r
c4378	13.8	0.5	17	1	AAX36644	Antisense oligomer
4379	13.8	0.5	17	1	AAX09151	Human biallelic po
4380	13.8	0.5	17	1	AAV97882	Human EGF-R target
c4381	13.8	0.5	17	1	AAV96447	Potato citrate syn
4382	13.8	0.5	17	1	AAV08636	Primer ANG/22RT fo
c4383	13.8	0.5	17	1	AAX23090	Primer #13. Synth
4384	13.8	0.5	17	1	AAA18461	Human TIE-2 substr
4385	13.8	0.5	17	1	AAA22593	Integrin subunit b
c4386	13.8	0.5	17	1	AAA20755	Integrin alpha 6 s
4387	13.8	0.5	17	1	AAA19040	Human TIE-2 substr
c4388	13.8	0.5	17	1	AAA21137	Integrin alpha 6 s
c4389	13.8	0.5	17	1	AAA22975	Integrin subunit b
4390	13.8	0.5	17	1	AAA22599	Integrin subunit b
4391	13.8	0.5	17	1	AAA20514	Integrin alpha 6 s
4392	13.8	0.5	17	1	AAA38264	Human angiotensino
4393	13.8	0.5	17	1	AAA25444	Oestrogen receptor
4394	13.8	0.5	17	1	AAA25445	Oestrogen receptor
c4395	13.8	0.5	17	1	AAA25445	Oestrogen receptor
4396	13.8	0.5	17	1	AAA25455	Oestrogen receptor
4397	13.8	0.5	17	1	AAA25180	Oestrogen receptor
c4398	13.8	0.5	17	1	AAA25180	Oestrogen receptor
4399	13.8	0.5	17	1	AAA25446	Oestrogen receptor
c4400	13.8	0.5	17	1	AAA25446	Oestrogen receptor
4401	13.8	0.5	17	1	AAC61264	Human ACE, AGT and
4402	13.8	0.5	17	1	AAF03220	Hammerhead ribozym
4403	13.8	0.5	17	1	AAF06382	Hammerhead ribozym
c4404	13.8	0.5	17	1	AAF06326	Hammerhead ribozym
c4405	13.8	0.5	17	1	AAF02388	Hammerhead ribozym
c4406	13.8	0.5	17	1	AAF05982	Hammerhead ribozym
c4407	13.8	0.5	17	1	ABK01191	Human NOGO Inozyme
c4408	13.8	0.5	17	1	ABK00928	Human NOGO Inozyme
c4409	13.8	0.5	17	1	ABK00932	Human NOGO Inozyme
c4410	13.8	0.5	17	1	ABK00933	Human NOGO Inozyme
c4411	13.8	0.5	17	1	ABK00930	Human NOGO Inozyme
c4412	13.8	0.5	17	1	ABK00237	Human NOGO Hammerh
c4413	13.8	0.5	17	1	ABK02172	Human NOGO DNAzyme
c4414	13.8	0.5	17	1	ABK03238	Human CD20 Inozyme
c4415	13.8	0.5	17	1	ABK00931	Human NOGO Inozyme
4416	13.8	0.5	17	1	ABK01789	Human NOGO Zinzyme
c4417	13.8	0.5	17	1	ABK00049	Human NOGO Hammerh
4418	13.8	0.5	17	1	ABK00904	Human NOGO Inozyme
4419	13.8	0.5	17	1	ABA80617	APOE mutation corr
c4420	13.8	0.5	17	1	ABA80616	APOE mutation corr
c4421	13.8	0.5	17	1	AAH27335	PCR primer #4. Ho
4422	13.8	0.5	17	1	ABN10667	Human GDMLP-1 17-m
4423	13.8	0.5	17	1	ABN02678	Human GDMLP-1 17-m
4424	13.8	0.5	17	1	ABN10666	Human GDMLP-1 17-m
c4425	13.8	0.5	17	1	ABN07651	Human GDMLP-1 17-m
4426	13.8	0.5	17	1	ABN09312	Human GDMLP-1 17-m
c4427	13.8	0.5	17	1	ABN02070	Human GDMLP-1 17-m
4428	13.8	0.5	17	1	ABN02679	Human GDMLP-1 17-m
4429	13.8	0.5	17	1	ABN09313	Human GDMLP-1 17-m
4430	13.8	0.5	17	1	ABN05947	Human GDMLP-1 17-m
4431	13.8	0.5	17	1	ABN07705	Human GDMLP-1 17-m
4432	13.8	0.5	17	1	ABN05946	Human GDMLP-1 17-m
c4433	13.8	0.5	17	1	ABN01354	Human GDMLP-1 17-m
c4434	13.8	0.5	17	1	ABN07650	Human GDMLP-1 17-m
4435	13.8	0.5	17	1	ABQ63368	Human KTOM1a porti
c4436	13.8	0.5	17	1	ABQ64270	Human KTOM1a porti
c4437	13.8	0.5	17	1	ABQ64271	Human KTOM1a porti
c4438	13.8	0.5	17	1	ABQ64272	Human KTOM1a porti
4439	13.8	0.5	17	1	ABQ63367	Human KTOM1a porti
4440	13.8	0.5	17	1	ABK27279	Reduced linolenic
c4441	13.8	0.5	17	1	ABK27280	Reduced linolenic
4442	13.8	0.5	17	1	ABV83073	Human HTPL scannin
4443	13.8	0.5	17	1	ABV83072	Human HTPL scannin
c4444	13.8	0.5	17	1	ABK17920	Human ERG hammerhe
c4445	13.8	0.5	17	1	ABK17919	Human ERG hammerhe
c4446	13.8	0.5	17	1	AAD41894	Target DNA #4 used
4447	13.8	0.5	17	1	ABS74958	Human PAPP-Ea asso
c4448	13.8	0.5	17	1	ABS74958	Human PAPP-Ea asso
4449	13.8	0.5	17	1	ABS74957	Human PAPP-Ea asso
4450	13.8	0.5	17	1	ABS76194	Human PAPP-Eb asso
4451	13.8	0.5	17	1	ABS76191	Human PAPP-Eb asso
4452	13.8	0.5	17	1	ABS76193	Human PAPP-Eb asso
c4453	13.8	0.5	17	1	ABS74686	Human PAPP-Ea asso
4454	13.8	0.5	17	1	ABS76192	Human PAPP-Eb asso
4455	13.8	0.5	17	1	ABL31395	Human HLA genotypi
c4456	13.8	0.5	17	1	ABL31540	Human HLA genotypi
c4457	13.8	0.5	17	1	ABL31783	Human HLA genotypi
c4458	13.8	0.5	17	1	ACC52674	Human tumour suppr
c4459	13.8	0.5	17	1	ACC52259	Human tumour suppr
4460	13.8	0.5	17	1	ACC53844	Human tumour suppr
4461	13.8	0.5	17	1	ACA99706	G-protein coupled
4462	13.8	0.5	17	1	ACA99704	G-protein coupled
4463	13.8	0.5	17	1	ACA99703	G-protein coupled
4464	13.8	0.5	17	1	ACA99705	G-protein coupled
c4465	13.8	0.5	17	1	ABT35213	Tumour suppression
c4466	13.8	0.5	17	1	ABT35699	Tumour suppression
c4467	13.8	0.5	17	1	ABT39123	Tumour suppression
4468	13.8	0.5	17	1	ABT39231	Tumour suppression
4469	13.8	0.5	17	1	ABT40168	Tumour suppression
4470	13.8	0.5	17	1	ABT40201	Tumour suppression
4471	13.8	0.5	17	1	ADA99204	Human MDZ3 scannin
4472	13.8	0.5	17	1	ADA99789	Human MDZ3 scannin
4473	13.8	0.5	17	1	ABZ65528	Human HER2 DNAzyme
4474	13.8	0.5	17	1	ABZ65527	Human HER2 DNAzyme
4475	13.8	0.5	17	1	ABZ61926	Human H-Ras DNAzym
4476	13.8	0.5	17	1	ABZ61300	Human H-Ras DNAzym
4477	13.8	0.5	17	1	ABZ61558	Human H-Ras DNAzym
c4478	13.8	0.5	17	1	ABZ61326	Human H-Ras DNAzym
c4479	13.8	0.5	17	1	ACD57046	HCV DNAzyme substr
4480	13.8	0.5	17	1	ACD56943	HCV DNAzyme substr
c4481	13.8	0.5	17	1	ACD65727	HCV minus strand D
4482	13.8	0.5	17	1	ACD65623	HCV minus strand D
4483	13.8	0.5	17	1	ACD56942	HCV DNAzyme substr
4484	13.8	0.5	17	1	ACC67022	Murine oligonucleo
4485	13.8	0.5	17	1	ACC68550	Murine oligonucleo
4486	13.8	0.5	17	1	ACC65305	Murine oligonucleo

4487	13.8	0.5	17	1	ADB41005	Tumour suppression
4488	13.8	0.5	17	1	ADB42684	Tumour suppression
c4489	13.8	0.5	17	1	ADB44777	Tumour suppression
c4490	13.8	0.5	17	1	ADB44262	Tumour suppression
c4491	13.8	0.5	17	1	ADD20961	Human GAP_N DNA 17
4492	13.8	0.5	17	1	ADE25221	Plant growth assoc
c4493	13.8	0.5	17	1	ADE25221	Plant growth assoc
4494	13.8	0.5	17	1	ADE30707	Cholesterol homeos
4495	13.8	0.5	18	1	AAQ20007	Oligonucleotide #3
c4496	13.8	0.5	18	1	AAQ20007	Oligonucleotide #3
4497	13.8	0.5	18	1	AAQ36431	GRP-R primer (EXT
4498	13.8	0.5	18	1	AAQ34456	DQA1 probe AG2.3,
4499	13.8	0.5	18	1	AAX15198	Triple helix formi
c4500	13.8	0.5	18	1	AAX15196	Triple helix formi
4501	13.8	0.5	18	1	AAT36431	Human papillomavir
4502	13.8	0.5	18	1	AAT93487	DQA1 allele determ
c4503	13.8	0.5	18	1	AAT93488	DQA1 allele determ
c4504	13.8	0.5	18	1	AAX71708	Human KDR VEGF rec
c4505	13.8	0.5	18	1	AAV13864	Oligonucleotide-cy
c4506	13.8	0.5	18	1	AAX63292	Delta-9 desaturase
c4507	13.8	0.5	18	1	AAT98144	Primer V-alpha(16)
c4508	13.8	0.5	18	1	AAV54725	Primer used to det
4509	13.8	0.5	18	1	AAV16008	PCR primer D-R use
c4510	13.8	0.5	18	1	AAX85987	PCR primer used to
4511	13.8	0.5	18	1	AAZ25592	Human RhoG antisen
c4512	13.8	0.5	18	1	AAX88163	T cell receptor al
4513	13.8	0.5	18	1	AAX90266	DQA1 gene PCR prim
c4514	13.8	0.5	18	1	AAX90267	DQA1 gene PCR prim
4515	13.8	0.5	18	1	AAD00540	Human adenine nucl
c4516	13.8	0.5	18	1	AAZ75194	Human biallelic ma
4517	13.8	0.5	18	1	AAZ43267	Murine Sox3 gene P
4518	13.8	0.5	18	1	AAA05252	PCR primer D-R use
c4519	13.8	0.5	18	1	AAZ93440	TRADD antisense ol
4520	13.8	0.5	18	1	AAZ93475	TRADD antisense ol
4521	13.8	0.5	18	1	AAH27102	Heltest4 cleavage
c4522	13.8	0.5	18	1	AAH27102	Heltest4 cleavage
4523	13.8	0.5	18	1	AAH56578	S. pneumoniae groE
4524	13.8	0.5	18	1	AAS08670	BsgI-AFLP primer/M
4525	13.8	0.5	18	1	AAF94740	Rho G antisense ph
4526	13.8	0.5	18	1	AAS05922	Human ANT-3 sequen
c4527	13.8	0.5	18	1	AAD11767	Human AAG6 DNA exo
4528	13.8	0.5	18	1	AAH91840	Human inflammatory
c4529	13.8	0.5	18	1	ABZ72262	Gene 216 SSCP sequ
4530	13.8	0.5	18	1	ABL54126	Cleavage product o
c4531	13.8	0.5	18	1	ABL54126	Cleavage product o
4532	13.8	0.5	18	1	AAS97605	Murine SAC1 gene-s
4533	13.8	0.5	18	1	ABL44451	Human chromosome 1
4534	13.8	0.5	18	1	ABQ78689	Cleavage product o
c4535	13.8	0.5	18	1	ABQ78689	Cleavage product o
c4536	13.8	0.5	18	1	ABS52682	mRNA display splin
4537	13.8	0.5	18	1	AAS95764	Human adenine nucl
4538	13.8	0.5	18	1	ABK94050	Cardiovascular reg
4539	13.8	0.5	18	1	AAD41291	Human C6ST gene am
4540	13.8	0.5	18	1	ABK87302	FEN 1 nuclease cle
c4541	13.8	0.5	18	1	ABK87302	FEN 1 nuclease cle
c4542	13.8	0.5	18	1	ABK98126	Triple helix formi
c4543	13.8	0.5	18	1	ABX75115	Human gene 216 seq
c4544	13.8	0.5	18	1	ABV75014	Nucleotide sequenc
4545	13.8	0.5	18	1	ADE39920	Human Midkine intr
4546	13.8	0.5	19	1	AAQ20028	Cross-linking olig
4547	13.8	0.5	19	1	AAQ20029	Cross-linking olig
4548	13.8	0.5	19	1	AAQ30375	Oligomer HUM beta
4549	13.8	0.5	19	1	AAQ30374	Oligomer HUM beta
4550	13.8	0.5	19	1	AAQ39059	S. nodosus 2634bp
4551	13.8	0.5	19	1	AAT49298	5' end fragment of
4552	13.8	0.5	19	1	AAT74905	5' end fragment of
4553	13.8	0.5	19	1	AAT47271	Capped RNA influen
4554	13.8	0.5	19	1	AAT47276	Capped RNA influen
4555	13.8	0.5	19	1	AAT47269	Capped RNA influen
4556	13.8	0.5	19	1	AAT47279	Capped RNA influen
4557	13.8	0.5	19	1	AAT47277	Capped RNA influen
4558	13.8	0.5	19	1	AAT47273	Capped RNA influen
4559	13.8	0.5	19	1	AAT47264	5' fragment of alf
4560	13.8	0.5	19	1	AAT47272	Capped RNA influen
4561	13.8	0.5	19	1	AAT47278	Capped RNA influen
4562	13.8	0.5	19	1	AAT47267	Capped RNA influen
4563	13.8	0.5	19	1	AAT47270	Capped RNA influen
4564	13.8	0.5	19	1	AAT50897	Probe #11 for inte
4565	13.8	0.5	19	1	AAX32232	Probe specific for
4566	13.8	0.5	19	1	AAZ00903	Primer for PG1 bia
4567	13.8	0.5	19	1	AAZ01223	PCR primer for PG1
c4568	13.8	0.5	19	1	AAA35512	Myrtaceae microsat
4569	13.8	0.5	19	1	AAZ37261	PCR primer for AV3
c4570	13.8	0.5	19	1	AAA86469	PCBA HH ribozyme b
c4571	13.8	0.5	19	1	AAA84405	Cyclin D3 ribozyme
c4572	13.8	0.5	19	1	AAA84723	Cyclin E ribozyme
c4573	13.8	0.5	19	1	AAA86472	PCBA HH ribozyme b
4574	13.8	0.5	19	1	AAZ70580	Human biallelic ma
4575	13.8	0.5	19	1	AAZ73500	Human biallelic ma
4576	13.8	0.5	19	1	AAA75956	PCR primer used to
c4577	13.8	0.5	19	1	AAH61634	PCNA HH ribozyme b
c4578	13.8	0.5	19	1	AAH61631	PCNA HH ribozyme b
c4579	13.8	0.5	19	1	AAH59885	Cyclin E ribozyme
c4580	13.8	0.5	19	1	AAH59567	Cyclin D3 ribozyme
4581	13.8	0.5	19	1	ABK41301	Human prostate can
4582	13.8	0.5	19	1	AAL42341	Novel sand pear mi
4583	13.8	0.5	19	1	ABK49173	F. oxysporum tryps
4584	13.8	0.5	19	1	ABK90099	Oestrogen response
4585	13.8	0.5	19	1	ACD06509	Forward RT-PCR pri
4586	13.8	0.5	19	1	ACD06722	Forward RT-PCR pri
c4587	13.8	0.5	19	1	ADA25723	Human REL-A short
4588	13.8	0.5	19	1	ADA26072	Human REL-A short
4589	13.8	0.5	19	1	ADA45472	Human BAP1 DNA pro
c4590	13.8	0.5	19	1	ACD99555	Immunostimulatory
4591	13.8	0.5	19	1	ACD07875	F. oxysporum tryps
4592	13.8	0.5	19	1	ADD00126	HCV coding region-
4593	13.8	0.5	19	1	ADD00278	HCV coding region-
4594	13.8	0.5	19	1	ADD19509	Salmo salar SNP PC
4595	13.8	0.5	19	1	ADE65619	Human c-fos transc
c4596	13.8	0.5	19	1	ADE65735	Human c-fos siNA 1
c4597	13.8	0.5	19	1	ADE36637	Human ERG gene PCR
4598	13.8	0.5	19	1	ADE43577	Human IDE sequenci
4599	13.8	0.5	19	1	ADE29797	Mitogen activated
c4600	13.8	0.5	19	1	ADE29902	Mitogen activated
c4601	13.8	0.5	20	1	AAA94537	Antisense oligonuc
4602	13.8	0.5	20	1	ABZ89720	Human oligonucleot
c4603	13.8	0.5	20	1	AAX32003	MSH2 gene specific
c4604	13.8	0.5	20	1	AAC82921	Human S-9 derived
c4605	13.8	0.5	20	1	ADA45244	Human MSH2 gene PC
4606	13.8	0.5	20	1	AAQ20027	Cross-linking olig
4607	13.8	0.5	20	1	AAQ30372	Oligomer HUM beta
4608	13.8	0.5	20	1	AAA94534	Antisense oligonuc
c4609	13.8	0.5	20	1	ABZ89084	Human oligonucleot
c4610	13.8	0.5	20	1	ACF57337	Human atlastin exo
c4611	13.8	0.5	20	1	AAA55978	Human G713 PCR pri
4612	13.8	0.5	20	1	ABZ89489	Human oligonucleot
4613	13.8	0.5	20	1	AAQ43126	HCV type 2 NS-4 se
c4614	13.8	0.5	20	1	AAQ41528	Antisense oligomer
c4615	13.8	0.5	20	1	AAQ47650	Mouse jun-B MUSJUN
c4616	13.8	0.5	20	1	AAQ56662	Bacteriophage lamb
4617	13.8	0.5	20	1	AAQ64082	NANBHV NS1/NS2 (EN
c4618	13.8	0.5	20	1	AAQ45269	Primer to amplify
4619	13.8	0.5	20	1	AAQ98982	H1 extra exon reve
c4620	13.8	0.5	20	1	AAT41105	Human gene signatu
4621	13.8	0.5	20	1	AAQ86599	HEV ORF2.0 PCR 5'
4622	13.8	0.5	20	1	AAQ86829	Antisense oligonuc
c4623	13.8	0.5	20	1	AAT39924	Maize acetyl CoA c
c4624	13.8	0.5	20	1	AAT44306	Primer 5 for ampli
c4625	13.8	0.5	20	1	AAV06314	Mouse gut RNA ampl
c4626	13.8	0.5	20	1	AAT88934	Detector probe 1 f
4627	13.8	0.5	20	1	AAT47265	5' fragment #2 of
4628	13.8	0.5	20	1	AAV20640	Primer Sf MI -25+
4629	13.8	0.5	20	1	AAV07136	Nucleotide sequenc
4630	13.8	0.5	20	1	AAV16787	Primer Sf MI -25+
4631	13.8	0.5	20	1	AAV53579	Nucleotide sequenc
4632	13.8	0.5	20	1	AAV19518	Retroviral DNA bas

c4633	13.8	0.5	20	1	AAV68581	Nucleotide sequenc
c4634	13.8	0.5	20	1	AAV28931	Bovine Nramp1 clon
4635	13.8	0.5	20	1	AAX36926	S. cereale microsa
4636	13.8	0.5	20	1	AAV74259	CpG-N motif oligon
c4637	13.8	0.5	20	1	AAV74259	CpG-N motif oligon
c4638	13.8	0.5	20	1	AAZ02544	PCR primer used to
c4639	13.8	0.5	20	1	AAZ02339	PCR primer used to
4640	13.8	0.5	20	1	AAZ03397	PCR primer used to
4641	13.8	0.5	20	1	AAZ02828	PCR primer used to
4642	13.8	0.5	20	1	AAX26623	PCR primer for amp
4643	13.8	0.5	20	1	AAZ23851	Rye mircrosatellit
c4644	13.8	0.5	20	1	AAX93392	PCR primer used to
4645	13.8	0.5	20	1	AAX95000	PCR primer used to
4646	13.8	0.5	20	1	AAX81592	PCR primer used to
4647	13.8	0.5	20	1	AAX29455	Rat JNK3-specific
c4648	13.8	0.5	20	1	AAZ86719	Antisense inhibito
c4649	13.8	0.5	20	1	AAZ49841	PCR primer 28sst-1
c4650	13.8	0.5	20	1	AAA40867	Murine TNFalpha an
c4651	13.8	0.5	20	1	AAZ28947	PCR primer c114 fo
c4652	13.8	0.5	20	1	AAZ59205	Forward PCR primer
c4653	13.8	0.5	20	1	AAZ59204	Second strand cDNA
c4654	13.8	0.5	20	1	AAA94533	Antisense oligonuc
4655	13.8	0.5	20	1	AAA38540	Jellyfish green fl
4656	13.8	0.5	20	1	AAZ29763	Human thymidylate
c4657	13.8	0.5	20	1	AAZ56191	Oligonucleotide A1
4658	13.8	0.5	20	1	ABK12263	Capra hircus aegag
4659	13.8	0.5	20	1	AAC62998	JNK antisense olig
c4660	13.8	0.5	20	1	AAC64800	Human plakophilin-
4661	13.8	0.5	20	1	AAA74057	Forward PCR primer
c4662	13.8	0.5	20	1	AAF31794	Human RANK antisen
c4663	13.8	0.5	20	1	AAH75301	Mouse inducible NO
c4664	13.8	0.5	20	1	AAK95000	Human cDNA clone-s
4665	13.8	0.5	20	1	AAF73065	Human daxx inhibit
c4666	13.8	0.5	20	1	AAS45802	Mouse PARP-2 antis
4667	13.8	0.5	20	1	AAC92903	Human PI3 kinase p
4668	13.8	0.5	20	1	AAC92905	Human PI3 kinase p
c4669	13.8	0.5	20	1	AAH77763	PCR primer for hum
4670	13.8	0.5	20	1	AAH21418	C. lanceolata KASI
c4671	13.8	0.5	20	1	AAS00481	Human FIRE cDNA PC
4672	13.8	0.5	20	1	AAH56777	S. aureus groE ope
4673	13.8	0.5	20	1	AAF99014	Immunostimulatory
c4674	13.8	0.5	20	1	AAF99014	Immunostimulatory
c4675	13.8	0.5	20	1	AAS43136	Human ERbeta gene,
4676	13.8	0.5	20	1	AAH39349	SNP specific upper
c4677	13.8	0.5	20	1	AAH40269	SNP specific upper
c4678	13.8	0.5	20	1	AAA54439	Primer for amplify
4679	13.8	0.5	20	1	AAD09639	Human PKA C-alpha
4680	13.8	0.5	20	1	AAD09640	Human PKA C-alpha
c4681	13.8	0.5	20	1	AAF54613	Human HLA Class I
c4682	13.8	0.5	20	1	AAF54596	Human HLA Class I
c4683	13.8	0.5	20	1	AAF54612	Human HLA Class I
c4684	13.8	0.5	20	1	AAF54615	Human HLA Class I
c4685	13.8	0.5	20	1	AAF54617	Human HLA Class I
4686	13.8	0.5	20	1	AAH40966	Primer SEQ ID 14 u
4687	13.8	0.5	20	1	AAS12283	DNA encoding class
4688	13.8	0.5	20	1	AAD17451	Human TNF-alpha cD
4689	13.8	0.5	20	1	AAH49468	D. melanogaster pe
c4690	13.8	0.5	20	1	ABK53147	HIV-1 Gag gene spe
c4691	13.8	0.5	20	1	ABQ82398	Human NOV4 forward
4692	13.8	0.5	20	1	ABK13157	En8183 EN transpos
4693	13.8	0.5	20	1	ABK11174	PCR primer #1 for
4694	13.8	0.5	20	1	AAD46658	Human ABCC11 exon2
4695	13.8	0.5	20	1	ABN74918	Mouse caspase 2 an
4696	13.8	0.5	20	1	ABS52754	Ferrocene-type pol
c4697	13.8	0.5	20	1	ABS52755	Ferrocene-type pol
c4698	13.8	0.5	20	1	AAS97619	Murine SAC1 gene-s
4699	13.8	0.5	20	1	ABN89247	Human Talin antise
4700	13.8	0.5	20	1	ABS77655	Angiogenesis inhib
c4701	13.8	0.5	20	1	ABS77655	Angiogenesis inhib
c4702	13.8	0.5	20	1	ABT07491	Rat protein phosph
4703	13.8	0.5	20	1	ABL38801	Immunostimulatory
c4704	13.8	0.5	20	1	ABL38801	Immunostimulatory
4705	13.8	0.5	20	1	ABL59017	Nucleotide sequenc
c4706	13.8	0.5	20	1	ABQ92966	T. tauschii/wheat
c4707	13.8	0.5	20	1	ABN99676	Human clusterin in
c4708	13.8	0.5	20	1	ABA89809	Human oestrogen re
4709	13.8	0.5	20	1	AAL40388	Mouse caspase 6 an
c4710	13.8	0.5	20	1	ABA02214	Human/mouse C/EBP
c4711	13.8	0.5	20	1	AAD29918	Mouse TID-1 cDNA 5
4712	13.8	0.5	20	1	ABK94486	Human BRCA1 gene r
4713	13.8	0.5	20	1	ABS59782	Human damage speci
4714	13.8	0.5	20	1	AAD30205	Human UGT1A6-1 gen
c4715	13.8	0.5	20	1	ABA97649	probe t. Unidenti
c4716	13.8	0.5	20	1	ABA97648	probe s. Unidenti
c4717	13.8	0.5	20	1	ABA97650	probe u. Unidenti
c4718	13.8	0.5	20	1	AAD39347	Human Von Willebra
4719	13.8	0.5	20	1	ABL94407	Mouse C/EBP beta p
4720	13.8	0.5	20	1	ABI95113	Capture oligonucle
4721	13.8	0.5	20	1	ABI95444	Capture oligonucle
c4722	13.8	0.5	20	1	ABI94329	Capture oligonucle
c4723	13.8	0.5	20	1	AAL41524	Oligonucleotide in
c4724	13.8	0.5	20	1	AAL45509	HIV-1 gag amplific
c4725	13.8	0.5	20	1	ABS59590	Real-time forward
c4726	13.8	0.5	20	1	ABZ85453	Human oligonucleot
4727	13.8	0.5	20	1	ABZ88060	Human oligonucleot
4728	13.8	0.5	20	1	ABZ89895	Human oligonucleot
4729	13.8	0.5	20	1	ABZ90674	Human oligonucleot
c4730	13.8	0.5	20	1	ABZ93123	Human oligonucleot
c4731	13.8	0.5	20	1	ABZ88828	Human oligonucleot
c4732	13.8	0.5	20	1	ABZ89594	Human oligonucleot
4733	13.8	0.5	20	1	ABZ90507	Human oligonucleot
c4734	13.8	0.5	20	1	ABZ97297	Human nucleic acid
4735	13.8	0.5	20	1	ABZ86168	Human oligonucleot
c4736	13.8	0.5	20	1	ABZ94127	Human oligonucleot
4737	13.8	0.5	20	1	ABZ85671	Human oligonucleot
4738	13.8	0.5	20	1	ABZ86919	Human oligonucleot
4739	13.8	0.5	20	1	ABZ99084	Human PDE4C oligon
c4740	13.8	0.5	20	1	ABZ93066	Human oligonucleot
4741	13.8	0.5	20	1	ABZ85437	Human oligonucleot
4742	13.8	0.5	20	1	ABZ91047	Human oligonucleot
c4743	13.8	0.5	20	1	ABZ91735	Human oligonucleot
4744	13.8	0.5	20	1	ABZ85702	Human oligonucleot
4745	13.8	0.5	20	1	ABZ85292	Human oligonucleot
4746	13.8	0.5	20	1	ABZ85546	Human oligonucleot
4747	13.8	0.5	20	1	ABZ89893	Human oligonucleot
4748	13.8	0.5	20	1	ABZ98459	Human ICAM oligonu
4749	13.8	0.5	20	1	ABZ88711	Human oligonucleot
c4750	13.8	0.5	20	1	ABZ87697	Human oligonucleot
4751	13.8	0.5	20	1	ABZ88668	Human oligonucleot
c4752	13.8	0.5	20	1	ABZ92288	Human oligonucleot
c4753	13.8	0.5	20	1	ABZ98730	Human tryptase a o
4754	13.8	0.5	20	1	ABX13312	Human NSDHL gene,
4755	13.8	0.5	20	1	ACC62221	Mouse alipoprotein
c4756	13.8	0.5	20	1	ABT34071	Human pigmentation
c4757	13.8	0.5	20	1	ACC55341	Human ADAMTS13 exo
4758	13.8	0.5	20	1	ACC45351	Escherichia coli s
4759	13.8	0.5	20	1	ADA26702	Rat Jun N-terminal
c4760	13.8	0.5	20	1	ABZ58576	Chitinase YM-3 for
4761	13.8	0.5	20	1	AAD55426	Human FGFR-3 antis
c4762	13.8	0.5	20	1	ABX12687	Human IL-4/IL-13 r
c4763	13.8	0.5	20	1	ACA60924	Caenorhabditis ele
c4764	13.8	0.5	20	1	ACF39518	BARCODE-MAT HPV re
4765	13.8	0.5	20	1	ACD99446	Immunostimulatory
c4766	13.8	0.5	20	1	ACD99446	Immunostimulatory
c4767	13.8	0.5	20	1	ACD05095	Tumour necrosis fa
4768	13.8	0.5	20	1	ADB36516	Immunostimulatory
c4769	13.8	0.5	20	1	ADB36516	Immunostimulatory
4770	13.8	0.5	20	1	ADB74233	Human GPR34 PCR pr
4771	13.8	0.5	20	1	ADC65850	Mouse TGF-beta rec
4772	13.8	0.5	20	1	AAD61201	Human Ship-1 antis
c4773	13.8	0.5	20	1	ADE43707	Human KNSL1 sequen
4774	13.8	0.5	20	1	ADE14470	HSD11B1 antisense
4775	13.8	0.5	21	1	AAZ26714	Human polymorphic
4776	13.8	0.5	21	1	AAQ10724	Mutagenising oligo
4777	13.8	0.5	21	1	AAQ22345	Antisense oligonuc
c4778	13.8	0.5	21	1	AAQ28771	HLA Class II gene

c4779	13.8	0.5	21	1	AAQ24706	J-beta-1b primer.
4780	13.8	0.5	21	1	AAT14900	Primer 6 for 3' po
4781	13.8	0.5	21	1	AAQ55571	Sequence of synthe
4782	13.8	0.5	21	1	AAQ67230	Triple helix-formi
4783	13.8	0.5	21	1	AAQ44571	Antisense oligonuc
4784	13.8	0.5	21	1	AAQ79210	Guanosine rich oli
4785	13.8	0.5	21	1	AAQ56046	Primer 5 to isolat
4786	13.8	0.5	21	1	AAQ70078	CZP2(487-713) prim
4787	13.8	0.5	21	1	AAT01778	Peptide nucleic ac
4788	13.8	0.5	21	1	AAT36683	Antisense oligonuc
4789	13.8	0.5	21	1	AAT51628	Viral integrase in
4790	13.8	0.5	21	1	AAT59010	beta3-adrenergic r
4791	13.8	0.5	21	1	AAT84680	KSHV glycoprotein
4792	13.8	0.5	21	1	AAT84689	KSHV glycoprotein
4793	13.8	0.5	21	1	AAT76136	Human eosinophil p
4794	13.8	0.5	21	1	AAV05263	Antisense primer u
4795	13.8	0.5	21	1	AAX79217	Oligonucleotide #1
c4796	13.8	0.5	21	1	AAV40572	Human TSC gene exo
4797	13.8	0.5	21	1	AAZ26192	Human polymorphic
4798	13.8	0.5	21	1	AAX99727	Human AUR2 inhibit
4799	13.8	0.5	21	1	AAV63682	HIV-2 ENV region P
4800	13.8	0.5	21	1	AAX53935	Eosinophil peroxid
4801	13.8	0.5	21	1	AAZ21762	Exemplary oligonuc
4802	13.8	0.5	21	1	AAA33375	Low adenosine anti
c4803	13.8	0.5	21	1	AAZ55720	Human caspase-9 PC
c4804	13.8	0.5	21	1	AAZ73879	Human biallelic ma
4805	13.8	0.5	21	1	AAZ75815	Human biallelic ma
4806	13.8	0.5	21	1	AAF19497	Human eosinophil p
c4807	13.8	0.5	21	1	AAA62937	Antisense oligonuc
4808	13.8	0.5	21	1	AAZ48932	Human ELAM-1 antis
4809	13.8	0.5	21	1	AAA57738	Oligonuleotide pro
c4810	13.8	0.5	21	1	AAA57739	Oligonuleotide pro
4811	13.8	0.5	21	1	AAA73988	HIV primer 2ENV-R2
c4812	13.8	0.5	21	1	ADE80908	Streptococcus pneu
c4813	13.8	0.5	21	1	AAS06843	SNP containing pro
4814	13.8	0.5	21	1	AAF97680	Human gene single
4815	13.8	0.5	21	1	AAF97544	Human gene single
c4816	13.8	0.5	21	1	AAF97617	Human gene single
4817	13.8	0.5	21	1	AAF97628	Human gene single
4818	13.8	0.5	21	1	AAF96104	Human gene single
4819	13.8	0.5	21	1	AAF96440	Human gene single
4820	13.8	0.5	21	1	AAF97321	Human gene single
c4821	13.8	0.5	21	1	AAH62300	GLI-kruppel family
4822	13.8	0.5	21	1	AAH28431	PCR primer for int
4823	13.8	0.5	21	1	AAD12205	Human CYP450 2C19
c4824	13.8	0.5	21	1	AAH91420	Human inflammatory
4825	13.8	0.5	21	1	AAF85206	PCR primer used to
c4826	13.8	0.5	21	1	AAH89104	Human polymorphic
4827	13.8	0.5	21	1	AAS11076	Bacterial 16s RNA
4828	13.8	0.5	21	1	AAS11058	Bacterial 16s RNA
c4829	13.8	0.5	21	1	AAS11038	Bacterial 16s RNA
c4830	13.8	0.5	21	1	ABK53146	HIV-1 Gag gene spe
c4831	13.8	0.5	21	1	ABK53111	HIV-1 Gag gene spe
4832	13.8	0.5	21	1	ABK65817	Human single nucle
c4833	13.8	0.5	21	1	ABK88537	Human cholecystoki
4834	13.8	0.5	21	1	ABQ78573	RT-PCR primer used
4835	13.8	0.5	21	1	ABV99452	Human NOV5 forward
c4836	13.8	0.5	21	1	ABL44206	Human chromosome 1
4837	13.8	0.5	21	1	ABK81198	Polyimmunoglobulin
c4838	13.8	0.5	21	1	AAD22905	Human soluble LIGH
4839	13.8	0.5	21	1	ABX04726	Human endogenous r
c4840	13.8	0.5	21	1	AAL45508	HIV-1 gag amplific
c4841	13.8	0.5	21	1	AAL45473	HIV-1 gag amplific
c4842	13.8	0.5	21	1	ADE53231	FEN-1 related DNA
4843	13.8	0.5	21	1	ABZ95191	Human eosinophil p
4844	13.8	0.5	21	1	ABQ83714	Exemplary oligonuc
c4845	13.8	0.5	21	1	ABT33998	Human pigmentation
4846	13.8	0.5	21	1	ACC70856	Human G-protein co
4847	13.8	0.5	21	1	ACA90032	Cardiovascular dis
c4848	13.8	0.5	21	1	ABZ23347	Forward PCR primer
4849	13.8	0.5	21	1	ADA26144	Human REL-A short
c4850	13.8	0.5	21	1	ACC78817	Human CD31 (PECAM)
4851	13.8	0.5	21	1	ADC39012	Human ELAM-1 targe
c4852	13.8	0.5	21	1	ADD14396	Human src biomarke
c4853	13.8	0.5	21	1	ADD24723	Human CYP2E1 mutan
c4854	13.8	0.5	21	1	ADE34494	Human G-protein co
c4855	13.8	0.5	22	1	AAT78996	Human Huntington's
4856	13.8	0.5	25	1	AAC96115	16s rRNA gene PCR
4857	13.8	0.5	25	1	AAC96598	HLA DRB345 gene PC
c4858	13.8	0.5	25	1	AAC96156	16s rRNA gene PCR
c4859	13.8	0.5	25	1	AAC96394	HLA DPB1 gene PCR
c4860	13.8	0.5	25	1	AAC96041	16s rRNA gene PCR
c4861	13.8	0.5	28	1	AAD41903	ON-41 oligonucleot
c4862	13.6	0.5	15	1	ABN87920	Human GSR allele s
4863	13.6	0.5	15	1	ABL01248	Human MMP3 gene po
4864	13.6	0.5	15	1	ABK32799	Human APPBP1 gene,
c4865	13.6	0.5	15	1	ABK32799	Human APPBP1 gene,
c4866	13.6	0.5	20	1	AAC82914	Human beta-actin d
c4867	13.6	0.5	20	1	AAC82912	Human beta-actin d
4868	13.6	0.5	20	1	ABZ87682	Human oligonucleot
c4869	13.6	0.5	20	1	ABZ89513	Human oligonucleot
c4870	13.6	0.5	20	1	ABZ85671	Human oligonucleot
c4871	13.6	0.5	20	1	AAN71012	Probe to 35kd pulm
4872	13.6	0.5	20	1	AAQ05898	Probe AD03 to dete
c4873	13.6	0.5	20	1	AAQ35728	EIV 5' fragment pr
4874	13.6	0.5	20	1	AAQ41529	Antisense oligomer
4875	13.6	0.5	20	1	AAQ46060	Sequence of PCR pr
c4876	13.6	0.5	20	1	AAQ34754	Blocker oligonucle
c4877	13.6	0.5	20	1	AAQ70719	C-myc gene antisen
4878	13.6	0.5	20	1	AAQ71313	Primer for the det
c4879	13.6	0.5	20	1	AAQ97446	Phage lambda J gen
4880	13.6	0.5	20	1	AAT41357	Human gene signatu
c4881	13.6	0.5	20	1	AAT41087	Human gene signatu
c4882	13.6	0.5	20	1	AAQ87813	Antisense oligomer
c4883	13.6	0.5	20	1	AAT60911	Multi-tumour aberr
c4884	13.6	0.5	20	1	AAT60649	Antisense oligonuc
c4885	13.6	0.5	20	1	AAT60650	Antisense oligonuc
c4886	13.6	0.5	20	1	AAT48940	Complementary huma
c4887	13.6	0.5	20	1	AAT50903	Probe #17 for inte
c4888	13.6	0.5	20	1	AAT95343	Treatment of human
c4889	13.6	0.5	20	1	AAT61084	Mouse Apo E forwar
4890	13.6	0.5	20	1	AAT47409	Primer #35 for cys
c4891	13.6	0.5	20	1	AAT76385	Human tumour necro
c4892	13.6	0.5	20	1	AAT48467	Third-strand oligo
4893	13.6	0.5	20	1	AAT68337	Loci-specific prim
4894	13.6	0.5	20	1	AAV40288	Rat insulin-like g
4895	13.6	0.5	20	1	AAV20979	Human PRCC-TFE3 co
c4896	13.6	0.5	20	1	AAV57186	Human Notch-3 muta
4897	13.6	0.5	20	1	AAV42472	PCR primer 1 used
c4898	13.6	0.5	20	1	AAV35081	Antisense MDR1 oli
c4899	13.6	0.5	20	1	AAV48864	ErbB-2 gene antise
c4900	13.6	0.5	20	1	AAV48673	junB gene antisens
4901	13.6	0.5	20	1	AAV70022	Mouse c-Fos protei
c4902	13.6	0.5	20	1	AAV57115	Human Notch3 mutan
4903	13.6	0.5	20	1	AAV42066	Mouse alpha 3 conn
4904	13.6	0.5	20	1	AAV79995	BMP-IA DNA amplify
c4905	13.6	0.5	20	1	AAZ37685	Human mdm2 phospho
c4906	13.6	0.5	20	1	AAX21637	Human N-ras specif
c4907	13.6	0.5	20	1	AAX57000	Ras gene modulatin
c4908	13.6	0.5	20	1	AAZ31287	CCR5 gene inhibiti
4909	13.6	0.5	20	1	AAZ31349	CXCR4 gene inhibit
c4910	13.6	0.5	20	1	AAX33699	DNA tandem nucleot
c4911	13.6	0.5	20	1	AAX54534	Tumour necrosis fa
c4912	13.6	0.5	20	1	AAX33260	PEBP2 alpha A gene
4913	13.6	0.5	20	1	AAZ01809	PCR primer used to
4914	13.6	0.5	20	1	AAZ04150	PCR primer used to
4915	13.6	0.5	20	1	AAZ05582	PCR primer used to
4916	13.6	0.5	20	1	AAZ06015	PCR primer used to
4917	13.6	0.5	20	1	AAZ03352	PCR primer used to
4918	13.6	0.5	20	1	AAZ05579	PCR primer used to
4919	13.6	0.5	20	1	AAZ02019	PCR primer used to
c4920	13.6	0.5	20	1	AAX76250	Peritoneal macroph
4921	13.6	0.5	20	1	AAX58467	PCR primer P38-S25
c4922	13.6	0.5	20	1	AAZ18677	ASTH1 gene intron/
c4923	13.6	0.5	20	1	AAX93060	PCR primer used to
4924	13.6	0.5	20	1	AAX92277	PCR primer used to

c4925	13.6	0.5	20	1	AAX95057	PCR primer used to
c4926	13.6	0.5	20	1	AAX94674	PCR primer used to
4927	13.6	0.5	20	1	AAZ28022	Seq ID No: 8 of WO
c4928	13.6	0.5	20	1	AAZ47566	Antisense oligonuc
4929	13.6	0.5	20	1	AAZ48056	Human IGF-II antis
c4930	13.6	0.5	20	1	AAA60405	Human telomerase a
c4931	13.6	0.5	20	1	AAA33978	Low adenosine anti
4932	13.6	0.5	20	1	AAZ46619	Reverse primer spe
4933	13.6	0.5	20	1	AAA46764	Oligonucleotide se
4934	13.6	0.5	20	1	AAA40976	Human TNFalpha ant
c4935	13.6	0.5	20	1	AAA59816	Primer for RIP 140
c4936	13.6	0.5	20	1	AAA90438	Mouse GANP reverse
4937	13.6	0.5	20	1	AAA99058	Porcine virus acti
4938	13.6	0.5	20	1	AAA09616	Primer SEQ ID 8 us
4939	13.6	0.5	20	1	AAA13090	PCR primer used fo
4940	13.6	0.5	20	1	AAZ99922	PCR primer used to
c4941	13.6	0.5	20	1	AAA94525	Antisense oligonuc
c4942	13.6	0.5	20	1	AAA94526	Antisense oligonuc
c4943	13.6	0.5	20	1	AAA95875	Human N-ras antise
4944	13.6	0.5	20	1	AAC61860	Antisense oligonuc
4945	13.6	0.5	20	1	AAA07904	Hs-UNC-53/2 specif
c4946	13.6	0.5	20	1	AAA07907	Hs-UNC-53/2 specif
4947	13.6	0.5	20	1	AAZ74552	Human biallelic ma
4948	13.6	0.5	20	1	AAZ75568	Human biallelic ma
4949	13.6	0.5	20	1	AAZ71396	Human biallelic ma
c4950	13.6	0.5	20	1	AAZ76490	Human biallelic ma
c4951	13.6	0.5	20	1	AAA80059	Hepatitis B virus
4952	13.6	0.5	20	1	AAA80060	Hepatitis B virus
4953	13.6	0.5	20	1	AAC55854	PCR primer used to
c4954	13.6	0.5	20	1	AAC55853	PCR primer used to
4955	13.6	0.5	20	1	AAZ95329	Human mtPEPCK phos
4956	13.6	0.5	20	1	AAA29832	Human jun N-termin
c4957	13.6	0.5	20	1	AAZ43999	Bacteria detecting
c4958	13.6	0.5	20	1	AAF20100	Human tumour necro
c4959	13.6	0.5	20	1	AAA15603	Reverse PCR primer
4960	13.6	0.5	20	1	AAA57980	Candida albicans T
c4961	13.6	0.5	20	1	AAA86885	Probe for wild typ
4962	13.6	0.5	20	1	AAC93192	Human STAT3 phosph
c4963	13.6	0.5	20	1	AAA80584	Human ASTH1J gene
c4964	13.6	0.5	20	1	ABL57553	Synthetic deoxyrib
4965	13.6	0.5	20	1	ABL57554	Synthetic deoxyrib
4966	13.6	0.5	20	1	AAA37705	Human Rad51 antise
c4967	13.6	0.5	20	1	AAF31770	Human RANK antisen
c4968	13.6	0.5	20	1	AAA91252	Antisense IGFBP-5
c4969	13.6	0.5	20	1	AAA91233	Antisense IGFBP-5
4970	13.6	0.5	20	1	AAS01198	Human RAD51 antise
c4971	13.6	0.5	20	1	AAI70304	Phage lambda vecto
4972	13.6	0.5	20	1	AAC67211	Human E2F transcri
c4973	13.6	0.5	20	1	AAF73008	Human daxx inhibit
c4974	13.6	0.5	20	1	AAD11311	Human cot oncogene
4975	13.6	0.5	20	1	AAC92738	Human hnRNP A1 pho
4976	13.6	0.5	20	1	AAH57066	Human oestrogen re
4977	13.6	0.5	20	1	AAH57065	Human oestrogen re
4978	13.6	0.5	20	1	AAA91571	Adaptor molecule #
c4979	13.6	0.5	20	1	AAF59983	Rabbit beta-globin
4980	13.6	0.5	20	1	AAH25808	Human ibaI DNA PCR
4981	13.6	0.5	20	1	AAH25827	Adipogenesis inhib
4982	13.6	0.5	20	1	AAH56682	Streptococcus pyog
4983	13.6	0.5	20	1	AAH56570	S. pneumoniae groE
c4984	13.6	0.5	20	1	AAH56423	Escherichia coli g
c4985	13.6	0.5	20	1	AAF80839	Human mdm2 phospho
4986	13.6	0.5	20	1	AAS10664	Human caspase 3 an
4987	13.6	0.5	20	1	AAF29930	Human estrogen rec
c4988	13.6	0.5	20	1	AAF99650	Immunostimulatory
c4989	13.6	0.5	20	1	AAF99396	Immunostimulatory
4990	13.6	0.5	20	1	AAF99576	Immunostimulatory
c4991	13.6	0.5	20	1	AAF99225	Immunostimulatory
c4992	13.6	0.5	20	1	AAH41798	RIP 140 gene PCR p
c4993	13.6	0.5	20	1	AAS43108	Human ERbeta gene,
4994	13.6	0.5	20	1	AAC67698	Oligonucleotide #9
c4995	13.6	0.5	20	1	AAD11966	Human PTP1B antise
c4996	13.6	0.5	20	1	AAD12126	Rat PTP1B antisens
4997	13.6	0.5	20	1	AAF24291	Complementary nucl
4998	13.6	0.5	20	1	AAH47246	Human C-PLACE10032
4999	13.6	0.5	20	1	AAC82915	Human beta-actin d
c5000	13.6	0.5	20	1	AAC82915	Human beta-actin d
c5001	13.6	0.5	20	1	AAF91308	Human E2F transcri
5002	13.6	0.5	20	1	AAD09641	Human PKA C-alpha
5003	13.6	0.5	20	1	AAS08796	Human PD-ABC form
5004	13.6	0.5	20	1	AAS08736	Human PD-ABC form
5005	13.6	0.5	20	1	AAS08827	Human PD-ABC form
5006	13.6	0.5	20	1	AAI98550	Genomic DNA methyl
c5007	13.6	0.5	20	1	AAF75050	Primer #22. Homo
5008	13.6	0.5	20	1	AAS12922	Human BCMP 11 cDNA
5009	13.6	0.5	20	1	AAH62087	PDGF B hairpin/ham
5010	13.6	0.5	20	1	AAS43046	Breast cancer-asso
c5011	13.6	0.5	20	1	AAS29454	Human mdm2 antisen
5012	13.6	0.5	20	1	AAH80587	Oligonucleotide hy
c5013	13.6	0.5	20	1	AAH80390	Oligonucleotide hy
c5014	13.6	0.5	20	1	AAH80810	Oligonucleotide hy
c5015	13.6	0.5	20	1	AAH80812	Oligonucleotide hy
c5016	13.6	0.5	20	1	AAH80811	Oligonucleotide hy
5017	13.6	0.5	20	1	ABA81742	PCR primer KP212.
5018	13.6	0.5	20	1	ABK90287	Bcl-2-targeting an
5019	13.6	0.5	20	1	AAD43244	Antisense oligonuc
c5020	13.6	0.5	20	1	ABA91531	DNA oligonucleotid
c5021	13.6	0.5	20	1	ABA91533	DNA oligonucleotid
5022	13.6	0.5	20	1	ABA91527	DNA-RNA-DNA oligon
c5023	13.6	0.5	20	1	ABA91536	DNA oligonucleotid
5024	13.6	0.5	20	1	ABQ65299	Human gene methyla
5025	13.6	0.5	20	1	ABK85429	Oligonucleotide #7
5026	13.6	0.5	20	1	AAD41025	Mouse PI3K p85 ant
5027	13.6	0.5	20	1	AAD40874	Human hepsin antis
5028	13.6	0.5	20	1	AAS96809	Human STAT3 antise
5029	13.6	0.5	20	1	AAS97811	Murine SAC1 gene-s
c5030	13.6	0.5	20	1	AAS97626	Murine SAC1 gene-s
c5031	13.6	0.5	20	1	ABK37098	Human lysophosphol
5032	13.6	0.5	20	1	ABK37112	Human lysophosphol
5033	13.6	0.5	20	1	ABK37064	Human lysophosphol
c5034	13.6	0.5	20	1	AAD41793	Human RECQL2 antis
c5035	13.6	0.5	20	1	ABS77869	Angiogenesis inhib
c5036	13.6	0.5	20	1	ABS78371	Angiogenesis inhib
5037	13.6	0.5	20	1	ABS78292	Angiogenesis inhib
c5038	13.6	0.5	20	1	ABS78041	Angiogenesis inhib
c5039	13.6	0.5	20	1	ABT07437	Mammalian protein
c5040	13.6	0.5	20	1	ABT07470	Human protein phos
c5041	13.6	0.5	20	1	ABL38651	Immunostimulatory
c5042	13.6	0.5	20	1	ABL39120	Immunostimulatory
5043	13.6	0.5	20	1	ABL38654	Immunostimulatory
c5044	13.6	0.5	20	1	ABL38650	Immunostimulatory
5045	13.6	0.5	20	1	ABK34037	Human CSNK2B PCR p
5046	13.6	0.5	20	1	ABK67993	Mutant DNA library
c5047	13.6	0.5	20	1	ABK85201	Rat PTPB1 antisens
5048	13.6	0.5	20	1	ABK85319	Human PTP1B antise
c5049	13.6	0.5	20	1	ABK85041	Human PTP1B antise
5050	13.6	0.5	20	1	AAD40692	Human hepsin antis
c5051	13.6	0.5	20	1	ABA89781	Human oestrogen re
5052	13.6	0.5	20	1	ABN79650	Mouse Fas chimeric
c5053	13.6	0.5	20	1	ABS54903	Bovine breed discr
5054	13.6	0.5	20	1	ABL43506	Human chromosome 1
c5055	13.6	0.5	20	1	ABL43971	Human chromosome 1
5056	13.6	0.5	20	1	ABL43508	Human chromosome 1
5057	13.6	0.5	20	1	ABA98707	PCR primer R1. Sy
5058	13.6	0.5	20	1	ABV72239	Antisense oligonuc
c5059	13.6	0.5	20	1	ABQ81884	Kaposi's Sarcoma r
c5060	13.6	0.5	20	1	ABK37370	Rat PTP1B mRNA lev
c5061	13.6	0.5	20	1	ABK37210	Human PTP1B mRNA l
5062	13.6	0.5	20	1	AAD35748	Human hIbeta4BP an
5063	13.6	0.5	20	1	ABL60762	Human SPHK1 cDNA c
5064	13.6	0.5	20	1	ABA97633	Poly o nucleotide
c5065	13.6	0.5	20	1	ABA97638	Poly t nucleotide
5066	13.6	0.5	20	1	ABA97639	Poly u nucleotide
5067	13.6	0.5	20	1	ABQ78543	Antisense oligodeo
c5068	13.6	0.5	20	1	ABT13059	Human apolipoprote
5069	13.6	0.5	20	1	ABK28025	Human CSNK2B methy
5070	13.6	0.5	20	1	ABK69224	Human phosphorylas

5071	13.6	0.5	20	1	ABK88956	Interleukin-10 (IL
5072	13.6	0.5	20	1	ABQ74646	Ki67 gene antisens
c5073	13.6	0.5	20	1	ABL94461	Mouse C/EBP beta p
5074	13.6	0.5	20	1	ABL94394	Mouse C/EBP beta p
c5075	13.6	0.5	20	1	ABL94252	Human C/EBP beta p
5076	13.6	0.5	20	1	ABS70610	Dendritic cell sti
c5077	13.6	0.5	20	1	ABI94166	Capture oligonucle
5078	13.6	0.5	20	1	ABI94468	Capture oligonucle
5079	13.6	0.5	20	1	ABL54171	Oligonucleotide.
c5080	13.6	0.5	20	1	ABZ89486	Human oligonucleot
5081	13.6	0.5	20	1	ABZ89718	Human oligonucleot
5082	13.6	0.5	20	1	ABZ99083	Human PDE4C oligon
5083	13.6	0.5	20	1	ABZ91619	Human oligonucleot
c5084	13.6	0.5	20	1	ABZ91619	Human oligonucleot
c5085	13.6	0.5	20	1	ABZ92183	Human oligonucleot
c5086	13.6	0.5	20	1	ABZ86522	Human oligonucleot
5087	13.6	0.5	20	1	ABZ88944	Human oligonucleot
c5088	13.6	0.5	20	1	ABZ89490	Human oligonucleot
5089	13.6	0.5	20	1	ABZ89503	Human oligonucleot
c5090	13.6	0.5	20	1	ABZ90826	Human oligonucleot
5091	13.6	0.5	20	1	ABZ98749	Human tryptase a o
5092	13.6	0.5	20	1	ABZ98961	Human PDE4A oligon
5093	13.6	0.5	20	1	ABZ88835	Human oligonucleot
5094	13.6	0.5	20	1	ABZ90740	Human oligonucleot
c5095	13.6	0.5	20	1	ABZ99023	Human PDE4A oligon
c5096	13.6	0.5	20	1	ABZ90288	Human oligonucleot
c5097	13.6	0.5	20	1	ABZ91627	Human oligonucleot
c5098	13.6	0.5	20	1	ABZ89922	Human oligonucleot
c5099	13.6	0.5	20	1	ABZ97376	Human IL4-R oligon
c5100	13.6	0.5	20	1	ABZ89225	Human oligonucleot
5101	13.6	0.5	20	1	ABZ90987	Human oligonucleot
c5102	13.6	0.5	20	1	ABZ95794	Human tumour necro
5103	13.6	0.5	20	1	ABZ89376	Human oligonucleot
c5104	13.6	0.5	20	1	ABZ92584	Human oligonucleot
c5105	13.6	0.5	20	1	ABZ98728	Human tryptase a o
c5106	13.6	0.5	20	1	ABZ98829	Human tryptase b o
c5107	13.6	0.5	20	1	ABZ87741	Human oligonucleot
c5108	13.6	0.5	20	1	ABZ90974	Human oligonucleot
c5109	13.6	0.5	20	1	ABZ91436	Human oligonucleot
5110	13.6	0.5	20	1	ABZ88937	Human oligonucleot
5111	13.6	0.5	20	1	ABZ98627	Human tryptase a o
5112	13.6	0.5	20	1	ABZ85307	Human oligonucleot
c5113	13.6	0.5	20	1	ABZ85307	Human oligonucleot
c5114	13.6	0.5	20	1	ABZ93877	Human oligonucleot
c5115	13.6	0.5	20	1	ABZ99269	Human PDE4C oligon
5116	13.6	0.5	20	1	ABZ88750	Human oligonucleot
5117	13.6	0.5	20	1	ABZ92509	Human oligonucleot
c5118	13.6	0.5	20	1	ABZ92815	Human oligonucleot
5119	13.6	0.5	20	1	ABZ98578	Human ICAM oligonu
c5120	13.6	0.5	20	1	ABZ98645	Human tryptase a o
c5121	13.6	0.5	20	1	ABZ87698	Human oligonucleot
c5122	13.6	0.5	20	1	ABZ88388	Human oligonucleot
c5123	13.6	0.5	20	1	ABZ80359	CD45 antisense PCR
5124	13.6	0.5	20	1	ABQ84589	DPP10 related PSQ
5125	13.6	0.5	20	1	AAD50403	Mouse HPRT DNA amp
5126	13.6	0.5	20	1	ABZ77107	Human stearoyl-CoA
5127	13.6	0.5	20	1	ADA26838	Human ZD52F10 reve
5128	13.6	0.5	20	1	ACC68889	Human TGR23 phosph
c5129	13.6	0.5	20	1	ACA92598	Human N ras antise
5130	13.6	0.5	20	1	ABZ79328	Acetyl-Coenzyme A-
c5131	13.6	0.5	20	1	ADA00265	RIP 140 gene PCR p
c5132	13.6	0.5	20	1	ABQ77167	Human ABCC12 exon
5133	13.6	0.5	20	1	ABZ10372	Haematopoietic cel
5134	13.6	0.5	20	1	ABZ10249	Haematopoietic cel
5135	13.6	0.5	20	1	ADA20472	Prostate tumour re
5136	13.6	0.5	20	1	ADA20493	Prostate tumour re
5137	13.6	0.5	20	1	ADA84290	Human CSNK2B PCR p
5138	13.6	0.5	20	1	ADA84294	Human DBCCR1 PCR p
5139	13.6	0.5	20	1	ACA10235	Human NOVX DNA PCR
5140	13.6	0.5	20	1	ABT43367	Neuroblastoma-rela
5141	13.6	0.5	20	1	ABT43222	Neuroblastoma-rela
c5142	13.6	0.5	20	1	ABX34233	Antisense oligonuc
c5143	13.6	0.5	20	1	ABX10779	Human dual specifi
c5144	13.6	0.5	20	1	ABX10791	Human dual specifi
5145	13.6	0.5	20	1	AAD55805	Major ampullate sp
5146	13.6	0.5	20	1	AAL53961	DNA mutation detec
5147	13.6	0.5	20	1	AAL53959	DNA mutation detec
c5148	13.6	0.5	20	1	AAL53967	DNA mutation detec
5149	13.6	0.5	20	1	AAL53958	DNA mutation detec
c5150	13.6	0.5	20	1	AAL53962	DNA mutation detec
5151	13.6	0.5	20	1	AAL53960	DNA mutation detec
c5152	13.6	0.5	20	1	AAL53964	DNA mutation detec
c5153	13.6	0.5	20	1	AAL53966	DNA mutation detec
5154	13.6	0.5	20	1	ABT32534	Neuroblastoma-rela
5155	13.6	0.5	20	1	ABT32356	Neuroblastoma-rela
c5156	13.6	0.5	20	1	AAL61847	Human ETBR-LP-2 an
c5157	13.6	0.5	20	1	ACD99656	Immunostimulatory
5158	13.6	0.5	20	1	ACH03114	Immunostimulatory
c5159	13.6	0.5	20	1	ACD99816	Immunostimulatory
c5160	13.6	0.5	20	1	ACH03191	Immunostimulatory
5161	13.6	0.5	20	1	ACF06256	Human NOV4 probe S
c5162	13.6	0.5	20	1	ABT43815	Human PIP5KIa anti
5163	13.6	0.5	20	1	ACF05559	Human secreted pro
5164	13.6	0.5	20	1	ACD05204	Tumour necrosis fa
c5165	13.6	0.5	20	1	AAL61587	Human inhibitor-ka
5166	13.6	0.5	20	1	ADB93133	Human Type II coll
c5167	13.6	0.5	20	1	ADB37152	Immunostimulatory
c5168	13.6	0.5	20	1	ADB36727	Immunostimulatory
c5169	13.6	0.5	20	1	ADB36898	Immunostimulatory
5170	13.6	0.5	20	1	ADB37078	Immunostimulatory
5171	13.6	0.5	20	1	ADC23725	Antisense PCR prim
c5172	13.6	0.5	20	1	ADC13699	Human NOVX forward
c5173	13.6	0.5	20	1	ADC53902	Pediococcus detect
5174	13.6	0.5	20	1	AAD60260	Oligonucleotide 16
5175	13.6	0.5	20	1	ADD20133	Oreochromis niloti
c5176	13.6	0.5	20	1	ADD21650	Human mdm2 antisen
c5177	13.6	0.5	20	1	ADD68563	SNP typing-related
5178	13.6	0.5	20	1	ADD68537	SNP typing-related
c5179	13.6	0.5	20	1	ADD56647	Human gene express
5180	13.6	0.5	20	1	ADE28930	Forward Ag5892 RT-
c5181	13.6	0.5	20	1	ADE86164	HRAS gene regulato
c5182	13.6	0.5	20	1	ADE86160	RET gene regulator
c5183	13.6	0.5	20	1	ADD81701	HIV PRT antisense
c5184	13.6	0.5	20	1	ADD81702	HIV PRT antisense
c5185	13.6	0.5	20	1	ADD81281	HIV PRT antisense
5186	13.6	0.5	20	1	ADD81478	HIV PRT antisense
c5187	13.6	0.5	20	1	ADD81703	HIV PRT antisense
c5188	13.6	0.5	20	1	ADE10334	Plasmid pKN108-der
5189	13.6	0.5	20	1	ADE10335	Plasmid pKN108-der
5190	13.6	0.5	20	1	ADE84223	Human lymphoid cel
c5191	13.6	0.5	21	1	AAZ26573	Human polymorphic
5192	13.6	0.5	21	1	ADD24723	Human CYP2E1 mutan
c5193	13.6	0.5	22	1	AAX14678	Triple helix formi
c5194	13.6	0.5	24	1	AAT03687	Homopyrimidine pro
c5195	13.6	0.5	24	1	AAL42406	Human ORC413-64 PC
c5196	13.6	0.5	25	1	AAC96455	HLA DQB1 gene PCR
5197	13.6	0.5	25	1	AAC96092	16s rRNA gene PCR
5198	13.6	0.5	25	1	AAC96353	HLA DPB1 gene PCR
5199	13.6	0.5	25	1	AAC95751	HLA DQB1 gene PCR
5200	13.4	0.5	15	1	AAT52142	Human ICAM hammerh
5201	13.4	0.5	15	1	AAA11718	Human MIF gene D5k
5202	13.4	0.5	15	1	AAF60455	Oligonucleotide cl
c5203	13.4	0.5	16	1	ABL57076	Molecular beacon t
c5204	13.4	0.5	16	1	AAD57846	Target oligonucleo
c5205	13.4	0.5	17	1	AAF03225	Hammerhead ribozym
c5206	13.4	0.5	17	1	AAF03224	Hammerhead ribozym
c5207	13.4	0.5	17	1	AAF03226	Hammerhead ribozym
c5208	13.4	0.5	17	1	ADB40890	Tumour suppression
c5209	13.4	0.5	20	1	AAC82922	Human S-9 derived
c5210	13.4	0.5	20	1	AAF87713	Human glutathione
c5211	13.4	0.5	20	1	AAQ52305	FKBP12C PCR primer
5212	13.4	0.5	20	1	ABZ94127	Human oligonucleot
c5213	13.4	0.5	21	1	AAF87033	Anchored 3' oligo
5214	13.4	0.5	21	1	AAF80105	Nucleotide sequenc
c5215	13.4	0.5	21	1	ABL57072	Molecular beacon t
5216	13.4	0.5	21	1	ABS58234	Sequence surroundi

5217	13.4	0.5	21	1	AAT42561	3' primer #1087-11
5218	13.4	0.5	21	1	AAZ26403	Human polymorphic
c5219	13.4	0.5	24	1	ABA04964	Human FD14 PCR pri
c5220	13.4	0.5	25	1	AAC96197	16s rRNA gene PCR
5221	13.4	0.5	25	1	ABS75770	Human PAPP-Ea asso
c5222	13.2	0.5	18	1	AAX87332	Reverse transcript
c5223	13.2	0.5	18	1	AAX15198	Triple helix formi
5224	13.2	0.5	18	1	AAX15196	Triple helix formi
5225	13.2	0.5	18	1	ABS52682	mRNA display splin
5226	13.2	0.5	18	1	ABK98126	Triple helix formi
c5227	13.2	0.5	19	1	AAQ20030	Cross-linking olig
c5228	13.2	0.5	19	1	AAQ30373	Oligomer HUM beta
c5229	13.2	0.5	19	1	AAQ30376	Oligomer HUM beta
5230	13.2	0.5	19	1	ABA97625	Probe d. Unidenti
c5231	13.2	0.5	19	1	ADE27307	Stearoyl-CoA desat
5232	13.2	0.5	19	1	ADE27597	Stearoyl-CoA desat
c5233	13.2	0.5	19	1	AAQ20028	Cross-linking olig
c5234	13.2	0.5	19	1	AAQ20029	Cross-linking olig
c5235	13.2	0.5	19	1	AAQ30375	Oligomer HUM beta
c5236	13.2	0.5	19	1	AAQ30374	Oligomer HUM beta
c5237	13.2	0.5	19	1	AAT49298	5' end fragment of
c5238	13.2	0.5	19	1	AAT74905	5' end fragment of
c5239	13.2	0.5	19	1	AAT47271	Capped RNA influen
c5240	13.2	0.5	19	1	AAT47276	Capped RNA influen
c5241	13.2	0.5	19	1	AAT47269	Capped RNA influen
c5242	13.2	0.5	19	1	AAT47279	Capped RNA influen
c5243	13.2	0.5	19	1	AAT47277	Capped RNA influen
c5244	13.2	0.5	19	1	AAT47273	Capped RNA influen
c5245	13.2	0.5	19	1	AAT47264	5' fragment of alf
c5246	13.2	0.5	19	1	AAT47272	Capped RNA influen
c5247	13.2	0.5	19	1	AAT47278	Capped RNA influen
c5248	13.2	0.5	19	1	AAT47267	Capped RNA influen
c5249	13.2	0.5	19	1	AAT47270	Capped RNA influen
5250	13.2	0.5	20	1	ABA91534	DNA oligonucleotid
c5251	13.2	0.5	20	1	ABZ85667	Human oligonucleot
5252	13.2	0.5	20	1	ABZ90373	Human oligonucleot
5253	13.2	0.5	20	1	AAQ30371	Oligomer HUM beta
5254	13.2	0.5	20	1	AAQ68869	Self paired oligon
c5255	13.2	0.5	20	1	AAT47265	5' fragment #2 of
c5256	13.2	0.5	20	1	ABL57554	Synthetic deoxyrib
c5257	13.2	0.5	20	1	ABA97633	Poly o nucleotide
c5258	13.2	0.5	20	1	ABA97639	Poly u nucleotide
c5259	13.2	0.5	20	1	ABZ88937	Human oligonucleot
5260	13.2	0.5	20	1	ABZ87698	Human oligonucleot
c5261	13.2	0.5	21	1	AAH91825	Human inflammatory
c5262	13.2	0.5	21	1	ABK70498	In-situ analysis s
c5263	13.2	0.5	21	1	ABQ78573	RT-PCR primer used
c5264	13.2	0.5	22	1	AAT28045	3'-primer B for hu
c5265	13.2	0.5	22	1	AAT28046	3'-primer C for hu
c5266	13.2	0.5	22	1	AAT28044	3'-primer A for hu
c5267	13.2	0.5	22	1	AAT58484	First primer #1 fo
c5268	13.2	0.5	22	1	AAT58485	First primer #2 fo
c5269	13.2	0.5	22	1	AAT58486	First primer #3 fo
c5270	13.2	0.5	22	1	AAV03675	Oligo dT primer.
c5271	13.2	0.5	22	1	AAZ47342	PCR primer A used
c5272	13.2	0.5	22	1	AAZ47344	PCR primer C used
c5273	13.2	0.5	22	1	AAZ47343	PCR primer B used
c5274	13.2	0.5	22	1	AAH22185	Human hepatocyte a
c5275	13.2	0.5	22	1	AAH22187	Human hepatocyte a
c5276	13.2	0.5	22	1	AAH22186	Human hepatocyte a
c5277	13.2	0.5	22	1	AAT93818	Antitumoural phosp
c5278	13.2	0.5	23	1	AAF60331	Human liver RNA re
c5279	13.2	0.5	23	1	ABQ81205	Human endostatin c
5280	13.2	0.5	23	1	AAA53817	Primer BTU1-75 hyb
c5281	13.2	0.5	24	1	ABZ25620	Human zinc finger
c5282	13.2	0.5	24	1	ABN86391	Basophilic nucleop
c5283	13.2	0.5	25	1	ABQ94378	Tumour suppression
c5284	13.2	0.5	25	1	ABQ94374	Tumour suppression
c5285	13.2	0.5	25	1	ABQ94375	Tumour suppression
c5286	13.2	0.5	27	1	AAT90275	Pyrimidine ring mo
c5287	13.2	0.5	28	1	AAH91554	Human inflammatory
5288	13	0.5	14	1	ABQ83276	EGI cDNA tag relat
c5289	13	0.5	14	1	ABQ83275	EGI cDNA tag relat
5290	13	0.5	14	1	ABQ83271	EGI cDNA tag relat
5291	13	0.5	14	1	ABX79769	EST polymorphic DN
5292	13	0.5	15	1	AAX18361	RT-PCR primer of t
c5293	13	0.5	17	1	AAX69797	Human flt1 VEGF re
c5294	13	0.5	18	1	ADC64943	Camellia sinensis
c5295	13	0.5	18	1	ADC64941	Camellia sinensis
c5296	13	0.5	19	1	AAC83562	DNA synthesis meth
5297	13	0.5	20	1	ABZ92288	Human oligonucleot
c5298	13	0.5	20	1	AAZ74552	Human biallelic ma
c5299	13	0.5	21	1	AAH88904	Human polymorphic
c5300	13	0.5	21	1	AAQ61989	HIV replication in
c5301	13	0.5	21	1	AAT35001	HIV inhibitor #4.
c5302	13	0.5	21	1	AAZ26572	Human polymorphic
c5303	13	0.5	22	1	AAV58375	Biotinylated prime
c5304	13	0.5	22	1	AAA99617	(T)-primer for fir
c5305	13	0.5	22	1	AAL56810	T(13) bio-primer o
c5306	13	0.5	24	1	AAC96274	HLA DPB1 gene PCR
5307	13	0.5	25	1	AAC96374	HLA DPB1 gene PCR
c5308	13	0.5	25	1	AAC96070	16s rRNA gene PCR
5309	12.8	0.5	17	1	AAX69805	Human flt1 VEGF re
5310	12.8	0.5	17	1	AAQ20006	Oligonucleotide #2
c5311	12.8	0.5	17	1	AAQ20005	Oligonucleotide #1
5312	12.8	0.5	17	1	AAA22975	Integrin subunit b
c5313	12.8	0.5	17	1	AAA25444	Oestrogen receptor
c5314	12.8	0.5	17	1	AAA25455	Oestrogen receptor
5315	12.8	0.5	17	1	AAF02388	Hammerhead ribozym
c5316	12.8	0.5	17	1	ABS74957	Human PAPP-Ea asso
c5317	12.8	0.5	17	1	ABZ65528	Human HER2 DNAzyme
c5318	12.8	0.5	17	1	ABZ65527	Human HER2 DNAzyme
5319	12.8	0.5	19	1	AAZ59379	Forward PCR primer
c5320	12.8	0.5	20	1	ABZ92287	Human oligonucleot
c5321	12.8	0.5	20	1	ABX12581	Human cytochrome P
c5322	12.8	0.5	20	1	AAS03670	PCR primer re012,
5323	12.8	0.5	20	1	AAA94533	Antisense oligonuc
c5324	12.8	0.5	20	1	ABZ99084	Human PDE4C oligon
5325	12.8	0.5	20	1	ABZ87697	Human oligonucleot
c5326	12.8	0.5	20	1	AAV42066	Mouse alpha 3 conn
c5327	12.8	0.5	20	1	AAF99576	Immunostimulatory
c5328	12.8	0.5	20	1	ABS78292	Angiogenesis inhib
c5329	12.8	0.5	20	1	ABL38654	Immunostimulatory
c5330	12.8	0.5	20	1	ABS70610	Dendritic cell sti
c5331	12.8	0.5	20	1	ACH03114	Immunostimulatory
c5332	12.8	0.5	20	1	ADB37078	Immunostimulatory
c5333	12.8	0.5	20	1	AAD60260	Oligonucleotide 16
c5334	12.8	0.5	21	1	AAH91826	Human inflammatory
c5335	12.8	0.5	21	1	AAZ75372	Human biallelic ma
5336	12.8	0.5	23	1	AAC83568	Human FMR1 gene 5'
c5337	12.8	0.5	23	1	AAH28300	3' untranslated re
5338	12.8	0.5	23	1	ABT05505	NOVX related probe
c5339	12.8	0.5	25	1	AAS20313	Human Cgamma gene
c5340	12.8	0.5	25	1	ABK90953	PCR primer, 25657,
c5341	12.8	0.5	25	1	ACI27529	Human microarray D
5342	12.6	0.4	20	1	ABA91535	DNA oligonucleotid
c5343	12.6	0.4	20	1	AAH80594	Oligonucleotide hy
5344	12.6	0.4	20	1	ABA91532	DNA oligonucleotid
c5345	12.6	0.4	20	1	ADD81485	HIV PRT antisense
5346	12.6	0.4	20	1	AAL53965	DNA mutation detec
c5347	12.6	0.4	20	1	AAH80593	Oligonucleotide hy
5348	12.6	0.4	20	1	AAL53963	DNA mutation detec
c5349	12.6	0.4	20	1	ADD81484	HIV PRT antisense
c5350	12.6	0.4	20	1	AAV69993	Mouse c-jun protei
5351	12.6	0.4	20	1	AAC65597	Human uteroglobin
5352	12.6	0.4	20	1	ABZ85536	Human oligonucleot
5353	12.6	0.4	20	1	ABQ92966	T. tauschii/wheat
5354	12.6	0.4	20	1	AAV48864	ErbB-2 gene antise
c5355	12.6	0.4	20	1	AAA40976	Human TNFalpha ant
5356	12.6	0.4	20	1	ABL57553	Synthetic deoxyrib
c5357	12.6	0.4	20	1	AAF24291	Complementary nucl
5358	12.6	0.4	20	1	ABA91531	DNA oligonucleotid
5359	12.6	0.4	20	1	ABA91533	DNA oligonucleotid
c5360	12.6	0.4	20	1	ABA91527	DNA-RNA-DNA oligon
5361	12.6	0.4	20	1	ABA91536	DNA oligonucleotid
c5362	12.6	0.4	20	1	ABK85429	Oligonucleotide #7

5363	12.6	0.4	20	1	ABA97638	Poly t nucleotide
5364	12.6	0.4	20	1	ABL94461	Mouse C/EBP beta p
5365	12.6	0.4	20	1	ABZ89486	Human oligonucleot
c5366	12.6	0.4	20	1	ABZ89718	Human oligonucleot
c5367	12.6	0.4	20	1	AAL53961	DNA mutation detec
c5368	12.6	0.4	20	1	AAL53959	DNA mutation detec
5369	12.6	0.4	20	1	AAL53967	DNA mutation detec
c5370	12.6	0.4	20	1	AAL53958	DNA mutation detec
5371	12.6	0.4	20	1	AAL53962	DNA mutation detec
c5372	12.6	0.4	20	1	AAL53960	DNA mutation detec
5373	12.6	0.4	20	1	AAL53964	DNA mutation detec
5374	12.6	0.4	20	1	AAL53966	DNA mutation detec
c5375	12.6	0.4	20	1	ACD05204	Tumour necrosis fa
c5376	12.6	0.4	21	1	AAA14463	AUUUA RNA target s
c5377	12.6	0.4	21	1	AAL50228	Human ARE-mRNA seq
c5378	12.6	0.4	21	1	AAL53707	Adenylate Uridylat
c5379	12.6	0.4	21	1	AAD49639	Human adenylate ur
c5380	12.6	0.4	21	1	ACC83520	AU rich element (A
c5381	12.6	0.4	21	1	ADE86000	AU-rich element mo
5382	12.6	0.4	21	1	AAH91420	Human inflammatory
c5383	12.6	0.4	22	1	AAT28053	3'-primer K for hu
c5384	12.6	0.4	22	1	AAT58493	First primer #10 f
c5385	12.6	0.4	22	1	AAZ47351	PCR primer K used
c5386	12.6	0.4	22	1	AAH22194	Human hepatocyte a
c5387	12.6	0.4	22	1	AAS01584	Human fibrillin-1
5388	12.6	0.4	22	1	AAS01637	Human fibrillin-1
c5389	12.6	0.4	22	1	AAT28049	3'-primer F for hu
c5390	12.6	0.4	22	1	AAT58489	First primer #6 fo
c5391	12.6	0.4	22	1	AAZ47347	PCR primer F used
c5392	12.6	0.4	22	1	AAH22190	Human hepatocyte a
c5393	12.6	0.4	22	1	AAV47448	Antisense oligonuc
c5394	12.6	0.4	23	1	ADC66134	Human CFTR exon 21
c5395	12.6	0.4	24	1	ABL56411	PCR primer F used
c5396	12.4	0.4	14	1	AAV09230	3' poly(T) primer
5397	12.4	0.4	14	1	AAV09234	3' poly(T) primer
c5398	12.4	0.4	14	1	AAV12222	Poly(T) oligonucle
5399	12.4	0.4	14	1	AAV12226	Poly(T) oligonucle
5400	12.4	0.4	14	1	AAT99552	Oligo-dT primer us
5401	12.4	0.4	14	1	AAX02696	Barley HPPD primer
c5402	12.4	0.4	14	1	AAX19465	Human senescence f
5403	12.4	0.4	14	1	AAX19467	Human senescence f
c5404	12.4	0.4	14	1	ABL88471	Oligo dT 3P1 prime
5405	12.4	0.4	14	1	AAD24496	Retinoid-regulated
c5406	12.4	0.4	14	1	AAD24492	Retinoid-regulated
5407	12.4	0.4	15	1	AAT52144	Human ICAM hammerh
c5408	12.4	0.4	17	1	AAX69796	Human flt1 VEGF re
c5409	12.4	0.4	17	1	AAF03223	Hammerhead ribozym
5410	12.4	0.4	17	1	ABQ99687	Murine Ikbkap exon
5411	12.4	0.4	18	1	AAF56305	Human mGluR1alpha
5412	12.4	0.4	20	1	ABA02214	Human/mouse C/EBP
5413	12.4	0.4	20	1	ABZ86522	Human oligonucleot
c5414	12.4	0.4	20	1	ABQ84589	DPP10 related PSQ
c5415	12.4	0.4	21	1	AAZ26823	Human polymorphic
c5416	12.4	0.4	21	1	AAT14900	Primer 6 for 3' po
c5417	12.4	0.4	21	1	AAQ56046	Primer 5 to isolat
c5418	12.4	0.4	21	1	AAQ70078	CZP2(487-713) prim
c5419	12.4	0.4	22	1	AAT28050	3'-primer G for hu
c5420	12.4	0.4	22	1	AAT28051	3'-primer H for hu
c5421	12.4	0.4	22	1	AAT58490	First primer #7 fo
c5422	12.4	0.4	22	1	AAT58491	First primer #8 fo
c5423	12.4	0.4	22	1	AAZ47348	PCR primer G used
c5424	12.4	0.4	22	1	AAZ47349	PCR primer H used
c5425	12.4	0.4	22	1	AAH22191	Human hepatocyte a
c5426	12.4	0.4	22	1	AAH22192	Human hepatocyte a
c5427	12.4	0.4	22	1	AAT28055	3'-primer M for hu
c5428	12.4	0.4	22	1	AAT28047	3'-primer D for hu
c5429	12.4	0.4	22	1	AAT58487	First primer #4 fo
c5430	12.4	0.4	22	1	AAT58495	First primer #12 f
c5431	12.4	0.4	22	1	AAX55049	C/EBP-beta antisen
c5432	12.4	0.4	22	1	AAA34496	Human adenosine re
c5433	12.4	0.4	22	1	AAZ47353	PCR primer M used
c5434	12.4	0.4	22	1	AAZ47345	PCR primer D used
c5435	12.4	0.4	22	1	AAF20618	Human C/EBP polynu
c5436	12.4	0.4	22	1	AAH22188	Human hepatocyte a
c5437	12.4	0.4	22	1	ABZ96312	Human C/EBP antise
c5438	12.4	0.4	23	1	AAX55048	C/EBP-beta antisen
c5439	12.4	0.4	23	1	AAA34495	Human adenosine re
5440	12.4	0.4	23	1	AAZ47417	Probe 1 used to co
c5441	12.4	0.4	23	1	AAF20617	Human C/EBP polynu
c5442	12.4	0.4	23	1	ABZ96311	Human C/EBP antise
c5443	12.4	0.4	24	1	AAZ24999	Sense probe to Fra
c5444	12.4	0.4	25	1	AAC96355	HLA DPB1 gene PCR
c5445	12.4	0.4	25	1	AAZ49618	PCR primer-2 for s
c5446	12.2	0.4	17	1	AAF06381	Hammerhead ribozym
5447	12.2	0.4	17	1	AAX69806	Human flt1 VEGF re
c5448	12.2	0.4	17	1	AAA22593	Integrin subunit b
5449	12.2	0.4	17	1	ABK00237	Human NOGO Hammerh
5450	12.2	0.4	17	1	ABK02172	Human NOGO DNAzyme
c5451	12.2	0.4	17	1	ABZ61926	Human H-Ras DNAzym
c5452	12.2	0.4	18	1	ABL57566	Synthetic deoxyrib
c5453	12.2	0.4	18	1	ABA97651	Poly w nucleotide
c5454	12.2	0.4	18	1	ABL95913	Probe poly w for a
c5455	12.2	0.4	18	1	ABL44451	Human chromosome 1
c5456	12.2	0.4	19	1	AAV44620	Human uncoupling p
5457	12.2	0.4	19	1	AAAB4722	Cyclin E ribozyme
5458	12.2	0.4	19	1	AAH59884	Cyclin E ribozyme
5459	12.2	0.4	20	1	AAL62285	Human transcriptio
c5460	12.2	0.4	20	1	AAT91100	Bovine lysosomal a
c5461	12.2	0.4	20	1	ABZ90451	Human oligonucleot
5462	12.2	0.4	20	1	AAZ70845	Human biallelic ma
5463	12.2	0.4	20	1	ABQ84614	DPP10 related PSQ
c5464	12.2	0.4	20	1	AAH56777	S. aureus groE ope
c5465	12.2	0.4	20	1	ABZ89895	Human oligonucleot
c5466	12.2	0.4	20	1	AAA57980	Candida albicans T
5467	12.2	0.4	20	1	AAH56423	Escherichia coli g
5468	12.2	0.4	20	1	ABZ90288	Human oligonucleot
c5469	12.2	0.4	21	1	AAZ99642	Nucleotide sequenc
5470	12.2	0.4	21	1	AAF30891	Mismatched target
c5471	12.2	0.4	21	1	AAZ26192	Human polymorphic
5472	12.2	0.4	21	1	ADE53231	FEN-1 related DNA
c5473	12.2	0.4	22	1	AAT28052	3'-primer J for hu
c5474	12.2	0.4	22	1	AAT58492	First primer #9 fo
c5475	12.2	0.4	22	1	AAZ47350	PCR primer I used
c5476	12.2	0.4	22	1	AAH22193	Human hepatocyte a
c5477	12.2	0.4	22	1	AAT28048	3'-primer E for hu
c5478	12.2	0.4	22	1	AAT58488	First primer #5 fo
c5479	12.2	0.4	22	1	AAX77101	GC6 gene 3' primer
c5480	12.2	0.4	22	1	AAZ47346	PCR primer E used
c5481	12.2	0.4	22	1	AAH22189	Human hepatocyte a
5482	12.2	0.4	22	1	AAQ42237	PCR primer Gelo-19
5483	12.2	0.4	22	1	AAA12754	5' PCR primer for
5484	12.2	0.4	23	1	AAC80383	Forward primer #15
c5485	12.2	0.4	24	1	AAQ43999	HIV-1 LTR region a
5486	12.2	0.4	25	1	AAL61680	Oligonucleotide #3
5487	12.2	0.4	29	1	ACD18468	Human zinc finger
c5488	12.2	0.4	29	1	ACD18467	Human zinc finger
c5489	12	0.4	15	1	AAF81549	Dye-labeled molecu
c5490	12	0.4	15	1	AAH23587	Dye-labeled dideox
c5491	12	0.4	15	1	AAD30518	Oligonucleotide us
c5492	12	0.4	16	1	AAT75138	Arbitrary anchor p
c5493	12	0.4	16	1	AAX19464	Human senescence f
c5494	12	0.4	16	1	AAA60992	Rapid analysis of
c5495	12	0.4	16	1	AAA94103	Fruit-associated b
c5496	12	0.4	16	1	AAF83582	B. gymnorrhiza sal
c5497	12	0.4	16	1	AAS06650	Human cDNA synthes
c5498	12	0.4	16	1	ABK87149	Scarlet runner bea
c5499	12	0.4	16	1	AAD34284	Mouse E2 cDNA ampl
c5500	12	0.4	16	1	AAD32156	H-T11-C PCR primer
c5501	12	0.4	16	1	ABK12622	Mouse E4 protein,
c5502	12	0.4	16	1	ABK87932	Anchored oligo-dT
c5503	12	0.4	16	1	ABZ21815	Anti-cancer drug r
c5504	12	0.4	16	1	ABZ70966	Human cervical can
c5505	12	0.4	16	1	ADD26194	Primer relating to
c5506	12	0.4	16	1	ABK87931	Anchored oligo-dT
c5507	12	0.4	17	1	AAS06656	Human cDNA synthes
c5508	12	0.4	17	1	AAS06657	Human cDNA synthes

c5509	12	0.4	17	1	ACC64290	Murine oligonucleo
c5510	12	0.4	20	1	AAH00614	Staphylococcus det
5511	12	0.4	20	1	ABI94721	Capture oligonucle
c5512	12	0.4	20	1	ABZ88600	Human oligonucleot
c5513	12	0.4	20	1	AAD09639	Human PKA C-alpha
5514	12	0.4	20	1	AAF54617	Human HLA Class I
5515	12	0.4	20	1	ABT07491	Rat protein phosph
5516	12	0.4	20	1	ABA97649	probe t. Unidenti
5517	12	0.4	20	1	ABA97650	probe u. Unidenti
c5518	12	0.4	20	1	ABZ90674	Human oligonucleot
5519	12	0.4	20	1	ABZ89594	Human oligonucleot
c5520	12	0.4	20	1	AAX92277	PCR primer used to
5521	12	0.4	20	1	AAA94525	Antisense oligonuc
5522	12	0.4	20	1	AAA94526	Antisense oligonuc
5523	12	0.4	20	1	AAA80059	Hepatitis B virus
c5524	12	0.4	20	1	AAA37705	Human Rad51 antise
c5525	12	0.4	20	1	AAS01198	Human RAD51 antise
5526	12	0.4	20	1	AAH80810	Oligonucleotide hy
5527	12	0.4	20	1	AAH80811	Oligonucleotide hy
c5528	12	0.4	20	1	AAD43244	Antisense oligonuc
5529	12	0.4	20	1	ADD81701	HIV PRT antisense
5530	12	0.4	20	1	ADD81702	HIV PRT antisense
5531	12	0.4	21	1	AAA80353	Human ASTH1I 5' re
5532	12	0.4	21	1	AAT76513	Endothelial nitric
5533	12	0.4	21	1	AAX54304	Endothelial nitric
5534	12	0.4	21	1	AAA33748	Low adenosine anti
5535	12	0.4	21	1	AAF19870	Human endothelial
5536	12	0.4	21	1	ABZ95564	Human endothelial
c5537	12	0.4	21	1	AAQ55571	Sequence of synthe
c5538	12	0.4	21	1	AAQ67230	Triple helix-formi
c5539	12	0.4	21	1	AAQ79210	Guanosine rich oli
c5540	12	0.4	21	1	AAT51628	Viral integrase in
c5541	12	0.4	21	1	AAX79217	Oligonucleotide #1
c5542	12	0.4	21	1	ADA26144	Human REL-A short
5543	12	0.4	22	1	AAV26091	Mandarin mb2ch1 ge
c5544	12	0.4	22	1	AAQ90036	Human SMP30 gene P
c5545	12	0.4	22	1	AAT62686	Primer for human s
5546	12	0.4	22	1	ABS52173	Human forward prim
c5547	12	0.4	23	1	ABL51554	Human NSAID regula
5548	12	0.4	24	1	AAZ24998	Antisense probe to
c5549	12	0.4	24	1	AAC91733	Human pollinosis-a
5550	12	0.4	25	1	ADE64628	Recombinant blood
c5551	11.8	0.4	17	1	AAX69437	Human flt1 VEGF re
c5552	11.8	0.4	17	1	AAF06380	Hammerhead ribozym
c5553	11.8	0.4	17	1	AAX69438	Human flt1 VEGF re
5554	11.8	0.4	17	1	ABK02792	Human CD20 Hammerh
5555	11.8	0.4	17	1	ABK02791	Human CD20 Hammerh
c5556	11.8	0.4	17	1	AAF03220	Hammerhead ribozym
5557	11.8	0.4	17	1	ABK00932	Human NOGO Inozyme
5558	11.8	0.4	17	1	ABK00933	Human NOGO Inozyme
5559	11.8	0.4	17	1	ABK00049	Human NOGO Hammerh
c5560	11.8	0.4	19	1	ADE65656	Human c-fos transc
5561	11.8	0.4	19	1	ADE65772	Human c-fos siNA 1
5562	11.8	0.4	20	1	AAA50702	Sense strand encod
c5563	11.8	0.4	20	1	AAH80592	Oligonucleotide hy
c5564	11.8	0.4	20	1	AAH80591	Oligonucleotide hy
c5565	11.8	0.4	20	1	AAH80590	Oligonucleotide hy
c5566	11.8	0.4	20	1	ABZ88121	Human oligonucleot
c5567	11.8	0.4	20	1	ADD81483	HIV PRT antisense
c5568	11.8	0.4	20	1	ADD81482	HIV PRT antisense
c5569	11.8	0.4	20	1	ADD81481	HIV PRT antisense
5570	11.8	0.4	20	1	ADE43612	Human KNSL1 sequen
5571	11.8	0.4	20	1	AAQ70719	C-myc gene antisen
5572	11.8	0.4	20	1	AAQ87813	Antisense oligomer
5573	11.8	0.4	20	1	AAT60649	Antisense oligonuc
5574	11.8	0.4	20	1	AAT60650	Antisense oligonuc
5575	11.8	0.4	20	1	AAT95343	Treatment of human
5576	11.8	0.4	20	1	ABZ89225	Human oligonucleot
c5577	11.8	0.4	21	1	AAL56640	S36 primer to ampl
c5578	11.8	0.4	21	1	AAF96326	Human gene single
5579	11.8	0.4	21	1	AAF96504	Human gene single
5580	11.8	0.4	22	1	ADD21875	Protein translatio
5581	11.8	0.4	23	1	ABK90968	PCR primer, 22164,
c5582	11.8	0.4	24	1	ADD06134	N-acetylgalactosam
c5583	11.8	0.4	24	1	ABL56688	PCR primer #2 for
5584	11.8	0.4	25	1	AAC90736	Human secretory pr
c5585	11.8	0.4	25	1	ACI62001	Human microarray D
5586	11.8	0.4	25	1	ACK11064	Human microarray D
5587	11.8	0.4	25	1	ABL43221	Human chromosome 1
c5588	11.6	0.4	16	1	AAA99205	Human apoptosis re
c5589	11.6	0.4	16	1	AAA99206	Human apoptosis re
c5590	11.6	0.4	16	1	AAA97561	Reverse transcript

ALIGNMENTS

RESULT 1
AAL07489/c
ID AAL07489 standard; DNA; 47 BP.
XX
AC AAL07489;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 10177.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001339.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
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PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
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PR 30-JUN-2000; 2000US-0215135P.
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PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
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PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
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PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
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PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
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PR 26-SEP-2000; 2000US-0235484P.
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PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
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PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249264P.
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PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; SEQ ID NO 10177; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX
SQ Sequence 47 BP; 36 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 31.4; DB 1; Length 47;
Best Local Similarity 85.4%; Pred. No. 31;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2147 CTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTA 2187
| |||| ||||||| | ||||||||||||||||||||||
Db 46 CAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTA 6

RESULT 2
ADD33791
ID ADD33791 standard; DNA; 44 BP.
XX
AC ADD33791;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mouse mitochondrial DNA sequence SEQ ID NO:1564.
XX
KW ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
KW mitochondrial disease; oxidative phosphorylation dysfunction;
KW oxidative stress; apoptosis; aging.
XX
OS Mus musculus.
XX
PN WO2003020220-A2.
XX
PD 13-MAR-2003.

XX
PF 30-AUG-2002; 2002WO-US027886.
XX
PR 30-AUG-2001; 2001US-0316323P.
PR 31-AUG-2001; 2001CA-02356540.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Wallace DC, Levy S, Kerstann K, Procaccio V;
XX
DR WPI; 2003-300821/29.
XX
PT Array containing probes for genes involved in mitochondrial biology,
PT useful for determining mitochondrial biology gene expression profiles for
PT use in diagnosing pathologies and identifying biochemical pathways.
XX
PS Claim 2; SEQ ID NO 1564; 201pp; English.
XX
CC The invention relates to a novel array comprising at least two isolated
CC nucleotide molecules, each molecule having a sequence capable of uniquely
CC hybridising to a nucleic acid molecule which is an expression product of
CC a gene involved in mitochondrial biology. The array comprises two or more
CC isolated nucleic acid molecules or spots, each molecule having a sequence
CC chosen from sequence of 994 human probes and 2046 mouse probes. An array
CC of the invention is useful for determining an expression profile of a
CC mouse or human sample containing nucleic acid, by contacting the array
CC with the sample under conditions allowing selective hybridisation, and
CC measuring hybridisation of nucleic acid in the sample to the array to
CC produce an expression profile. The array is also useful for determining
CC an expression profile of a first labelled sample containing nucleic acid
CC relative to a second, differently labelled sample containing nucleic
CC acid. The second sample is a reference or a standard. An array is useful
CC for determining an expression profile diagnostic of an energy-metabolism-
CC related physiological condition. An array of the invention is useful for
CC determining mitochondrial biology gene expression profiles of organisms,
CC such as human, mice and closely related species, tissue and organs of
CC such organisms, which are useful for determining expression profiles
CC diagnostic of energy metabolism-related physiological conditions,
CC diagnosing such physiological conditions, identifying biochemical
CC pathways, genes, and mutations involved in such physiological conditions,
CC identifying therapeutic agents useful for preventing and/or treating such
CC physiological conditions, evaluating and/or monitoring the efficacy of
CC such therapies, and creating and identifying animal models of human
CC energy metabolism-related physiological conditions. An array is also
CC useful for defining expression signatures or profiles for mitochondrial
CC diseases, as well as distinguishing clinical disorders that result from
CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
CC apoptosis and aging. An array of the invention contains probes of genes
CC not previously recognised to participate in mitochondrial biology. The
CC sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA
CC clones used to make the probes of the invention. Some sequences are not
CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
CC 1906, 2408 and 2643.
XX
SQ Sequence 44 BP; 1 A; 1 C; 0 G; 42 T; 0 U; 0 Other;

Query Match 1.1%; Score 30.4; DB 1; Length 44;
Best Local Similarity 85.0%; Pred. No. 40;
Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2147 CTGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
|| || |||||||| | ||||||||||||||||||||
Db 1 CTTTTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 40

RESULT 3
AAS95728
ID AAS95728 standard; DNA; 45 BP.
XX
AC AAS95728;
XX
DT 14-FEB-2002 (first entry)
XX
DE Allele discrimination P1 primer #12.
XX
KW Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW melanoma; PCR primer; sequencing primer; probe.
XX
OS Homo sapiens.
XX
PN WO200177390-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US011151.
XX
PR 05-APR-2000; 2000US-0194843P.
XX
PA (MOLE-) MOLECULAR STAGING INC.
XX
PI Abarzua P;
XX
DR WPI; 2002-049157/06.
XX
PT Detecting single nucleotide polymorphism involves amplifying target
PT sequences using small primer probe that matches or mismatches to target
PT sequence and extending primer probe which is then detected.
XX
PS Claim 15; Page 41; 67pp; English.
XX
CC The invention relates to detecting single nucleotide polymorphisms by
CC contacting an allele-specific oligonucleotide primer (P1) with a target
CC polynucleotide to form a hybridisation complex, where the target sequence
CC is complementary to P1 at one end but the terminal nucleotide and the
CC third nucleotide from the terminal at the other end of P1 may not be
CC complementary. The complex is then contacted with an exonuclease
CC deficient DNA polymerase enzyme under conditions that promote extension
CC of P1 with the target DNA as the template, thereby forming an extended
CC segment of P1. Oligonucleotide probes hybridising to one or more target
CC polynucleotides distinguish between matched and mismatched 3' ends, hence
CC the absence of sequence amplification indicates the presence of a single
CC nucleotide mismatch. Primer sequences complementary to a sequence on an
CC amplification target circle can be used in rolling circle amplification
CC (RCA). The method is useful for diagnosing a disease caused by, induced
CC by or related to a mutation in at least one gene, such as Parkinson's
CC disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC fluorescence decorators used in the detection of RCA products
XX
SQ Sequence 45 BP; 2 A; 5 C; 0 G; 38 T; 0 U; 0 Other;

Query Match 1.1%; Score 30; DB 1; Length 45;
Best Local Similarity 86.8%; Pred. No. 51;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
||||||| | ||||||||||||||||||||| || ||
Db 4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41

RESULT 4
AAS95724
ID AAS95724 standard; DNA; 45 BP.
XX
AC AAS95724;
XX
DT 14-FEB-2002 (first entry)
XX

```
DE   Allele discrimination P1 primer #8.
XX
KW   Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW   exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW   Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW   Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW   diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW   lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW   melanoma; PCR primer; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200177390-A2.
XX
PD   18-OCT-2001.
XX
PF   05-APR-2001; 2001WO-US011151.
XX
PR   05-APR-2000; 2000US-0194843P.
XX
PA   (MOLE-) MOLECULAR STAGING INC.
XX
PI   Abarzua P;
XX
DR   WPI; 2002-049157/06.
XX
PT   Detecting single nucleotide polymorphism involves amplifying target
PT   sequences using small primer probe that matches or mismatches to target
PT   sequence and extending primer probe which is then detected.
XX
PS   Claim 15; Page 41; 67pp; English.
XX
CC   The invention relates to detecting single nucleotide polymorphisms by
CC   contacting an allele-specific oligonucleotide primer (P1) with a target
CC   polynucleotide to form a hybridisation complex, where the target sequence
CC   is complementary to P1 at one end but the terminal nucleotide and the
CC   third nucleotide from the terminal at the other end of P1 may not be
CC   complementary. The complex is then contacted with an exonuclease
CC   deficient DNA polymerase enzyme under conditions that promote extension
CC   of P1 with the target DNA as the template, thereby forming an extended
CC   segment of P1. Oligonucleotide probes hybridising to one or more target
CC   polynucleotides distinguish between matched and mismatched 3' ends, hence
CC   the absence of sequence amplification indicates the presence of a single
CC   nucleotide mismatch. Primer sequences complementary to a sequence on an
CC   amplification target circle can be used in rolling circle amplification
CC   (RCA). The method is useful for diagnosing a disease caused by, induced
CC   by or related to a mutation in at least one gene, such as Parkinson's
CC   disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC   disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC   obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC   lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC   melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC   fluorescence decorators used in the detection of RCA products
XX
SQ   Sequence 45 BP; 1 A; 6 C; 0 G; 38 T; 0 U; 0 Other;

  Query Match             1.1%;  Score 30;  DB 1;  Length 45;
  Best Local Similarity   86.8%;  Pred. No. 51;
  Matches   33;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  |||||||||||||||||||| || ||
Db          4 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCACCTT 41


RESULT 5
ABQ80395/c
ID   ABQ80395 standard; DNA; 33 BP.
XX
AC   ABQ80395;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Probe APC 1-MUT.
XX
KW   Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW   infection; screening; colour change; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Gold-S'-A"
XX
PN   WO2003048769-A1.
XX
PD   12-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038069.
XX
PR   30-NOV-2001; 2001US-0334644P.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Storhoff JJ,  Fritz BM,  Herrmann M;
XX
DR   WPI; 2003-617993/58.
XX
PT   Detecting target polynucleotide in a sample, by amplifying target,
PT   hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
PT   detection system, and determining amount of signal generated due to
PT   binding.
XX
PS   Example 1; Page 35; 74pp; English.
XX
CC   The sequences given in ABQ80394-99 represent probes and targets which
CC   were used in the method of the invention for detecting a target
CC   polynucleotide in a sample. The method comprises amplifying the target,
CC   hybridizing the target to oligonucleotides bound to nanoparticles in a
CC   nanoparticle detection system, determining the amount of signal generated
CC   as a result of binding, optionally repeating the above steps, and
CC   detecting the presence of the target oligonucleotide by analysing for the
CC   amount of signal produced after at least one amplification cycle. The
CC   method is useful for detecting target polynucleotide in a sample, and for
CC   determining the quantity of target polynucleotide in a sample. The method
CC   is useful in research and analytical laboratories in DNA sequencing, in
CC   the field to detect the presence of specific pathogens, in the doctor's
CC   office for quick identification of an infection to assist in prescribing
CC   a drug for treatment, and in homes and health centres for inexpensive
CC   first-line screening. The method is based on observing colour change with
CC   the naked eye, hence the method is cheap, fast, simple, robust, do not
CC   require specialized or expensive equipment, and little or no
CC   instrumentation is required
XX
SQ   Sequence 33 BP; 29 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 29.4;  DB 1;  Length 33;
  Best Local Similarity   96.8%;  Pred. No. 28;
  Matches   30;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||||| ||||||||||||||||||||
Db         31 TTTTTTTCTGCTTTTTTTTTTTTTTTTTT 1


RESULT 6
AAD17216
ID   AAD17216 standard; DNA; 43 BP.
XX
AC   AAD17216;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Human mRNA hybridisation selection reaction biotin-dT3 oligonucleotide.
XX
```

```
KW   Human; multiplex ligation-dependent amplification; amplicon;
KW   single nucleotide polymorphism; hybridisation selection reaction; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Biotin-labelled Thymidine"
XX
PN   WO200161033-A2.
XX
PD   23-AUG-2001.
XX
PF   15-FEB-2001; 2001WO-EP001739.
XX
PR   15-FEB-2000; 2000EP-00200506.
XX
PA   (SCHO/) SCHOUTEN J P.
XX
PI   Schouten JP;
XX
DR   WPI; 2001-550053/61.
XX
PT   An improved multiplex ligation-dependent amplification method for
PT   detecting specific single stranded target nucleic acids in samples.
XX
PS   Example 8; Page 137; 158pp; English.
XX
CC   The invention relates to an improved multiplex ligation-dependent
CC   amplification method for detecting specific single stranded target
CC   nucleic acids in samples using a plurality of probe sets comprising at
CC   least 2 probes. Each probe comprises a target specific region and a non-
CC   complementary region comprising a primer binding site. The probes in each
CC   set are ligated when hybridised to a target nucleic acid and amplified by
CC   a primer set. The method is used for detecting a nucleotide polymorphism,
CC   especially a single nucleotide polymorphism; detecting multiple single
CC   stranded target nucleic acid sequences (through the detection of multiple
CC   amplicons); determining the absolute or relative abundance of multiple
CC   single stranded nucleic acids in a sample; and detection of a break point
CC   region in rearranged nucleic acids. By using a femtomolar amount of the
CC   probes, a large number of different probe sets can be used to
CC   simultaneously detect and quantify a corresponding large number of target
CC   sequences with high specificity. The present DNA sequence is biotin-dT3
CC   labelled fluorescent oligonucleotide which is used for the hybridisation
CC   selection reaction of human mRNA samples
XX
SQ   Sequence 43 BP; 0 A; 0 C; 0 G; 43 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 43;
  Best Local Similarity   81.0%;  Pred. No. 63;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||  |||||||  |  ||||||||||||||||||||   |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 42


RESULT 7
AAV09273/c
ID   AAV09273 standard; cDNA; 44 BP.
XX
AC   AAV09273;
XX
DT   07-JUL-1998  (first entry)
XX
DE   Nucleotide sequence of the 3' portion of the BG513_19 protein.
XX
KW   BG513_19 protein; human adult brain cDNA library; nutritional activity;
KW   cytokine activity; cell proliferation/differentiation activity; homology;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9748801-A2.
XX
PD   24-DEC-1997.
XX
PF   16-JUN-1997;   97WO-US010501.
XX
PR   17-JUN-1996;   96US-00664596.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Racie LA,  Merberg D,  Treacy M;
PI   Evans C,  Spaulding V,  Bowman M;
XX
DR   WPI; 1998-063142/06.
XX
PT   Poly:nucleotide(s) and proteins obtained from human PBMC, dendritic cell,
PT   adult brain, foetal brain and adult testes cDNA libraries - used in
PT   research, detection and therapy of, e.g. cytokine and cell proliferation
PT   or differentiation.
XX
PS   Claim 19; Page 51; 78pp; English.
XX
CC   This nucleotide sequence encodes the 3' portion of the BG513_19 protein
CC   which was isolated from a human adult brain cDNA library. The products of
CC   the polynucleotides of the invention can be used in research, detection
CC   and therapy, as they may have nutritional activity, cytokine and cell
CC   proliferation/differentiation activity. A search against the Genbank
CC   database demonstrated that this sequence has no homology with known
CC   sequences
XX
SQ   Sequence 44 BP; 44 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 29.2;  DB 1;  Length 44;
  Best Local Similarity   81.0%;  Pred. No. 67;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||  |||||||  |  ||||||||||||||||||||   |||
Db         44 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 8
AAL07488/c
ID   AAL07488 standard; DNA; 38 BP.
XX
AC   AAL07488;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human reproductive system related antigen DNA SEQ ID NO: 10176.
XX
KW   Human; reproductive system related antigen; reproductive system disorder;
KW   cancer; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155320-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001339.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
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PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; SEQ ID NO 10176; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX
SQ Sequence 38 BP; 35 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

```
  Query Match             1.0%;  Score 29;  DB 1;  Length 38;
  Best Local Similarity   86.5%;  Pred. No. 49;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              |||| | ||||||||||||||||||||||||   |||
Db         38 TTTTCTTTCCTTTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 9
AAL31948/c
ID   AAL31948 standard; DNA; 43 BP.
XX
AC   AAL31948;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #5156.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035498.
XX
PR   28-DEC-1999;   99US-0173419P.
PR   27-DEC-2000; 2000US-00173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT   autoimmune diseases and infections.
XX
PS   Claim 1; Page 2871; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC   protein coupled receptors and thioesterases. The present sequence is one
CC   such oligonucleotide. The oligonucleotides and the peptides encoded by
CC   them may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate expression of the proteins listed above.
CC   Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms
XX
SQ   Sequence 43 BP; 9 A; 4 C; 2 G; 28 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 28.8;  DB 1;  Length 43;
  Best Local Similarity   82.5%;  Pred. No. 75;
  Matches   33;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2764 AAAAGTATTCTTGTTAGAATTGAAAAAAAAAAAAAAAAAA 2803
              |||||| || |  | ||||  ||||||||||||||||||
Db         40 AAAAGTTTTTTCTTCAGAAAGGAAAAAAAAAAAAAAAAAA 1

RESULT 10
AAQ25031
ID   AAQ25031 standard; DNA; 40 BP.
XX
AC   AAQ25031;
XX
DT   13-JUL-1992  (first entry)
XX
DE   Oligonucleotide specific for HIV proviral DNA.
XX
KW   HIV; thiolation; reverse transcriptase; primer; inhibition; homooligomer;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9203127-A.
XX
PD   05-MAR-1992.
XX
PF   15-AUG-1991;   91WO-US005919.
XX
PR   16-AUG-1990;   90US-00568131.
XX
PA   (UYNY-) RES FOUND UNIV NEW.
XX
PI   Bardos TJ,  Ho YK,  Aradi J,  Schinazi RF;
XX
DR   WPI; 1992-096567/12.
XX
PT   Compsn. contg. 5-thiolated (oligo-poly-)-nucleotide(s) - for treating HIV
PT   infection, AIDS and for preventing HIV-1 infection.
XX
PS   Disclosure; Page 11; 42pp; English.
XX
CC   The oligomer comprises a non-thiolated (binding) homooligonucleotide
CC   region ( d(T)12 ) to promote the binding of the remaining portion of the
CC   5-thiolated oligonucleotide ( MdU_28 ) to a homopurine site of the viral
CC   genome via triple-helix formations. The oligo is used to in the treatment
CC   of HIV. See also AAQ22624-27 and AAQ25017-Q25032
XX
SQ   Sequence 40 BP; 0 A; 0 C; 0 G; 12 T; 28 U; 0 Other;

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   23.7%;  Pred. No. 73;
  Matches    9;  Conservative   23;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  |:::::::::::::::::::   :::
Db          1 TTTTTTTTTTTTUUUUUUUUUUUUUUUUUUUUUUUUUU 38

RESULT 11
AAA39649
ID   AAA39649 standard; DNA; 40 BP.
XX
AC   AAA39649;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Primer used in construction of hybrid CAT RNA.
XX
KW   Control element; translation enhancer; pestivirus homology box IV;
KW   immune response; viral infection; primer; ss.
XX
OS   Unidentified.
XX
```

```
PN   US6057093-A.
XX
PD   02-MAY-2000.
XX
PF   12-MAY-1995;   95US-00439996.
XX
PR   28-SEP-1992;   92US-00952799.
PR   28-SEP-1993;   93US-00128583.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Han JH,  Spaete RR,  Suh BS,  Selby MJ,  Houghton M,  Yoo BJ;
XX
DR   WPI; 2000-338599/29.
XX
PT   Enhancing translation of coding region of hepatitis C virus involves
PT   making RNA molecule comprising the coding region and 5' untranslated
PT   region comprising a sequence fully homologous to pestivirus homology box
PT   IV.
XX
PS   Disclosure; Col 19-20; 16pp; English.
XX
CC   This invention describes a novel method for enhancing translation of a
CC   coding region which involves making an RNA molecule, comprising the
CC   coding region operably linked to a 5' untranslated region (UTR)
CC   comprising a sequence fully homologous to pestivirus homology box IV, and
CC   then translating it so that the translation of the coding region is
CC   enhanced. The method is useful for enhancing or controlling the
CC   translation of HCV nucleic acid, which allows stronger immune responses,
CC   where blocking or decreasing translation of viral nucleic acid may
CC   decrease the pathology of viral infection. This sequence represents a
CC   primer which is used in the construction of hybrid CAT RNA's described in
CC   the method of the invention
XX
SQ   Sequence 40 BP; 0 A; 0 C; 0 G; 40 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 28.4;  DB 1;  Length 40;
  Best Local Similarity   84.2%;  Pred. No. 73;
  Matches   32;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||| |  ||||||||||||||||||||    |||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 12
ABK99273/c
ID   ABK99273 standard; RNA; 36 BP.
XX
AC   ABK99273;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #3.
XX
KW   Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS   Synthetic.
XX
PN   US2002064771-A1.
XX
PD   30-MAY-2002.
XX
PF   06-APR-2001; 2001US-00828034.
XX
PR   07-APR-2000; 2000US-0195852P.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (FERR/) FERRARI E.
XX
PI   Zhong W,  Hong Z,  Ferrari E;
XX
DR   WPI; 2002-582330/62.
XX
PT   Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT   nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT   and template and primer which do not form a stable duplex in the absence
PT   of HCV NS5B.
XX
PS   Example; Page 6; 17pp; English.
XX
CC   The invention relates to a replicase complex comprising a hepatitis C
CC   virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC   complementary nucleic acid primer which is annealed to the 3' terminus of
CC   the template, where the template is at least three nucleotides and the
CC   primer is two or three nucleotides, and the template and primer do not
CC   form a stable duplex in solution in the absence of the HCV NS5B protein.
CC   The complex is useful for detecting HCV replicase activity and permits
CC   establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC   and evaluate antiviral inhibitors and to improve the specificity and
CC   efficacy of the inhibitors. The complex is also useful in the development
CC   of a reliable system for determining kinetic and thermodynamic constants
CC   of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC   mechanistic inhibitors for mis-incorporation or chain termination.
CC   Specifically, the short RNA template and primer pairs are useful in
CC   screening assays which are used for determining kinetic, thermodynamic
CC   and mechanistic properties of NS5B replication and ultimately in the
CC   development of inhibitors of NS5B. Newly identified inhibitors of
CC   replicase activity may be used for developing anti-HCV pharmaceuticals.
CC   Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC   templates
XX
SQ   Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 36;
  Best Local Similarity   90.9%;  Pred. No. 60;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              |||||||| |  ||||||||||||||||||||
Db         36 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4


RESULT 13
AAD27117/c
ID   AAD27117 standard; RNA; 36 BP.
XX
AC   AAD27117;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, AU used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z.  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
```

```
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 1A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, AU used to direct RNA synthesis by RNA
CC   polymerase proteins of HCV, BVDV and polivirus. This sequence is used in
CC   the exemplification of the invention
XX
SQ   Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 36;
  Best Local Similarity   90.9%;  Pred. No. 60;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              |||||||| |  ||||||||||||||||||||
Db         36 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 4


RESULT 14
AAD27125/c
ID   AAD27125 standard; RNA; 37 BP.
XX
AC   AAD27125;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, (AU)2 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 2A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, (AU)2 used to direct RNA synthesis by
CC   RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used
CC   in the exemplification of the invention
XX
SQ   Sequence 37 BP; 33 A; 0 C; 2 G; 0 T; 2 U; 0 Other;

  Query Match             1.0%;  Score 28.2;  DB 1;  Length 37;
  Best Local Similarity   90.9%;  Pred. No. 65;
  Matches   30;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              |||||||| |  ||||||||||||||||||||
Db         35 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 15
AAL62267
ID   AAL62267 standard; DNA; 28 BP.
XX
AC   AAL62267;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human TFAP2C DNA specific PCR probe.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; PCR; probe; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "FAM labelled"
FT   modified_base    28
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "TAMRA labelled"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
```

```
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 14; Page 77; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is a PCR probe specific for human
CC   TFAP2C DNA. This sequence is used to illustrate the method of the
CC   invention
XX
SQ   Sequence 28 BP; 4 A; 6 C; 8 G; 10 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 28;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 33;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1093 AGCTGTTCATTTGGCTAGGGACTTTGCC 1120
              ||||||||||||||||||||||||||||
Db          1 AGCTGTTCATTTGGCTAGGGACTTTGCC 28


RESULT 16
ABQ80394/c
ID   ABQ80394 standard; DNA; 33 BP.
XX
AC   ABQ80394;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Probe APC 1-WT.
XX
KW   Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW   infection; screening; colour change; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Gold-S'-A"
XX
PN   WO2003048769-A1.
XX
PD   12-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038069.
XX
PR   30-NOV-2001; 2001US-0334644P.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Storhoff JJ,  Fritz BM,  Herrmann M;
XX
DR   WPI; 2003-617993/58.
XX
PT   Detecting target polynucleotide in a sample, by amplifying target,
PT   hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
PT   detection system, and determining amount of signal generated due to
PT   binding.
XX
PS   Example 1; Page 35; 74pp; English.
XX
CC   The sequences given in ABQ80394-99 represent probes and targets which
CC   were used in the method of the invention for detecting a target
CC   polynucleotide in a sample. The method comprises amplifying the target,
CC   hybridizing the target to oligonucleotides bound to nanoparticles in a
CC   nanoparticle detection system, determining the amount of signal generated
CC   as a result of binding, optionally repeating the above steps, and
CC   detecting the presence of the target oligonucleotide by analysing for the
CC   amount of signal produced after at least one amplification cycle. The
CC   method is useful for detecting target polynucleotide in a sample, and for
CC   determining the quantity of target polynucleotide in a sample. The method
CC   is useful in research and analytical laboratories in DNA sequencing, in
CC   the field to detect the presence of specific pathogens, in the doctor's
CC   office for quick identification of an infection to assist in prescribing
CC   a drug for treatment, and in homes and health centres for inexpensive
CC   first-line screening. The method is based on observing colour change with
CC   the naked eye, hence the method is cheap, fast, simple, robust, do not
CC   require specialized or expensive equipment, and little or no
CC   instrumentation is required
XX
SQ   Sequence 33 BP; 28 A; 1 C; 3 G; 1 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.8;  DB 1;  Length 33;
  Best Local Similarity   93.5%;  Pred. No. 56;
  Matches   29;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||| ||||| ||||||||||||||||||||
Db         31 TTTATTTCTGCTTTTTTTTTTTTTTTTTT 1


RESULT 17
AAA37946
ID   AAA37946 standard; DNA; 42 BP.
XX
AC   AAA37946;
XX
DT   18-AUG-2000  (first entry)
XX
DE   DNA synthesis primer used in PTAN gene isolation.
XX
KW   PTAN; testis specific; prostate cancer; overexpress; chromosome 1q22;
KW   diagnose; cancer; breast; vaccine; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200020589-A2.
XX
PD   13-APR-2000.
XX
PF   30-SEP-1999;   99WO-US022985.
XX
PR   30-SEP-1998;   98US-0102556P.
PR   02-OCT-1998;   98US-0102910P.
PR   21-DEC-1998;   98US-0113229P.
PR   14-APR-1999;   99US-0129518P.
XX
PA   (UROG-) UROGENESYS INC.
PA   (AFAR/) AFAR D E.
PA   (HUBE/) HUBERT R S.
PA   (RAIT/) RAITANO A B.
PA   (MITC/) MITCHELL S C.
XX
PI   Afar DE,  Hubert RS,  Raitano AB,  Mitchell SC;
XX
DR   WPI; 2000-317715/27.
XX
PT   PTAN proteins, and sequences encoding them, used for diagnosing and
PT   treating cancers, especially breast and prostate cancers.
XX
PS   Example 1; Page 31; 71pp; English.
XX
CC   This sequence represents a primer used in the isolation of cDNA fragments
CC   of the PTAN (testis specific protein expressed in prostate cancer) gene.
```

```
CC   PTAN is expressed in 3 isoforms PTAN-1, 2, and 3. The PTAN gene is
CC   located on chromosome 1q22. PTAN is overexpressed in prostate cancer, and
CC   has a testis specific expression pattern in adult tissues. PTAN shows no
CC   homology to any known gene. PTAN can be used in methods for the diagnosis
CC   of cancer, especially prostate or breast cancer, where the normal tissue
CC   samples are prostate tissue, or breast tissue, bone tissue, lymphatic
CC   tissue, serum, blood, or urine. A vector containing the PTAN nucleotide
CC   sequence, a vaccine composition targeting PTAN, PTAN, ribozymes specific
CC   for PTAN mRNA and antisense sequences, can be used to treat cancer,
CC   especially breast and prostate cancers. Cancer development can be
CC   inhibited by a vaccine composition targeting PTAN
XX
SQ   Sequence 42 BP; 3 A; 2 C; 2 G; 35 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.8;  DB 1;  Length 42;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+02;
  Matches   32;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||||  |  |||||  |  ||||||||||||||||||||
Db          3 TGATCAAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 41


RESULT 18
AAZ57404
ID   AAZ57404 standard; DNA; 38 BP.
XX
AC   AAZ57404;
XX
DT   07-APR-2000  (first entry)
XX
DE   Hepatitis C virus PCR primer CAC-T35 SEQ ID NO:19.
XX
KW   Hepatitis C virus; RNA virus; replication; viral infection; PCR primer;
KW   ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9967394-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003380.
XX
PR   24-JUN-1998;   98JP-00177820.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Kohara M,  Kohara K,  Taira K,  Matsuzaki J,  Ohmori H;
XX
DR   WPI; 2000-106296/09.
XX
PT   Vectors expressing full-length gene of RNA viruses, useful in clarifying
PT   mechanisms of RNA viral replication, infection, and developing remedies
PT   and therapeutics.
XX
PS   Example 2; Page 20; 46pp; Japanese.
XX
CC   The present invention describes a vector comprising a cDNA encoding an
CC   RNA virus gene, constructed to ensure the exact and homogeneous
CC   transcription of both terminals of the RNA virus gene. Also described is
CC   a method for screening drugs for inhibiting the replication of RNA virus
CC   by using the RNA viral infection model animal, particularly one with
CC   hepatitis C viral infection. The vector is useful in clarifying the
CC   mechanism of RNA viral replication, onset of RNA viral infection, and
CC   developing remedies and therapeutics for RNA viral infections,
CC   particularly of a hepatitis C virus. The present sequence represents a
CC   PCR primer which is used in the exemplification of the present invention
XX
SQ   Sequence 38 BP; 1 A; 2 C; 0 G; 35 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.4;  DB 1;  Length 38;
  Best Local Similarity   83.8%;  Pred. No. 98;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              |  |  |||||||  |  ||||||||||||||||||||
Db          2 ACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 38


RESULT 19
AAZ98722
ID   AAZ98722 standard; cDNA; 40 BP.
XX
AC   AAZ98722;
XX
DT   20-JUN-2000  (first entry)
XX
DE   PCR primer used for swine vesicular disease virus gene synthesis.
XX
KW   Swine vesicular disease virus; SVDV; swine vesicular disease;
KW   Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
KW   differentiation; vaccine; prevent; PCR primer; ss.
XX
OS   Swine vesicular disease virus.
XX
PN   EP982403-A1.
XX
PD   01-MAR-2000.
XX
PF   14-AUG-1998;   98EP-00306486.
XX
PR   14-AUG-1998;   98EP-00306486.
XX
PA   (BIOT-) DEV CENT BIOTECHNOLOGY.
XX
PI   Hwong CL,  Lo C,  Yang Y,  Jeng K,  Chang EL;
XX
DR   WPI; 2000-258616/23.
XX
PT   Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
PT   to prevent swine vesicular disease.
XX
PS   Example 2; Page 6; 66pp; English.
XX
CC   This sequence represents a PCR primer used to determine the full length
CC   cDNA sequence of the swine vesicular disease virus (SVDV) gene sequence
CC   of Taiwan Yu-Li strain (see AAZ98717). SVDV is the causative agent of
CC   swine vesicular disease, which is very similar to foot and mouth disease.
CC   The invention relates to the wild-type Taiwan Yu-Li strain cDNA sequence,
CC   and the gene sequences of the mutant SVDV strains N3, H21 and SP7. The
CC   mutant SVDV nucleotide sequence can be used in a vaccine for the
CC   prophylaxis of swine vesicular disease. The invention also includes a
CC   method for differentiating the mutant SVDV nucleotide sequences from the
CC   wild type strain of SVDV, coxsackievirus and foot-and-mouth disease virus
CC   through the use of polymerase chain reaction
XX
SQ   Sequence 40 BP; 1 A; 3 C; 3 G; 33 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.4;  DB 1;  Length 40;
  Best Local Similarity   83.8%;  Pred. No. 1.1e+02;
  Matches   31;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2149 GATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||   |||||||  |  ||||||||||||||||||||
Db          4 GATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 40


RESULT 20
AAN70278
ID   AAN70278 standard; DNA; 32 BP.
XX
AC   AAN70278;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
```

```
XX
DE   Sequence of scissile link probe MRC068 (HL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   65.6%;  Pred. No. 67;
  Matches   21;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  |||:::::::|||||||||
Db          1 TTTTTTTTTTTTTTUUUUUUUUTTTTTTTTT 32


RESULT 21
AAN92244
ID   AAN92244 standard; DNA; 32 BP.
XX
AC   AAN92244;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRC068.
XX
KW   Probe MRC068; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .14
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    15. .22
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    23. .32
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRC068 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 32;
  Best Local Similarity   65.6%;  Pred. No. 67;
  Matches   21;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  |||:::::::|||||||||
Db          1 TTTTTTTTTTTTTTUUUUUUUUTTTTTTTTT 32


RESULT 22
ADC33445
ID   ADC33445 standard; DNA; 32 BP.
XX
AC   ADC33445;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Template oligonucleotide #SEQ ID 2.
XX
KW   Binding; tandem repeat; label; analyte detection; ss.
XX
OS   Synthetic.
XX
PN   WO2003072721-A2.
XX
PD   04-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005301.
XX
PR   21-FEB-2002; 2002US-0359223P.
PR   08-MAY-2002; 2002US-0379360P.
XX
PA   (DISC-) DISCOVERX INC.
XX
PI   Wu M,  Ullman E;
XX
DR   WPI; 2003-712717/67.
XX
```

PT Detecting a label comprising employing (as the label) a reagent having a
PT 3' extendable terminus hybridized to a tandem repeat template in
PT combination with a DNA polymerase and dNTPs necessary for repetitively
PT replicating the tandem repeat.
XX
PS Example; SEQ ID NO 2; 38pp; English.
XX
CC The invention relates to a method for detecting a label, comprising
CC employing (as the label) a reagent having a 3' extendable terminus
CC hybridised to a tandem repeat template in combination with a DNA
CC polymerase and dNTPs necessary for repetitively replicating the tandem
CC repeat. The method involves detecting a binding event between first and
CC second binding members, employing a label to determine the occurrence of
CC the binding event. The tandem repeating units are polyT. The method of
CC the invention is useful in detecting an analyte using repetitive
CC extension along a tandem repeat. The extended nucleic acid may be used
CC for detecting a moiety, particularly involved in a binding event
CC employing a reagent. The current sequence represents a template member
CC oligonucleotide containing a polyT tandem repeat that binds to the
CC extendable oligonucleotide given in ADC33444.
XX
SQ Sequence 32 BP; 0 A; 0 C; 0 G; 32 T; 0 U; 0 Other;

Query Match 1.0%; Score 27.2; DB 1; Length 32;
Best Local Similarity 90.6%; Pred. No. 67;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
||||||| | ||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 23
AAF29153
ID AAF29153 standard; DNA; 33 BP.
XX
AC AAF29153;
XX
DT 04-APR-2001 (first entry)
XX
DE PCR primer SEQ ID 24 used to amplify SRSV specific cDNA.
XX
KW Small round structured virus; SRSV; food poisoning; PCR primer; ss.
XX
OS Small round structured virus.
XX
PN WO200079280-A1.
XX
PD 28-DEC-2000.
XX
PF 22-JUN-2000; 2000WO-JP004095.
XX
PR 22-JUN-1999; 99JP-00175928.
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA (DENK-) DENKA SEIKEN KK.
XX
PI Takeda N, Natori K, Miyamura T, Kamata K, Sato T, Sato S;
XX
DR WPI; 2001-080848/09.
XX
PT Kit for the detection and typing of small round-structured virus (SRSV)
PT strains for investigation of food poisoning outbreaks, contains
PT antibodies.
XX
PS Example 1; Page 75; 84pp; Japanese.
XX
CC This invention relates to a kit for the detection and typing of small
CC round structured virus (SRSV) strains. The kit contains antibodies
CC directed against peptides represented in sequences AAB49700 - AAB49710,
CC which are each SRSV strain specific. Polynucleotide sequences AAF20141 -
CC AAF20151 represent cDNA encoding the strain specific proteins. The kit is
CC used for detecting and typing strains of SRSV in order to prevent the
CC spread of infection and to examine the epidemiology of outbreaks. PCR
CC primers AAF29152 - AAF29163 are used to amplify SRSV strain specific cDNA
CC sequences
XX
SQ Sequence 33 BP; 0 A; 0 C; 0 G; 33 T; 0 U; 0 Other;

Query Match 1.0%; Score 27.2; DB 1; Length 33;
Best Local Similarity 90.6%; Pred. No. 73;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
||||||| | ||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 24
ABK99272/c
ID ABK99272 standard; RNA; 36 BP.
XX
AC ABK99272;
XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #2.
XX
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS Synthetic.
XX
PN US2002064771-A1.
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-00828034.
XX
PR 07-APR-2000; 2000US-0195852P.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (FERR/) FERRARI E.
XX
PI Zhong W, Hong Z, Ferrari E;
XX
DR WPI; 2002-582330/62.
XX
PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT and template and primer which do not form a stable duplex in the absence
PT of HCV NS5B.
XX
PS Example; Page 6; 17pp; English.
XX
CC The invention relates to a replicase complex comprising a hepatitis C
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC complementary nucleic acid primer which is annealed to the 3' terminus of
CC the template, where the template is at least three nucleotides and the
CC primer is two or three nucleotides, and the template and primer do not
CC form a stable duplex in solution in the absence of the HCV NS5B protein.
CC The complex is useful for detecting HCV replicase activity and permits
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC and evaluate antiviral inhibitors and to improve the specificity and
CC efficacy of the inhibitors. The complex is also useful in the development
CC of a reliable system for determining kinetic and thermodynamic constants
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC mechanistic inhibitors for mis-incorporation or chain termination.
CC Specifically, the short RNA template and primer pairs are useful in
CC screening assays which are used for determining kinetic, thermodynamic
CC and mechanistic properties of NS5B replication and ultimately in the
CC development of inhibitors of NS5B. Newly identified inhibitors of
CC replicase activity may be used for developing anti-HCV pharmaceuticals.
CC Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC templates
XX

```
SQ   Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 36;
  Best Local Similarity   90.6%;  Pred. No. 92;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         36 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 5


RESULT 25
AAD27116/c
ID   AAD27116 standard; RNA; 36 BP.
XX
AC   AAD27116;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, AA used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 1A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, AA used to direct RNA synthesis by RNA
CC   polymerase proteins of HCV, BVDV and polivirus. This sequence is used in
CC   the exemplification of the invention
XX
SQ   Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 36;
  Best Local Similarity   90.6%;  Pred. No. 92;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||||||| |  ||||||||||||||||||||
Db         36 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 5


RESULT 26
AAL07487/c
ID   AAL07487 standard; DNA; 38 BP.
XX
AC   AAL07487;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human reproductive system related antigen DNA SEQ ID NO: 10175.
XX
KW   Human; reproductive system related antigen; reproductive system disorder;
KW   cancer; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155320-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001339.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
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PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; SEQ ID NO 10175; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX
SQ Sequence 38 BP; 34 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 1.0%; Score 27.2; DB 1; Length 38;
Best Local Similarity 90.6%; Pred. No. 1.1e+02;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
||||||| | ||||||||||||||||||||||
Db 34 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3

RESULT 27
ABN89412/c
ID ABN89412 standard; DNA; 40 BP.
XX
AC ABN89412;
XX
DT 30-AUG-2002 (first entry)
XX
DE Polymorphism detection related oligonucleotide SEQ ID NO:4.
XX
KW Polymorphism; detection; mass spectroscopy; ss.
XX
OS Synthetic.
XX
PN WO200250307-A1.
XX
PD 27-JUN-2002.
XX
PF 12-DEC-2001; 2001WO-JP010892.
XX
PR 12-DEC-2000; 2000JP-00378091.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Inoko H, Tamiya G, Nakajima K, Kimura N, Nagashima R, Morikawa M;
PI Okamoto K;

```
XX
DR   WPI; 2002-508814/54.
XX
PT   Detection of DNA polymorphism by mass spectroscopy for investigation and
PT   diagnosis of gene-related diseases.
XX
PS   Example 3; Page 28; 34pp; Japanese.
XX
CC   The present invention describes a method for detecting polymorphisms in
CC   DNA by: (a) preparing a DNA sample from patients containing the DNA
CC   region in which the target polymorphism is located; (b) hybridising to an
CC   appropriate oligonucleotide fragment, immobilised on a support; and (c)
CC   detecting the hybridised target DNA by mass spectroscopy. The method can
CC   be used for the investigation and diagnosis of gene-related diseases. The
CC   method allows polymorphisms to be detected rapidly and effectively in a
CC   large number of specimens. The present sequence represents an
CC   oligonucleotide which is used in an example from the present invention
XX
SQ   Sequence 40 BP; 30 A; 0 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 40;
  Best Local Similarity   90.6%;  Pred. No. 1.2e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTTAA 2188
              ||||| |  ||||||||||||||||||||||
Db         40 TTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 9


RESULT 28
ABZ46327
ID   ABZ46327 standard; DNA; 41 BP.
XX
AC   ABZ46327;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Human aldehyde dehydrogenase ALDH1A2 gene polymorphic site, #3111.
XX
KW   Human; drug metabolising enzyme; gene; drug metabolism; chromosome 15;
KW   polymorphic site; drug evaluation; drug screening; genotyping;
KW   genetic profiling; therapeutic customisation; adverse reaction;
KW   clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(21,G)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200252044-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-JP011592.
XX
PR   27-DEC-2000; 2000JP-00399443.
PR   02-MAY-2001; 2001JP-00135256.
PR   27-AUG-2001; 2001JP-00256862.
XX
PA   (RIKE ) RIKEN KK.
XX
PI   Nakamura Y,  Sekine A,  Iida A,  Saito S;
XX
DR   WPI; 2002-583571/62.
XX
PT   Identifying individuals having a polymorphism, useful for determining the
PT   effectiveness or side effect of a drug or treatment protocol, comprises
PT   detecting at least one polymorphism in the drug metabolizing enzyme
PT   nucleic acid.
XX
PS   Claim 23; Page 116; 2785pp; English.
XX
CC   Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC   encoding enzymes associated with drug metabolism. The invention relates
CC   to methods and compositions for identifying individuals who have at least
CC   one polymorphism in such drug metabolising enzyme-encoding genes. The
CC   polymorphisms may be identified in a nucleic acid sample using probes or
CC   primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC   variety of detection assays, including hybridisation assays, nucleic acid
CC   arrays and PCR-based methods. The invention also encompasses methods of
CC   evaluating and screening drugs using genetic polymorphism data. Genetic
CC   polymorphism data, particularly that relating to single nucleotide
CC   polymorphisms (SNPs), may be used in studying the relationship between
CC   DNA sequence variations and human diseases, conditions, and responses to
CC   drugs. SNPs are also useful as polymorphism markers for discovering genes
CC   that cause or exacerbate certain diseases. SNPs are particularly useful
CC   in the above respects as they are stable in populations, occur
CC   frequently, and have lower mutation rates than other genome variations
CC   such as repeating sequences. The detection and analysis of polymorphisms
CC   in genes encoding drug metabolising enzymes allows the customisation of
CC   drug therapies based upon the genetic profile of individual patients.
CC   This would not only take the guesswork out of selecting the drug with the
CC   greatest therapeutic effect for a particular patient, but would also
CC   reduce the likelihood of adverse reactions, thereby increasing safety.
CC   Methods of the invention are also useful in the drug discovery and
CC   approval processes. For example, individuals could be selected for
CC   clinical trials only if their genetic profiles indicate that they are
CC   capable of responding to a particular drug or drug class, and previously
CC   failed drug candidates could be revived if they were matched with more
CC   appropriate patient populations. The methods, data and compositions of
CC   the invention may therefore lead to a an increase in the range of
CC   possible drug targets and decreases in the number of adverse drug
CC   reactions, failed drug trials, the time taken for a drug to be approved,
CC   the length of time patients are on medication and the number of different
CC   medications a patient needs to take before finding an effective therapy
XX
SQ   Sequence 41 BP; 3 A; 2 C; 3 G; 33 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 41;
  Best Local Similarity   90.6%;  Pred. No. 1.3e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||| |||||  ||||||||||||||||||||
Db          8 TTTATTTCTGTTTTTTTTTTTTTTTTTTTT 39


RESULT 29
ABZ48839
ID   ABZ48839 standard; DNA; 41 BP.
XX
AC   ABZ48839;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Human aldehyde dehydrogenase ALDH1A2 gene polymorphic site, #5622.
XX
KW   Human; drug metabolising enzyme; gene; drug metabolism; polymorphic site;
KW   drug evaluation; drug screening; genotyping; genetic profiling;
KW   therapeutic customisation; adverse reaction; clinical trial;
KW   drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(21,G)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism (SNP)"
XX
PN   WO200252044-A2.
XX
PD   04-JUL-2002.
XX
PF   27-DEC-2001; 2001WO-JP011592.
```

```
XX
PR   27-DEC-2000; 2000JP-00399443.
PR   02-MAY-2001; 2001JP-00135256.
PR   27-AUG-2001; 2001JP-00256862.
XX
PA   (RIKE ) RIKEN KK.
XX
PI   Nakamura Y,  Sekine A,  Iida A,  Saito S;
XX
DR   WPI; 2002-583571/62.
XX
PT   Identifying individuals having a polymorphism, useful for determining the
PT   effectiveness or side effect of a drug or treatment protocol, comprises
PT   detecting at least one polymorphism in the drug metabolizing enzyme
PT   nucleic acid.
XX
PS   Claim 23; Page 175; 2785pp; English.
XX
CC   Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
CC   encoding enzymes associated with drug metabolism. The invention relates
CC   to methods and compositions for identifying individuals who have at least
CC   one polymorphism in such drug metabolising enzyme-encoding genes. The
CC   polymorphisms may be identified in a nucleic acid sample using probes or
CC   primers specific for a sequence selected from ABZ43217-ABZ50887 using a
CC   variety of detection assays, including hybridisation assays, nucleic acid
CC   arrays and PCR-based methods. The invention also encompasses methods of
CC   evaluating and screening drugs using genetic polymorphism data. Genetic
CC   polymorphism data, particularly that relating to single nucleotide
CC   polymorphisms (SNPs), may be used in studying the relationship between
CC   DNA sequence variations and human diseases, conditions, and responses to
CC   drugs. SNPs are also useful as polymorphism markers for discovering genes
CC   that cause or exacerbate certain diseases. SNPs are particularly useful
CC   in the above respects as they are stable in populations, occur
CC   frequently, and have lower mutation rates than other genome variations
CC   such as repeating sequences. The detection and analysis of polymorphisms
CC   in genes encoding drug metabolising enzymes allows the customisation of
CC   drug therapies based upon the genetic profile of individual patients.
CC   This would not only take the guesswork out of selecting the drug with the
CC   greatest therapeutic effect for a particular patient, but would also
CC   reduce the likelihood of adverse reactions, thereby increasing safety.
CC   Methods of the invention are also useful in the drug discovery and
CC   approval processes. For example, individuals could be selected for
CC   clinical trials only if their genetic profiles indicate that they are
CC   capable of responding to a particular drug or drug class, and previously
CC   failed drug candidates could be revived if they were matched with more
CC   appropriate patient populations. The methods, data and compositions of
CC   the invention may therefore lead to a an increase in the range of
CC   possible drug targets and decreases in the number of adverse drug
CC   reactions, failed drug trials, the time taken for a drug to be approved,
CC   the length of time patients are on medication and the number of different
CC   medications a patient needs to take before finding an effective therapy
XX
SQ   Sequence 41 BP; 3 A; 2 C; 3 G; 33 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27.2;  DB 1;  Length 41;
  Best Local Similarity   90.6%;  Pred. No. 1.3e+02;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||| |||||  |||||||||||||||||||||
Db          8 TTTATTTCTGTTTTTTTTTTTTTTTTTTT 39


RESULT 30
AAL62265
ID   AAL62265 standard; DNA; 27 BP.
XX
AC   AAL62265;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human TFAP2C DNA specific forward PCR primer.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 14; Page 77; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is a PCR primer specific for
CC   human TFAP2C DNA. This sequence is used to illustrate the method of the
CC   invention
XX
SQ   Sequence 27 BP; 6 A; 7 C; 5 G; 9 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 27;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   27;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1060 TGTGACTCTCCTGACATCCTTAGTAGA 1086
              |||||||||||||||||||||||||||
Db          1 TGTGACTCTCCTGACATCCTTAGTAGA 27


RESULT 31
AAD27124/c
ID   AAD27124 standard; RNA; 37 BP.
XX
AC   AAD27124;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, (AU)3 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
```

```
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 2A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, (AU)3 used to direct RNA synthesis by
CC   RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used
CC   in the exemplification of the invention
XX
SQ   Sequence 37 BP; 32 A; 0 C; 2 G; 0 T; 3 U; 0 Other;

  Query Match             1.0%;  Score 27;  DB 1;  Length 37;
  Best Local Similarity   85.7%;  Pred. No. 1.1e+02;
  Matches   30;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2184
              ||  |||||||| |  ||||||||||||||||||||
Db         37 ATATATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 32
AAV12483
ID   AAV12483 standard; DNA; 39 BP.
XX
AC   AAV12483;
XX
DT   15-MAY-1998  (first entry)
XX
DE   Oligonucleotide SEQ ID NO:6 from US5174320 Example 2.
XX
KW   Synthesis; selection; amplification; circular oligonucleotide;
KW   rolling circle synthesis; diagnosis; therapeutic agent; ss.
XX
OS   Synthetic.
XX
PN   US5714320-A.
XX
PD   03-FEB-1998.
XX
PF   23-FEB-1995;   95US-00393439.
XX
PR   15-APR-1993;   93US-00047860.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-144278/13.
XX
PT   Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
PT   template to produce oligonucleotide multimer for cleavage.
XX
PS   Example 2; Col 45; 38pp; English.
XX
CC   The present sequence represents an oligonucleotide used in an example of
CC   the present invention. The present invention describes a method for
CC   synthesising a selected oligonucleotide (I) having well defined ends. The
CC   method comprises: (a) annealing a primer to a single-stranded (ss)
CC   circular template to yield a primed circular template, where the template
CC   comprises: (i) at least one nucleotide sequence complementary to (I); and
CC   (ii) at least one nucleotide effective to produce a cleavage site in the
CC   oligonucleotide multimer; (b) combining the primed circular template with
CC   at least two types of nucleotide triphosphates and a polymerase enzyme
CC   without the addition of auxiliary proteins to yield a ss oligonucleotide
CC   multimer complementary to the circular oligonucleotide template,
CC   comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC   multimer at the cleavage site to produce (I) having well defined ends.
CC   The method is used for the large-scale synthesis of DNA and RNA oligomers
CC   for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX
SQ   Sequence 39 BP; 0 A; 0 C; 3 G; 36 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 39;
  Best Local Similarity   81.6%;  Pred. No. 1.4e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2149 GATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | ||  ||||||| |  |||||||| ||||||||||
Db          1 GTTTTTTTTTTTTGTTTTTTTTTTTGTTTTTTTTTT 38


RESULT 33
AAX30019
ID   AAX30019 standard; DNA; 39 BP.
XX
AC   AAX30019;
XX
DT   16-JUN-1999  (first entry)
XX
DE   Multimer SEQ ID NO:6.
XX
KW   Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.
XX
OS   Synthetic.
XX
PN   WO9909216-A2.
XX
PD   25-FEB-1999.
XX
PF   13-AUG-1998;   98WO-US016776.
XX
PR   13-AUG-1997;   97US-00910632.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1999-181062/15.
XX
PT   New detectably labelled oligonucleotide multimer, comprising multiple
PT   contiguous copies of a repeated oligonucleotide - useful for detecting
PT   target molecules in diagnosis and medicinal applications.
XX
PS   Example 2; Page 41; 103pp; English.
XX
CC   The present invention describes a detectably labelled oligonucleotide
CC   multimer, comprising multiple contiguous copies of a repeated
CC   oligonucleotides. The detectably labelled oligonucleotide multimer is
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CC   useful for detecting a target molecule. Oligonucleotide multimers may be
CC   produced in sufficient quantity to be useful for diagnostic and medical
CC   applications. The multimers are useful for affinity labelling of
CC   proteins, and for signal amplification in highly sensitive affinity
CC   capture and sequence identification applications. The method provides a
CC   faster, cheaper and simpler way for large-scale production of DNA and RNA
CC   oligomers and multimers. The incorporation of labels enables the
CC   oligonucleotide multimers to be useful in diagnostics and medicine. The
CC   present sequence represents an oligonucleotide used in an example from
CC   the present invention
XX
SQ   Sequence 39 BP; 0 A; 0 C; 3 G; 36 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 39;
  Best Local Similarity   81.6%;  Pred. No. 1.4e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2149 GATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | ||  ||||||| |  ||||||||| ||||||||||
Db          1 GTTTTTTTTTTTGTTTTTTTTTTTGTTTTTTTTTT 38


RESULT 34
AAQ55168
ID   AAQ55168 standard; DNA; 40 BP.
XX
AC   AAQ55168;
XX
DT   25-MAR-2003  (revised)
DT   21-JUL-1994  (first entry)
XX
DE   Sequence of primer for PCR amplification of HIV-LP Pt.1 isolate.
XX
KW   Human immunodeficiency virus; HIV-LP; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9400562-A1.
XX
PD   06-JAN-1994.
XX
PF   23-JUN-1993;   93WO-US006162.
XX
PR   24-JUN-1992;   92US-00903421.
XX
PA   (UYNY ) UNIV NEW YORK MT SINAI SCHOOL MEDICINE.
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Gelman IH,  Laurence JC;
XX
DR   WPI; 1994-026200/03.
XX
PT   HIV-LP useful in vaccine formulations - is novel HIV virus distinct from
PT   HIV-1 and or HIV-2 viruses.
XX
PS   Example; Page 7; 75pp; English.
XX
CC   HIV-LP is a new variant of the HIV family. A cDNA first strand was
CC   synthesised from Pt. 1 pellet using MLV RT. The product was converted
CC   into dsDNA and this cDNA was amplified by PCR using primers AAQ55167 and
CC   AAQ55168. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 40 BP; 3 A; 2 C; 3 G; 32 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 40;
  Best Local Similarity   81.6%;  Pred. No. 1.5e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2149 GATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||   ||| |||| |  ||||||||||||||||||||
Db          2 GAGGAATTCTTTTTTTTTTTTTTTTTTTTTTTTTTT 39


RESULT 35
AAV03013
ID   AAV03013 standard; DNA; 41 BP.
XX
AC   AAV03013;
XX
DT   17-AUG-1998  (first entry)
XX
DE   Aspergillus oryzae alpha-amylase transcription factor PCR primer.
XX
KW   alpha-amylase; promoter; filamentous fungi; transcription factor;
KW   expression; control; production; heterologous polypeptide; medicinal;
KW   industrial enzyme; PCR primer; amyR; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9801470-A1.
XX
PD   15-JAN-1998.
XX
PF   07-JUL-1997;   97WO-DK000305.
XX
PR   05-JUL-1996;   96DK-00000740.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Christensen T;
XX
DR   WPI; 1998-100998/09.
XX
PT   Transcription factor from Aspergillus oryzae which regulates alpha-
PT   amylase promoter - useful for producing heterologous proteins, especially
PT   medicinal proteins or enzymes, in filamentous fungi.
XX
PS   Example 1; Page 25; 64pp; English.
XX
CC   The sequence is that of PCR primer oligodT which was used in the analysis
CC   of a transcription factor (amyR) which regulates the expression of an
CC   alpha-amylase promoter
XX
SQ   Sequence 41 BP; 2 A; 1 C; 2 G; 36 T; 0 U; 0 Other;

  Query Match             1.0%;  Score 26.8;  DB 1;  Length 41;
  Best Local Similarity   81.6%;  Pred. No. 1.5e+02;
  Matches   31;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2148 TGATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||   | ||||||| |  |||||||||||||||||||
Db          4 TGTAAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 41


RESULT 36
AAQ25023
ID   AAQ25023 standard; DNA; 40 BP.
XX
AC   AAQ25023;
XX
DT   13-JUL-1992  (first entry)
XX
DE   Anti-sense oligonucleotide specific for tRNA_Lys anti-codon region.
XX
KW   HIV; thiolation; reverse transcriptase; primer; inhibition; homooligomer;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9203127-A.
XX
PD   05-MAR-1992.
XX
PF   15-AUG-1991;   91WO-US005919.
XX
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```
PR   16-AUG-1990;   90US-00568131.
XX
PA   (UYNY-) RES FOUND UNIV NEW.
XX
PI   Bardos TJ,  Ho YK,  Aradi J,  Schinazi RF;
XX
DR   WPI; 1992-096567/12.
XX
PT   Compsn. contg. 5-thiolated (oligo-poly-)-nucleotide(s) - for treating HIV
PT   infection, AIDS and for preventing HIV-1 infection.
XX
PS   Disclosure; Page 12; 42pp; English.
XX
CC   The oligomer comprises an 18-mer regional oligonucleotide corrre-
CC   sponding to the anti-codon region of the reverse transcriptase (RT)
CC   primer tRNA_Lys, with a 5' terminal thiolated 22-mer homooligomer. The
CC   homooligomer may be absent and the regional oligo may itself be thiolated
CC   (e.g. 5-Mercapto-), as in Claim 19. The oligos are used to inhibit
CC   reverse transcription in the treatment of HIV. See also AAQ22624-27 and
CC   AAQ25017-Q25032
XX
SQ   Sequence 40 BP; 7 A; 2 C; 3 G; 6 T; 22 U; 0 Other;

  Query Match             0.9%;  Score 26.6;  DB 1;  Length 40;
  Best Local Similarity   27.3%;  Pred. No. 1.6e+02;
  Matches    9;  Conservative   20;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
              ::::::::::::::::::::| |  || |||||
Db          3 UUUUUUUUUUUUUUUUUUUUUCAGATTAAAAGT 35


RESULT 37
AAT93827
ID   AAT93827 standard; DNA; 34 BP.
XX
AC   AAT93827;
XX
DT   25-MAR-2003  (revised)
DT   24-FEB-1998  (first entry)
XX
DE   Antitumoural phosphodiester oligonucleotide 17 with cytotoxic activity.
XX
KW   Phosphodiester; selective binding; cell viability; growth;
KW   tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW   lymphoblastic tumour; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .34
FT                    /*tag=  a
FT                    /note= "phosphodiester oligonucleotide"
XX
PN   WO9720924-A1.
XX
PD   12-JUN-1997.
XX
PF   04-DEC-1996;   96WO-EP005388.
XX
PR   04-DEC-1995;   95IT-MI002539.
XX
PA   (SAIC-) SAICOM SRL.
XX
PI   Scaggiante B,  Quadrifoglio F;
XX
DR   WPI; 1997-319771/29.
XX
PT   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT   selective cytotoxic effect on tumour cells, for treating both solid and
PT   liquid tumours.
XX
PS   Claim 10; Page 6; 38pp; English.
XX
CC   Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC   generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-
CC   (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''- (G-gTg')g''-N', where: N and
CC   N' = T or G, equal or different from each other; x = 0-8, equal or
CC   different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC   different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC   or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC   16, equal or different from each other; The oligonucleotides are believed
CC   to selectively bind and sequester some proteins which are essential to
CC   the viability and growth of tumoural cell line. They have specific and
CC   selective cytotoxic activity against tumour cells, and can be used for
CC   treating tumours of the liquid type, in particular of lymphoblastic
CC   origin, and of solid type, in particular lymphomas. The present
CC   phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC   reduced growth of CCRF-CEM tumoural cells by 71%, which is detectable 48
CC   hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 34 BP; 0 A; 0 C; 2 G; 32 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 26;  DB 1;  Length 34;
  Best Local Similarity   85.3%;  Pred. No. 1.3e+02;
  Matches   29;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              || ||||||| |  |||||||||||||||||| |
Db          1 TGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGT 34


RESULT 38
AAX88521
ID   AAX88521 standard; DNA; 33 BP.
XX
AC   AAX88521;
XX
DT   13-SEP-1999  (first entry)
XX
DE   Conus stercusmuscarum contryphan PCR primer DHOG 496.
XX
KW   Contryphan; leu-tryphan; anticonvulsant; neuroprotective; venom;
KW   cone snail; neurodegenerative disorder; epilepsy; neurotoxic injury;
KW   hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident;
KW   brain trauma; spinal chord trauma; myocardial infarct; physical trauma;
KW   drowning; suffocation; perinatal asphyxia; hypoglycaemia; migraine;
KW   senile dementia; Alzheimer's disease; amyotrophic lateral sclerosis;
KW   Parkinson's disease; Huntington's disease; Down's syndrome; PCR primer;
KW   Korsakoff's disease; schizophrenia; neuronal damage; seizure; ss.
XX
OS   Synthetic.
OS   Conus stercusmuscarum.
XX
PN   WO9933865-A1.
XX
PD   08-JUL-1999.
XX
PF   16-DEC-1998;   98WO-US026789.
XX
PR   24-DEC-1997;   97US-0068737P.
PR   16-APR-1998;   98US-00061026.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Jacobsen R,  Jimenez E,  Cruz LJ,  Olivera BM,  Gray WR,  Grilley M;
PI   Watkins M,  Hillyard DR;
XX
DR   WPI; 1999-419087/35.
XX
PT   New pure contryphan peptides.
XX
PS   Example 3; Page 20; 48pp; English.
XX
CC   The present sequence sequence represents a PCR primer for a contryphan
CC   peptide sequence. Contryphan peptides are found in the venom of cone
```

CC snails. The contryphan peptides are useful as anticonvulsant agents, as
CC neuroprotective agents, for managing pain, and for treating
CC neurodegenerative disorders, especially those resulting from an
CC overstimulation of excitatory amino acid receptors. The contryphans are
CC useful for the treatment and alleviation of epilepsy and as a general
CC anticonvulsant agent. The contryphans are also useful to reduce
CC neurotoxic injury associated with conditions of hypoxia, anoxia, or
CC ischaemia which typically follows stroke, cerebrovascular accident, brain
CC or spinal chord trauma, myocardial infarct, physical trauma, drownings,
CC suffocation, perinatal asphyxia, or hypoglycaemic events. The contryphans
CC are further useful for the treatment of Alzheimer's disease, senile
CC dementia, amyotrophic lateral sclerosis, Parkinson's disease,
CC Huntington's disease, Down's syndrome, Korsakoff's disease,
CC schizophrenia, AIDS dementia, multi-infarct dementia, and neuronal damage
CC associated with uncontrolled seizures. The contryphans are further useful
CC in controlling pain and are effective in the treatment of migraine. They
CC can be used prophylactically or to relieve the symptoms associated with a
CC migraine episode
XX
SQ Sequence 33 BP; 0 A; 1 C; 2 G; 30 T; 0 U; 0 Other;

Query Match 0.9%; Score 25.6; DB 1; Length 33;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 28; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              | ||||||| |  ||||||||||||||||||||
Db          2 GCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 33
```

RESULT 39
AAS17761
ID AAS17761 standard; DNA; 31 BP.
XX
AC AAS17761;
XX
DT 12-MAR-2002 (first entry)
XX
DE Oligo d(T) PCR primer.
XX
KW Oligo d(T); ss; differential subtraction; PCR primer;
KW double exponential elimination; tumour.
XX
OS Synthetic.
XX
PN US6316192-B1.
XX
PD 13-NOV-2001.
XX
PF 11-MAR-1999; 99US-00268505.
XX
PR 11-MAR-1999; 99US-00268505.
XX
PA (LUOJ/) LUO J.
XX
PI Luo J;
XX
DR WPI; 2002-074371/10.
XX
PT Selective elimination of non-targeted DNA sequences for rapid isolation
PT and enrichment of the differences of DNA fragments between two pools of
PT DNA, comprises converting testers to drivers.
XX
PS Claim 6; Col 5; 23pp; English.
XX
CC The invention comprises rapid isolation and enrichment of the differences
CC of DNA fragments between two pools of DNA, comprises converting
CC undesirable testers (DNA being subtracted) to drivers (DNA used to
CC subtract) and re-utilising converted drivers in repeats of subtraction to
CC achieve double exponential elimination of undesirable tester sequences.
CC The method comprises (a) attaching a nucleic acid fragment to 1 or more
CC polymerase chain reaction (PCR) adapters to form an adapter-attached
CC nucleic acid fragment, followed by amplifying the adapter-attached
CC nucleic acid fragment through PCR with primers containing nucleic acid
CC sequences complementary to nucleic acid sequences of the adapter to form
CC an adapter-attached nucleic acid tester, (b) mixing the adapter-attached
CC nucleic acid tester with a nucleic acid driver that contains no attached
CC adapter or contains an attached adapter whose sequence differs from the
CC adapter, to form a nucleic acid mixture, (c) denaturing and re-annealing
CC the tester/driver nucleic acid mixture, (d) adding to the nucleic acid
CC mixture an effective amount of reagents necessary for removing the
CC adapter sequence from the tester/ driver hetero-duplex and (e) repeating
CC step (c) to (d) at least once (no amplification takes place and no
CC additional driver is added). The method is used for rapid isolation and
CC enrichment of the differences of DNA fragments between two pools of DNA
CC e.g. in the search for tumour specific sequences. The method has 2
CC improvements over the methods disclosed by Yang et al. (1996), Lisitsyn
CC et al. (1993), Straus et al. (1990) by (i) bypassing the need of a
CC polymerase chain reaction (PCR) amplification or physical separation of
CC desirable testers from undesirable ones in each repeat of subtraction, it
CC eliminates the necessity of tester dilution in each repeat of
CC subtraction, and (ii) by utilising the convened driver from each repeat
CC of subtraction, it eliminates the need for re-introducing additional
CC driver into hybridisation in each repeat of subtraction. The present
CC sequence is an Oligo D(T) PCR primer used in the method of the invention
XX
SQ Sequence 31 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 1 Other;

Query Match 0.9%; Score 25.4; DB 1; Length 31;
Best Local Similarity 87.1%; Pred. No. 1.3e+02;
Matches 27; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTA 2187
              ||||| |  |||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTV 31
```

RESULT 40
AAS09500
ID AAS09500 standard; DNA; 32 BP.
XX
AC AAS09500;
XX
DT 24-OCT-2001 (first entry)
XX
DE SMART PCR primer #2.
XX
KW Heat-labile uracil-DNA glycolsylase; UNG; UDG; PCR primer; SMART;
KW PCR control; LCR control; ligase chain reaction; carry-over prevention;
KW ss.
XX
OS Synthetic.
XX
PN WO200151623-A1.
XX
PD 19-JUL-2001.
XX
PF 10-JAN-2001; 2001WO-NO000008.
XX
PR 12-JAN-2000; 2000NO-00000163.
PR 27-OCT-2000; 2000NO-00005428.
XX
PA (BIOT-) BIOTEC ASA.
XX
PI Lanes O, Willasen NP, Guddal PH, Gjellesvik DR;
XX
DR WPI; 2001-451854/48.
XX
PT New cod liver uracil-DNA glycosylase enzyme, useful in monitoring or
PT controlling a reaction system multiplying DNA sequences or in carry-over
PT prevention procedures.
XX
PS Example 2; Page 20; 59pp; English.
XX
CC The sequence represents a SMART PCR primer used to synthesise first
CC strand cDNA from Atlantic cod in order to isolate cDNAs encoding heat-

```
CC   labile uracil-DNA glycosylase, (UNG/UDG). The enzyme is useful in
CC   monitoring and/or controlling a reaction system multiplying DNA
CC   sequences, e.g. PCR (polymerase chain reaction) or LCR (ligase chain
CC   reaction). The enzyme is also useful in carry-over prevention procedures
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 2 Other;

  Query Match             0.9%;  Score 25.4;  DB 1;  Length 32;
  Best Local Similarity   84.4%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTTA 2187
              |||||| |  |||||||||||||||||||| :
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTNV 32


RESULT 41
ABA01204
ID   ABA01204 standard; DNA; 32 BP.
XX
AC   ABA01204;
XX
DT   11-SEP-2003  (revised)
DT   28-JAN-2002  (first entry)
XX
DE   Mamushi fibrinolytic enzyme, brevinase, PCR primer, BbRP1.
XX
KW   Fibrinolytic enzyme; brevinase; thermostable; thrombolytic agent;
KW   mamushi; PCR primer; ss.
XX
OS   Agkistrodon blomhoffi; brevicaudus.
XX
PN   KR2001045716-A.
XX
PD   05-JUN-2001.
XX
PF   06-NOV-1999;   99KR-00049115.
XX
PR   06-NOV-1999;   99KR-00049115.
XX
PA   (LEEJ/) LEE J W.
PA   (PARK/) PARK W.
XX
PI   Lee JW,  Park W;
XX
DR   WPI; 2001-636862/73.
XX
PT   Fibrinolytic enzyme, brevinase, separated from poison of viper,
PT   agkistrodon blomhoffi brevicaudus.
XX
PS   Example 5; Page 6; 23pp; Korean.
XX
CC   The present invention relates to fibrinolytic enzyme, brevinase (see
CC   AAG79000), which is separated from the poison of Agkistordon blomhoffi
CC   brevicaudus (mamushi). The enzyme shows stability at high temperatures
CC   and is thus useful in developing thrombolytic agents. The present
CC   sequence is a PCR primer, which was used in an example from the present
CC   invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 2 Other;

  Query Match             0.9%;  Score 25.4;  DB 1;  Length 32;
  Best Local Similarity   87.1%;  Pred. No. 1.5e+02;
  Matches   27;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTTA 2187
              ||||| |  ||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTV 31


RESULT 42
AAN70277
ID   AAN70277 standard; DNA; 30 BP.
XX
AC   AAN70277;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC064 (HL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   63.3%;  Pred. No. 1.3e+02;
  Matches   19;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  |::::::::|||||||||
Db          1 TTTTTTTTTTTTUUUUUUUUTTTTTTTTT 30


RESULT 43
AAN92243
ID   AAN92243 standard; DNA; 30 BP.
XX
AC   AAN92243;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRC064.
XX
KW   Probe MRC064; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .12
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
```

```
FT   misc_feature    13. .20
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    21. .30
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO64 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   63.3%;  Pred. No. 1.3e+02;
  Matches   19;  Conservative    8;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  |::::::::|||||||||||
Db          1 TTTTTTTTTTTTTUUUUUUUUTTTTTTTTTT 30


RESULT 44
AAQ36302
ID   AAQ36302 standard; DNA; 30 BP.
XX
AC   AAQ36302;
XX
DT   25-MAR-2003  (revised)
DT   07-JUN-1993  (first entry)
XX
DE   GST3anti, for GSTpi gene target sequence.
XX
KW   Glutathione-s-transferase pi; cancer; drug resistance; chemotherapy;
KW   sensitisation; triplex; target; duplex; ss.
XX
OS   Synthetic.
XX
PN   US5176996-A.
XX
PD   05-JAN-1993.
XX
PF   22-DEC-1989;   89US-00453532.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1993-035718/04.
XX
PT   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT   which bind to target sequence in duplex DNA forming colinear triplex by
PT   binding to major groove.
XX
PS   Example 8; Col 27; 29pp; English.
XX
CC   Overexpression of the enzyme glutathione-s-transferase pi has been
CC   implicated as being responsible for the broad range drug resistance which
CC   develops in a variety of cancers. Expression of the gene may be prevented
CC   by the formation of a triplex between the duplex target DNA sequence and
CC   an anti parallel or parallel synthetic oligonucleotide. A suitable target
CC   sequence is that from base -499 to -410 of GSTpi, an unusual repetitive
CC   DNA segment within the control domain. Oligonucleotides targetted against
CC   this sequence will repress GSTpi transcription. See also AAQ36219-362.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 45
AAQ36301
ID   AAQ36301 standard; DNA; 30 BP.
XX
AC   AAQ36301;
XX
DT   25-MAR-2003  (revised)
DT   07-JUN-1993  (first entry)
XX
DE   GST3par, for GSTpi gene target sequence.
XX
KW   Glutathione-s-transferase pi; cancer; drug resistance; chemotherapy;
KW   sensitisation; triplex; target; duplex; ss.
XX
OS   Synthetic.
XX
PN   US5176996-A.
XX
PD   05-JAN-1993.
XX
PF   22-DEC-1989;   89US-00453532.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1993-035718/04.
XX
PT   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT   which bind to target sequence in duplex DNA forming colinear triplex by
PT   binding to major groove.
XX
PS   Example 8; Col 27; 29pp; English.
XX
CC   Overexpression of the enzyme glutathione-s-transferase pi has been
CC   implicated as being responsible for the broad range drug resistance which
CC   develops in a variety of cancers. Expression of the gene may be prevented
CC   by the formation of a triplex between the duplex target DNA sequence and
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CC   an anti parallel or parallel synthetic oligonucleotide. A suitable target
CC   sequence is that from base -499 to -410 of GSTpi, an unusual repetitive
CC   DNA segment within the control domain. Oligonucleotides targetted against
CC   this sequence will repress GSTpi transcription. See also AAQ36219-362.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 46
AAX57020
ID   AAX57020 standard; DNA; 30 BP.
XX
AC   AAX57020;
XX
DT   19-JUL-1999  (first entry)
XX
DE   WO9923258 oligonucleotide primer 2.
XX
KW   Visual; nucleic acid detection; target; hybridisation; probe; primer;
KW   agglutination; bridging molecule; ss.
XX
OS   Synthetic.
XX
PN   WO9923258-A1.
XX
PD   14-MAY-1999.
XX
PF   30-OCT-1998;   98WO-US023267.
XX
PR   31-OCT-1997;   97US-0063969P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Weisburg WG,  Stull PD,  Reshatoff MR;
XX
DR   WPI; 1999-326994/27.
XX
PT   Optical detection of hybridization complexes for specific target nucleic
PT   acid sequences.
XX
PS   Example 1; Page 40; 46pp; English.
XX
CC   This invention describes a novel method for the visual detection of
CC   target nucleic acid presence in a sample. A preferred target is a
CC   Mycobacterium complex nucleic acid sequence. The detection method uses
CC   visual detection of a change in the hybridization without aid of
CC   instrumentation. Multiple copies of a target nucleic acid sequence are
CC   mixed with first and second detectable probes under hybridizing
CC   conditions favouring particle agglutination via a bridging molecule
CC   allowing for visual detection of the target nucleic acid sequence. The
CC   bridging molecule enhances or inhibits formation of a hybridization
CC   complex
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 47
AAF99889/c
ID   AAF99889 standard; DNA; 30 BP.
XX
AC   AAF99889;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #1005.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Example 6; Page 60; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 48
AAF99888
ID   AAF99888 standard; DNA; 30 BP.
XX
AC   AAF99888;
XX
DT   12-JUN-2001  (first entry)
XX
```

```
DE   Immunostimulatory nucleic acid #1004.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Example 6; Page 60; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 49
ABK10416/c
ID   ABK10416 standard; DNA; 30 BP.
XX
AC   ABK10416;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Synthetic primer sequence 5'-A30-3'.
XX
KW   ss; 5'-A30-3'; double stranded DNA generation; promiscuous base;
KW   target molecule; primer.
XX
OS   Synthetic.
XX
PN   US6326143-B1.
XX
PD   04-DEC-2001.
XX
PF   22-MAY-1998;   98US-00083123.
XX
PR   22-NOV-1996;   96WO-EP005149.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Orum H,  Seeger C;
XX
DR   WPI; 2002-214947/27.
XX
PT   Determining an analyte in a sample, for generating multiple double
PT   stranded nucleic acids, comprises employing a single primer sequence with
PT   a nucleobase sequence having affinity to the sequence contained in a
PT   target nucleic acid.
XX
PS   Example 1; Col 14; 25pp; English.
XX
CC   The invention relates to determining an analyte in a sample comprising
CC   (a) providing a target nucleic acid comprising a region A, a nucleobase
CC   sequence B, and a sequence I linked to the 5' terminus of the nucleobase
CC   sequence B, where the nucleobase sequence B is not specific for the
CC   analyte, and the region A specifically binds to the analyte, (b) binding
CC   the target nucleic acid to the analyte, separating the analyte bound to
CC   the target nucleic acid from the remaining part of the sample, (d)
CC   hybridising a primer to the target nucleic acid, where the primer
CC   comprises a nucleobase sequence B', and the nucleobase sequence B'
CC   hybridises to the nucleobase sequence B, (e) elongating the hybridised
CC   primer to produce an elongation product E using the target nucleic acid
CC   as a template and using nucleotides, where at least 30 % of the
CC   nucleotides contain at least one promiscuous base which is capable of
CC   base pairing with each of adenine, guanine, cytosine, and thymine, (f)
CC   separating the target nucleic acid from the elongation product E, (g)
CC   hybridising a further primer which comprises the nucleobase sequence B'
CC   to the elongation product E, where the elongation product E is capable of
CC   acting as a template for the elongation of the further primer, (h)
CC   elongating the hybridised further primer of step (g) to produce an
CC   elongation product E' using the elongation product E as a template and
CC   using nucleotides, where at least 30 % of the nucleotides contain at
CC   least one promiscuous base, (i) separating the elongation product E from
CC   the elongation product E', (j) hybridising a further primer comprising a
CC   nucleobase sequence B' to the target nucleic acid or the elongation
CC   product E, (k) elongating the further primer of step (j) to produce
CC   another elongation product E using the target nucleic acid or elongation
CC   product E as a template and using nucleotides, where at least 30 % of the
CC   nucleotides contain at least one promiscuous base, (l) separating product
CC   E of step (k) from the target nucleic acid or elongation product E, (m)
CC   optionally repeating steps (g) - (l) a sufficient number of times to
CC   generate a desired amount of double stranded nucleic acids and (n)
CC   determining the elongation product E and/or elongation product E' as a
CC   measure of the presence or amount of the analyte, where the lengths of
CC   the sequence I and the nucleobase sequence B are chosen such that, when
CC   the further primer hybridises to the elongation product E in step (g),
CC   the further primer spans a sequence formed by elongation of the
CC   hybridised primer of step (e) and overlaps at least a part of the 3'
CC   region of the hybridized primer of step (e) by an overlap length. The
CC   method is useful determining an analyte in a sample. In particular, the
CC   method is useful for generating multiple double stranded nucleic acids.
CC   The present sequence is a primer molecule used to exemplify the method of
CC   the invention
XX
SQ   Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          30 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1
```

```
RESULT 50
ABK10412
ID   ABK10412 standard; DNA; 30 BP.
XX
AC   ABK10412;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Synthetic primer sequence 5'-T30-3'.
XX
KW   ss; 5'-T30-3'; double stranded DNA generation; promiscuous base;
KW   target molecule; primer.
XX
OS   Synthetic.
XX
PN   US6326143-B1.
XX
PD   04-DEC-2001.
XX
PF   22-MAY-1998;   98US-00083123.
XX
PR   22-NOV-1996;   96WO-EP005149.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Orum H,  Seeger C;
XX
DR   WPI; 2002-214947/27.
XX
PT   Determining an analyte in a sample, for generating multiple double
PT   stranded nucleic acids, comprises employing a single primer sequence with
PT   a nucleobase sequence having affinity to the sequence contained in a
PT   target nucleic acid.
XX
PS   Example 1; Col 14; 25pp; English.
XX
CC   The invention relates to determining an analyte in a sample comprising
CC   (a) providing a target nucleic acid comprising a region A, a nucleobase
CC   sequence B, and a sequence I linked to the 5' terminus of the nucleobase
CC   sequence B, where the nucleobase sequence B is not specific for the
CC   analyte, and the region A specifically binds to the analyte, (b) binding
CC   the target nucleic acid to the analyte, separating the analyte bound to
CC   the target nucleic acid from the remaining part of the sample, (d)
CC   hybridising a primer to the target nucleic acid, where the primer
CC   comprises a nucleobase sequence B', and the nucleobase sequence B'
CC   hybridises to the nucleobase sequence B, (e) elongating the hybridised
CC   primer to produce an elongation product E using the target nucleic acid
CC   as a template and using nucleotides, where at least 30 % of the
CC   nucleotides contain at least one promiscuous base which is capable of
CC   base pairing with each of adenine, guanine, cytosine, and thymine, (f)
CC   separating the target nucleic acid from the elongation product E, (g)
CC   hybridising a further primer which comprises the nucleobase sequence B'
CC   to the elongation product E, where the elongation product E is capable of
CC   acting as a template for the elongation of the further primer, (h)
CC   elongating the hybridised further primer of step (g) to produce an
CC   elongation product E' using the elongation product E as a template and
CC   using nucleotides, where at least 30 % of the nucleotides contain at
CC   least one promiscuous base, (i) separating the elongation product E from
CC   the elongation product E', (j) hybridising a further primer comprising a
CC   nucleobase sequence B' to the target nucleic acid or the elongation
CC   product E, (k) elongating the further primer of step (j) to produce
CC   another elongation product E using the target nucleic acid or elongation
CC   product E as a template and using nucleotides, where at least 30 % of the
CC   nucleotides contain at least one promiscuous base, (l) separating product
CC   E of step (k) from the target nucleic acid or elongation product E, (m)
CC   optionally repeating steps (g) - (l) a sufficient number of times to
CC   generate a desired amount of double stranded nucleic acids and (n)
CC   determining the elongation product E and/or elongation product E' as a
CC   measure of the presence or amount of the analyte, where the lengths of
CC   the sequence I and the nucleobase sequence B are chosen such that, when
CC   the further primer hybridises to the elongation product E in step (g),
CC   the further primer spans a sequence formed by elongation of the
CC   hybridised primer of step (e) and overlaps at least a part of the 3'
CC   region of the hybridized primer of step (e) by an overlap length. The
CC   method is useful determining an analyte in a sample. In particular, the
CC   method is useful for generating multiple double stranded nucleic acids.
CC   The present sequence is a primer molecule used to exemplify the method of
CC   the invention
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 51
ABK70490
ID   ABK70490 standard; DNA; 30 BP.
XX
AC   ABK70490;
XX
DT   15-JUL-2002  (first entry)
XX
DE   In-situ analysis synthetic probe #58.
XX
KW   Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;
KW   Epstein-Barr virus; lambda-immunoglobulin light chain; hapten;
KW   kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;
KW   Epstein-Barr early RNA; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200222874-A2.
XX
PD   21-MAR-2002.
XX
PF   06-SEP-2001; 2001WO-US028014.
XX
PR   15-SEP-2000; 2000US-0233177P.
XX
PA   (VENT-) VENTANA MEDICAL SYSTEMS INC.
XX
PI   Utermohlen JG,  Connaughton J;
XX
DR   WPI; 2002-371972/40.
XX
PT   Novel oligonucleotide label-domain for incorporation into oligonucleotide
PT   probes useful for detecting or localizing nucleic acid target genes
PT   within a cell or tissue sample.
XX
PS   Disclosure; Page 69; 71pp; English.
XX
CC   The present invention relates to a new oligonucleotide label-domain
CC   comprising the sequence (CTATTTT)_n and its complement (AAAATAG)_n, where
CC   n is 1. The probe sets of the invention are useful for detecting kappa or
CC   lambda-immunoglobulin light chain mRNA or corresponding heteronuclear
CC   RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)
CC   early RNA 1 and RNA 2, and human Alu repetitive satellite genomic
CC   sequences. The invention is a useful generic sequence for incorporation
CC   into oligonucleotide probes for detecting gene-specific sequences within
CC   cells or tissue samples in in situ hybridisation analysis and for
CC   attaching a label to immunoglobulins or other proteins for detecting
CC   haptens and antigens in immunohistochemical analyses. The present nucleic
CC   acid sequence represents one of a collection (ABK70376-ABK70501) of
CC   oligonucleotide probes that were used in the invention for detecting or
CC   localising a plurality nucleic acid target gene or antigen within a cell
CC   or tissue sample
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;
```

```
  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 52
ABS53961
ID   ABS53961 standard; DNA; 30 BP.
XX
AC   ABS53961;
XX
DT   26-NOV-2002  (first entry)
XX
DE   Method of measuring nucleic acid related oligonucleotide dT30mer.
XX
KW   Fluorescent intercalative dye; nucleic acid detection; gene diagnosis;
KW   clinical diagnostics; Stokes shift; ds.
XX
OS   Synthetic.
XX
PN   EP1223226-A2.
XX
PD   17-JUL-2002.
XX
PF   11-JAN-2002; 2002EP-00000723.
XX
PR   11-JAN-2001; 2001JP-00003432.
XX
PA   (TOYJ ) TOSOH CORP.
XX
PI   Tokunaga T,  Ishiguro T,  Horie R;
XX
DR   WPI; 2002-645688/70.
XX
PT   Fluorescent dye or its salt, hydrate, solvate or stereoisomer for nucleic
PT   acid probe for measuring nucleic acid(s) containing specific nucleic acid
PT   sequence in sample, has specific formula.
XX
PS   Example 5; Page 33; 40pp; English.
XX
CC   The invention describes a novel fluorescent dye and method of detecting
CC   nucleic acid. The dye and method are useful for nucleic acid probes for
CC   measuring nucleic acid(s) containing a specific nucleic acid sequence in
CC   a sample, and for qualitative/quantitative assay of target RNA containing
CC   specific base sequence anticipated in gene mixture. The assay is useful
CC   in gene diagnosis and other areas of clinical diagnostics and in
CC   identification/quantification microorganisms in biological samples such
CC   as serum, plasma and urine, microbially contaminated samples from food,
CC   rooms, soil, rivers and sea. The fluorescent intercalative dye shows a
CC   large fluorescent enhancement upon intercalation into double-stranded
CC   nucleic acid, and shows a great difference between excitation and
CC   emission wavelengths (has a large Stokes shift) and does not have a
CC   fluorescent spectrum that overlaps with those of conventionally known
CC   fluorescent intercalation dyes. Viruses, microbial RNAs, specific
CC   sequences in one RNA, are detected or quantified in a short time, hence
CC   the detection method is applicable to clinical diagnosis which requires
CC   high reliability. Amplification and extraction efficiencies of the target
CC   nucleic acid, are checked. This sequence represents a synthetic DNA used
CC   as the target in an assay to detect double stranded DNA
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 25.2;  DB 1;  Length 30;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+02;
  Matches   27;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2184
              ||||||| |  ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 30


RESULT 53
ABN89412
ID   ABN89412 standard; DNA; 40 BP.
XX
AC   ABN89412;
XX
DT   30-AUG-2002  (first entry)
XX
DE   Polymorphism detection related oligonucleotide SEQ ID NO:4.
XX
KW   Polymorphism; detection; mass spectroscopy; ss.
XX
OS   Synthetic.
XX
PN   WO200250307-A1.
XX
PD   27-JUN-2002.
XX
PF   12-DEC-2001; 2001WO-JP010892.
XX
PR   12-DEC-2000; 2000JP-00378091.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Inoko H,  Tamiya G,  Nakajima K,  Kimura N,  Nagashima R,  Morikawa M;
PI   Okamoto K;
XX
DR   WPI; 2002-508814/54.
XX
PT   Detection of DNA polymorphism by mass spectroscopy for investigation and
PT   diagnosis of gene-related diseases.
XX
PS   Example 3; Page 28; 34pp; Japanese.
XX
CC   The present invention describes a method for detecting polymorphisms in
CC   DNA by: (a) preparing a DNA sample from patients containing the DNA
CC   region in which the target polymorphism is located; (b) hybridising to an
CC   appropriate oligonucleotide fragment, immobilised on a support; and (c)
CC   detecting the hybridised target DNA by mass spectroscopy. The method can
CC   be used for the investigation and diagnosis of gene-related diseases. The
CC   method allows polymorphisms to be detected rapidly and effectively in a
CC   large number of specimens. The present sequence represents an
CC   oligonucleotide which is used in an example from the present invention
XX
SQ   Sequence 40 BP; 30 A; 0 C; 0 G; 10 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 24.8;  DB 1;  Length 40;
  Best Local Similarity   80.6%;  Pred. No. 3.4e+02;
  Matches   29;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2769 TATTCTTGTTAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | || || ||| ||   ||||||||||||||||||
Db          1 TTTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAA 36


RESULT 54
AAX14632
ID   AAX14632 standard; DNA; 35 BP.
XX
AC   AAX14632;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Triple helix forming nucleotides 4791-4725 of the n-myc gene.
XX
KW   Triple-helix forming region; Triplex formation; DNA detection;
KW   identification; bacteria; oncogene; virus; ds.
XX
OS   Homo sapiens.
XX
PN   US5861244-A.
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XX
PD   19-JAN-1999.
XX
PF   22-DEC-1993;   93US-00173489.
XX
PR   29-OCT-1992;   92US-00968436.
XX
PA   (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PI   Hepburn AG,  Wang C;
XX
DR   WPI; 1999-130384/11.
XX
PT   Assay of genetic sequences based on triplex formation from double
PT   stranded analyte - and hybrid of anchor and reporter sequences, with
PT   reporter released if triplex formation occurs, used e.g. to identify
PT   bacteria.
XX
PS   Disclosure; Col 13-14; 168pp; English.
XX
CC   The present sequence represents a potential triple-helix forming region.
CC   It can be used to demonstrate the assay of the invention. The assay
CC   comprises adding a sample containing double-stranded DNA test sequences,
CC   e.g. containing the present sequence, to an aqueous medium containing at
CC   least one complex of anchor DNA, attached to a solid support, and
CC   reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC   designed to form a triple-strand structure with part of the test
CC   sequence. Triplex formation results in displacement of the reporter DNA
CC   which is detected as an indication of the presence of the DNA test
CC   sequence. The method is used to detect DNA sequences, particularly for
CC   identification of bacteria (by detecting genes for ribosomal RNA) in
CC   clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ   Sequence 35 BP; 1 A; 4 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 24.6;  DB 1;  Length 35;
  Best Local Similarity   87.1%;  Pred. No. 2.6e+02;
  Matches   27;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              |||| | | |||||| ||||||||||||||||
Db          1 TTTTCTATTCTTTTTCTTTTTTTTTTTTTT 31


RESULT 55
ABQ95487/c
ID   ABQ95487 standard; DNA; 36 BP.
XX
AC   ABQ95487;
XX
DT   28-OCT-2002  (first entry)
XX
DE   Tumour suppression-related oligonucleotide #1138.
XX
KW   Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW   tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW   viral infection; cell degeneration disease; neurodegeneration; ds;
KW   Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS   Homo sapiens.
XX
PN   FR2819824-A1.
XX
PD   26-JUL-2002.
XX
PF   23-JAN-2001; 2001FR-00000899.
XX
PR   23-JAN-2001; 2001FR-00000899.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI   Telerman A,  Amson R,  Tuijnder M,  Susini L;
XX
DR   WPI; 2002-610803/66.
XX
PT   New nucleic acid implicated e.g. in tumor suppression, useful for
PT   diagnosis of tumors, viral infection and cellular degeneration and for
PT   drug screening.
XX
PS   Claim 1; Page 323; 623pp; French.
XX
CC   The present invention relates to novel human nucleic acid sequences (I).
CC   The present sequence is one such nucleic acid sequence. Expression of (I)
CC   are implicated in tumour suppression or reversion and apoptosis and viral
CC   resistance. (I) are useful as probes or primers for detecting,
CC   identifying, measuring and/or amplifying nucleic acid sequences, as
CC   antisense reagents and for recombinant production of polypeptides. (I),
CC   polypeptides (II) encoded by (I), vector containing (I), cells containing
CC   these vectors and antibodies (Ab) against (II) are all useful for
CC   treatment/prevention of viral, tumour and cell degeneration diseases
CC   (especially neurodegeneration, such as Alzheimer's disease and
CC   schizophrenia). Analysing the expression of (I) is also useful for
CC   diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC   (I) are used for studying the aetiology of these diseases (also immune
CC   and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC   to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC   in the specification
XX
SQ   Sequence 36 BP; 27 A; 2 C; 2 G; 4 T; 0 U; 1 Other;

  Query Match             0.9%;  Score 24.6;  DB 1;  Length 36;
  Best Local Similarity   84.4%;  Pred. No. 2.8e+02;
  Matches   27;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTTAACTTT 2192
              | |  |||||||||||||||||||||||| || |
Db         34 TTTANTTTTTTTTTTTTTTTTTTTTACCTGT 3


RESULT 56
AAA71190
ID   AAA71190 standard; RNA; 29 BP.
XX
AC   AAA71190;
XX
DT   27-APR-2001  (first entry)
XX
DE   Molecular interaction site RNA #227.
XX
KW   Modulator; identification; molecular interaction; virtual library; ss.
XX
OS   Canis familiaris.
XX
PN   WO9958947-A2.
XX
PD   18-NOV-1999.
XX
PF   12-MAY-1999;   99WO-US010361.
XX
PR   12-MAY-1998;   98US-00076404.
PR   12-MAY-1998;   98US-0085092P.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Ecker DJ,  Griffey R,  Crooke ST,  Sampath R,  Swayze E,  Mohan V;
PI   Hofstadler S,  Mcneil J;
XX
DR   WPI; 2000-086439/07.
XX
PT   Identifying compounds which modulate activity of target biomolecules,
PT   used to provide compounds which can be used as pharmacological,
PT   agricultural and industrial compounds.
XX
PS   Example 8; Fig 135; 405pp; English.
XX
CC   This invention describes a novel method for identifying compounds which
```

CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAACAUAAUCUAGUUUACAGAAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 29 BP; 22 A; 1 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.9%; Score 24.4; DB 1; Length 29;
Best Local Similarity 88.5%; Pred. No. 1.7e+02;
Matches 23; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2803
:|||| :|||||||||||||||||||
Db 4 UAGAACUGAAAAAAAAAAAAAAAAAAA 29

RESULT 57
AAA71173
ID AAA71173 standard; DNA; 29 BP.
XX
AC AAA71173;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #154.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Canis familiaris.
XX
PN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Example 8; Fig 134; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAACAUAAUCUAGUUUACAGAAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 29 BP; 22 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 24.4; DB 1; Length 29;
Best Local Similarity 96.2%; Pred. No. 1.7e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2803
||||| |||||||||||||||||||
Db 4 TAGAACTGAAAAAAAAAAAAAAAAAAA 29

RESULT 58
AAD27121/c
ID AAD27121 standard; RNA; 36 BP.
XX
AC AAD27121;
XX
DT 09-APR-2002 (first entry)
XX
DE RNA template, (AU)4 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW lead compound; RNA polymerase; ss.
XX
OS Unidentified.
XX
PN US6322966-B1.
XX
PD 27-NOV-2001.
XX
PF 11-MAY-1999; 99US-00309670.
XX
PR 11-MAY-1999; 99US-00309670.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (LAUJ/) LAU J Y N.
XX
PI Zhong W, Hong Z, Lau JYN;
XX
DR WPI; 2002-096587/13.
XX
PT Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.
XX
PS Example 1; Fig 1C; 10pp; English.
XX
CC The present invention relates to an assay system for hepatitis C virus

```
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, (AU)4 used to direct RNA synthesis by
CC   RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used
CC   in the exemplification of the invention
XX
SQ   Sequence 36 BP; 30 A; 0 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match              0.9%;  Score 24.4;  DB 1;  Length 36;
  Best Local Similarity   82.4%;  Pred. No. 3e+02;
  Matches   28;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2183
              ||  || ||||| |  ||||||||||||||||||
Db         36 ATATATATTTTTTTTTTTTTTTTTTTTTTTTTTT 3


RESULT 59
AAQ05003
ID   AAQ05003 standard; DNA; 29 BP.
XX
AC   AAQ05003;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-1990  (first entry)
XX
DE   Sequence binding to and inhibiting the GSTpi gene.
XX
KW   C-myc; cancer; HIV-I; AIDS; collagenase; Alzheimers disease; EGF;
KW   epidermal growth factor; GSTpi; HMGCoA; thallasemia;
KW   Herpes simplex virus; nerve growth factor receptor; globin; ss.
XX
OS   Synthetic.
XX
PN   EP375408-A.
XX
PD   27-JUN-1990.
XX
PF   20-DEC-1989;   89EP-00313391.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (HOGA/) HOGAN M E.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1990-195509/26.
XX
PT   Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-
PT   linear triplex to control transcription process in gene-specific fashion.
XX
PS   Claim 39; Page 30; 40pp; English.
XX
CC   Sequence forms triplex with the double stranded target sequence with G
CC   binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel
CC   orientation and when targeted to a specific sequence will deactivate it.
CC   This allows for growth inhibition in cancerous cells; manipulation of
CC   cellular structural protein content; inhibition of IL-2 chain receptor;
CC   disbursing plaque formation in Alzheimer's disease; inhibiting EGF gene;
CC   modulating cholestrol synthesis through the HMGCoA gene; suppressing NGF
CC   gene expression; arresting HSV-I replication and suppressing Beta- globin
CC   expression in thallassaemia and sicle cell anaemia patients. (Updated on
CC   25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC   field.)
XX
SQ   Sequence 29 BP; 0 A; 0 C; 0 G; 29 T; 0 U; 0 Other;

  Query Match              0.9%;  Score 24.2;  DB 1;  Length 29;
  Best Local Similarity   89.7%;  Pred. No. 1.9e+02;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              ||||||| |  ||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTTTT 29


RESULT 60
ADA26181
ID   ADA26181 standard; DNA; 30 BP.
XX
AC   ADA26181;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice semi-dwarf (sd-1) DNA fragment SEQ ID NO:26.
XX
KW   genotype; plant; rice; semi-dwarf; sd-1; polymorphism; detection;
KW   characteristic; single nucleotide polymorphism; SNP; genotyping;
KW   chromosome 1; gene; ds.
XX
OS   Synthetic.
OS   Oryza sativa.
XX
PN   WO2003070934-A1.
XX
PD   28-AUG-2003.
XX
PF   07-FEB-2003; 2003WO-JP001317.
XX
PR   25-FEB-2002; 2002JP-00048115.
XX
PA   (PLAN-) PLANT GENOME CENT CO LTD.
XX
PI   Minobe Y,  Monna L,  Kitazawa N,  Yoshino R,  Suzuki J;
XX
DR   WPI; 2003-697617/66.
XX
PT   Judging the genotype of a region around a plant sd-1 gene with
PT   polymorphism-obtained markers isolated by positional cloning, useful in
PT   genotyping for examination of semi-dwarf character of rice.
XX
PS   Disclosure; Page 15; 104pp; Japanese.
XX
CC   The present invention describes a method for judging the genotype of a
CC   region around a plant semi-dwarf (sd-1) gene in which polymorphisms are
CC   present, by detecting the polymorphisms. Also described: (1) examining
CC   semi-dwarf characteristics of a plant using the judgment method with
CC   detection of polymorphisms; (2) oligonucleotides for amplifying sd-1 DNA
CC   regions, which are primers for judging the genotype of a region around a
CC   plant sd-1 gene; (3) reagents for judging the genotype of a region around
CC   a plant sd-1 gene containing these oligonucleotides; and (4) reagents for
CC   examining the semi-dwarf character of a plant containing the
CC   oligonucleotides. The method is for judging the genotype of a region
CC   around a plant sd-1 gene, which is applicable in genotyping by (d)CAPS
CC   ((derived) cleaved amplified polymorphic sequence) for examination of the
CC   semi-dwarf character of rice to identify desirable strains e.g. with high
CC   crop yield, pest resistance and resistance to flooded water. The method
CC   is easy and quick, in which a seedling is required for studying single
CC   nucleotide polymorphisms (SNPs) for genotyping, without needing
CC   cultivation of seedling to fully-grown plant for judging heterozygote and
CC   distinguishing morphology. The present sequence represents a rice sd-1
CC   DNA fragment, which is given in the exemplification of the present
```

```
CC   invention. Rice sd-1 is located on chromosome 1.
XX
SQ   Sequence 30 BP; 0 A; 3 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 24.2;  DB 1;  Length 30;
  Best Local Similarity   89.7%;  Pred. No. 2e+02;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
              ||||||||  |||||| ||||||||||||
Db          2 TTTTTTCTTTTTTTTTCTTTTTTTTTTT 30


RESULT 61
AAF85682
ID   AAF85682 standard; DNA; 37 BP.
XX
AC   AAF85682;
XX
DT   25-JUN-2001  (first entry)
XX
DE   Pea blight resistance protein related oligonucleotide #1.
XX
KW   Pea; blight resistance; nucleotide triphosphate decomposition; ds.
XX
OS   Unidentified.
XX
PN   JP2001017176-A.
XX
PD   23-JAN-2001.
XX
PF   02-JUL-1999;   99JP-00189129.
XX
PR   02-JUL-1999;   99JP-00189129.
XX
PA   (KYOU ) UNIV KYOTO.
XX
DR   WPI; 2001-320697/34.
XX
PT   New blight-resistant polypeptide useful for giving blight resistance to a
PT   plant.
XX
PS   Example; Page 6; 20pp; Japanese.
XX
CC   The present invention provides the protein and coding sequences of a pea
CC   protein with nucleotide triphosphate decomposing activity. The gene can
CC   be used for conferring blight resistance on a plant
XX
SQ   Sequence 37 BP; 2 A; 3 C; 3 G; 29 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 24.2;  DB 1;  Length 37;
  Best Local Similarity   89.7%;  Pred. No. 3.5e+02;
  Matches   26;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTT 2179
              ||||||||||| |  |||||||||||||
Db          9 TTGATTTTTTTTTTTTTTTTTTTTTTTT 37


RESULT 62
AAF26222
ID   AAF26222 standard; DNA; 30 BP.
XX
AC   AAF26222;
XX
DT   26-APR-2001  (first entry)
XX
DE   APC binding protein associated primer ON-AT- SEQ ID 7.
XX
KW   APC binding protein; cell proliferation; adenomatous polyposis coli;
KW   tumor cell detection; primer; ss.
XX
OS   Unidentified.
XX
PN   DE19933237-A1.
XX
PD   18-JAN-2001.
XX
PF   15-JUL-1999;   99DE-01033237.
XX
PR   15-JUL-1999;   99DE-01033237.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI   Mueller O;
XX
DR   WPI; 2001-148321/16.
XX
PT   Determining proliferative capacity of cells, useful e.g. for detecting
PT   tumor cells, by measuring concentration and subcellular localization of
PT   adenomatous polyposis coli protein.
XX
PS   Claim 10; Page 13; 26pp; German.
XX
CC   This invention describes a novel method for determining the proliferative
CC   activity of cells, comprising detecting, in a sample, the concentration
CC   and/or subcellular localization of APC (adenomatous polyposis coli)
CC   protein (I). The invention also describes (1) determining function of (I)
CC   in a sample by detecting presence of the C-terminal, DNA-binding domain
CC   of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting
CC   the DNA-binding domain of (I); (3) purifying, enriching and/or detecting
CC   (I) or its fragments by reaction with a probe; (4) double-stranded DNA
CC   (II) that contains the sequence GGCCGCA_2_3G (S1) and/or GATCCT_2_3GC
CC   (S2); (5) peptide fragment of (I) containing at least the DNA-binding
CC   domain; (6) antibodies (Ab) directed against an epitope of positions 1340
CC   -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,
CC   one of which is Ab and the other directed against the N-terminal region
CC   (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or
CC   its fragments in a sample consisting of (II), Ab or the set of (7). The
CC   method is used to detect proliferative, especially tumor (precursor),
CC   cells, to detect function of (I) and mutations in (I), and to purify
CC   and/or enrich (I), or its fragments, from a sample. The method allows
CC   simple, rapid and reliable detection of proliferation, without the need
CC   for polymerase chain reaction or sequencing
XX
SQ   Sequence 30 BP; 1 A; 3 C; 2 G; 24 T; 0 U; 0 Other;

  Query Match             0.9%;  Score 24;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||||||
Db          3 TCCTTTTTTTTTTTTTTTTTTTTT 26


RESULT 63
AAL44170
ID   AAL44170 standard; DNA; 33 BP.
XX
AC   AAL44170;
XX
DT   03-OCT-2002  (first entry)
XX
DE   Porphyra yezoensis cytochrome C - related PCR primer, SEQ ID NO 4.
XX
KW   Cytochrome C; ss; maturation protein; nitrogen oxide trapping;
KW   polluted atmosphere purification; PCR; primer.
XX
OS   Porphyra yezoensis.
XX
PN   WO200259339-A1.
XX
PD   01-AUG-2002.
XX
PF   23-JAN-2002; 2002WO-JP000467.
```

XX
PR 23-JAN-2001; 2001JP-00014510.
XX
PA (UYNI-) UNIV NIPPON.
XX
PI Oku T, Nishio T, Satoh T;
XX
DR WPI; 2002-557951/59.
XX
PT Production of cytochrome c by culturing prokaryote transformed with
PT vector containing e.g. DNA of signal peptide and of eukaryotic cytochrome
PT c maturation protein for use in reagents and drugs for trapping nitrogen
PT oxide.
XX
PS Example 1; Page 7-8; 27pp; Japanese.
XX
CC The invention comprises a method for the production of cytochrome C. The
CC method involves culturing a prokaryote that has been transformed with a
CC vector encoding a signal peptide and a cytochrome C maturation protein.
CC The method of the invention is useful for producing cytochrome C.
CC Cytochrome C produced by the method of the invention is used in reagents
CC and drugs for trapping nitrogen oxide (e.g. in purifying polluted
CC atmosphere by trapping nitrogen oxide). The present DNA sequence
CC represents a Porphyra yezoensis cytochrome C - related PCR primer
XX
SQ Sequence 33 BP; 1 A; 3 C; 3 G; 26 T; 0 U; 0 Other;

Query Match 0.9%; Score 24; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||||||
Db 6 TCCTTTTTTTTTTTTTTTTTTTTT 29

RESULT 64
AAA75564
ID AAA75564 standard; DNA; 34 BP.
XX
AC AAA75564;
XX
DT 22-JAN-2001 (first entry)
XX
DE PCR primer for DNA encoding zeocin selective marker gene fragment.
XX
KW zalpha11 ligand; cytokine; haematopoietic cell proliferation; lymphoma;
KW tumourigenesis; leukaemia; hematopoiesis; B cell tumour; PCR primer; ss.
XX
OS Unidentified.
XX
PN WO200053761-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006067.
XX
PR 09-MAR-1999; 99US-00264908.
PR 11-MAR-1999; 99US-00265992.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI; 2000-565600/52.
XX
PT New human cytokine, designated zalpha11 ligand, useful for stimulating
PT the proliferation and/or development of hematopoietic cells in vitro and
PT in vivo, and for treating tumorigenesis.
XX
PS Example 6; Page 213; 256pp; English.
XX
CC The present PCR primer was used to amplify DNA encoding a fragment of
CC zeocin selective marker. The amplified fragment was used to construct a
CC vector for expression of zalpha11 ligand polypeptide. Zalpha11 ligand is
CC a cytokine. The zalpha11 ligand is useful for stimulating the
CC proliferation and development of haematopoietic cells in vitro and in
CC vivo. Zalpha11 ligand polynucleotides can be used as primers or probes
CC for cloning the zalpha11 gene. The zalpha11 ligand is useful for treating
CC tumourigenesis. A zalpha11 ligand-saporin fusion toxin may be used for
CC treating leukaemias and lymphomas. Antagonists against zalpha11 ligand
CC are useful as research reagents for characterizing ligand-receptor
CC interaction. Antagonists are also useful for inhibiting expansion,
CC proliferation, activation and differentiation of cells involved in
CC regulating hematopoiesis. The zalpha11 ligand may also be used to
CC stimulate an immune response against B cell tumour, a virus, a parasite
CC or a bacterium. The zalpha11 polypeptides, polynucleotides, antagonists,
CC agonists and antibodies are also useful for the detection, diagnosis,
CC prevention, and treatment of diseases associated with a zalpha11 ligand
CC genetic defect
XX
SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.9%; Score 24; DB 1; Length 34;
Best Local Similarity 84.4%; Pred. No. 3.1e+02;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2186
|||||||||| ||||||||||||||||
Db 1 TTTTTTTCTCGAGACTTTTTTTTTTTTTTTT 32

RESULT 65
AAD09727
ID AAD09727 standard; DNA; 34 BP.
XX
AC AAD09727;
XX
DT 10-SEP-2001 (first entry)
XX
DE ZC18698 primer, to synthesise human activated CD3+ selected cell cDNA.
XX
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US035308.
XX
PR 23-DEC-1999; 99US-00471767.
PR 01-DEC-2000; 2000US-0250841P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
DR WPI; 2001-408648/43.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer.
XX
PS Example 4B; Page 145; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity in
CC K5626 cells. ZCYTO18 DNA is useful for detecting a genetic abnormality in
CC a patient. ZCYTO18 DNA and its antibodies are useful for detecting cancer
CC and inflammation. ZCYTO18 protein is useful for killing cancer cells. It
CC is useful for increasing platelets in a patient or injured tissue. It is
CC also used in gene therapy. The present sequence is a PCR primer, ZC18698

CC used to synthesise a cDNA strand from human activated CD3+ selected
CC cells. This primer is used for the identification of human ZCYTO18
CC message in activated T-cell library
XX
SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.9%; Score 24; DB 1; Length 34;
Best Local Similarity 84.4%; Pred. No. 3.1e+02;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
||||||||||| ||||||||||||||||
Db 1 TTTTTTTCTCGAGACTTTTTTTTTTTTTTTT 32

RESULT 66
AAS20662
ID AAS20662 standard; DNA; 34 BP.
XX
AC AAS20662;
XX
DT 09-APR-2002 (first entry)
XX
DE Primer ZC18698 ued to create XhoI site into human zalpha11 Ligand cDNA.
XX
KW Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytostatic; human; primer; ss.
XX
OS Synthetic.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI; 2002-040208/05.
XX
PT New zalpha11 ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
PS Example 6; Col 135; 105pp; English.
XX
CC The present invention relates to the isolation of a novel cytokine,
CC zalpha11 Ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalpha11 receptor and the polynucleotide
CC encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC zalpha11 Ligand polypeptide is also useful in preparing antibodies that
CC bind to zalpha11 Ligand epitopes. The zalpha11 Ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalpha11 Ligand gene,
CC and in gene therapy. Zalpha11 Ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC a primer used in the methods of the present invention
XX

SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.9%; Score 24; DB 1; Length 34;
Best Local Similarity 84.4%; Pred. No. 3.1e+02;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
||||||||||| ||||||||||||||||
Db 1 TTTTTTTCTCGAGACTTTTTTTTTTTTTTTT 32

RESULT 67
ADD68172
ID ADD68172 standard; DNA; 34 BP.
XX
AC ADD68172;
XX
DT 15-JAN-2004 (first entry)
XX
DE PCR primer relating to the invention ZC18698 SEQ ID NO:30.
XX
KW ss; PCR; primer; zcytor17; antiinflammatory; dermatological;
KW immunosuppressive; antimicrobial; vaccine; inflammatory disease;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW atopic dermatitis; eczema; psoriasis; endotoxaemia; septicaemia;
KW toxic shock syndrome; infectious disease.
XX
OS Synthetic.
XX
PN WO2003060090-A2.
XX
PD 24-JUL-2003.
XX
PF 21-JAN-2003; 2003WO-US001984.
XX
PR 18-JAN-2002; 2002US-0350325P.
PR 25-APR-2002; 2002US-0375323P.
PR 19-DEC-2002; 2002US-0435315P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Sprecher CA, Kuijper JL, Dasovich MM, Grant FJ, Hammond AK;
PI Novak JE, Gross JA, Dillon SR;
XX
DR WPI; 2003-618179/58.
XX
PT New zcytor17 ligand polypeptides, useful for treating inflammatory
PT diseases, such as inflammatory bowel disease, ulcerative colitis, Crohn's
PT disease, atopic dermatitis, eczema, psoriasis, endotoxemia, septicemia.
XX
PS Example 6; SEQ ID NO 30; 372pp; English.
XX
CC The invention relates to a novel isolated zcytor17 ligand polypeptide. A
CC polypeptide of the invention has antiinflammatory, dermatological,
CC immunosuppressive, and antimicrobial activity, and may have a use in a
CC vaccine. The polypeptide is useful for treating inflammatory diseases,
CC such as inflammatory bowel disease, ulcerative colitis, Crohn's disease,
CC atopic dermatitis, eczema, psoriasis, endotoxaemia, septicaemia, toxic
CC shock syndrome or infectious diseases. The present sequence is used in
CC the exemplification of the invention.
XX
SQ Sequence 34 BP; 2 A; 3 C; 2 G; 27 T; 0 U; 0 Other;

Query Match 0.9%; Score 24; DB 1; Length 34;
Best Local Similarity 84.4%; Pred. No. 3.1e+02;
Matches 27; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
||||||||||| ||||||||||||||||
Db 1 TTTTTTTCTCGAGACTTTTTTTTTTTTTTTT 32

RESULT 68

```
ADC65905
ID   ADC65905 standard; DNA; 34 BP.
XX
AC   ADC65905;
XX
DT   18-DEC-2003  (first entry)
XX
DE   DNA oligonucleotide #38.
XX
KW   RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW   electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW   cation-mediated delivery; bacterial infection; viral infection;
KW   drug resistant infection; double stranded DNA oligomer; ss.
XX
OS   Synthetic.
XX
PN   US2003087241-A1.
XX
PD   08-MAY-2003.
XX
PF   30-NOV-2001; 2001US-00997931.
XX
PR   15-APR-1993;   93US-00047860.
PR   23-FEB-1995;   95US-00393439.
PR   26-FEB-1997;   97US-00805631.
PR   11-MAY-2000; 2000US-00569344.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 2003-755141/71.
XX
PT   Synthesizing RNA oligonucleotide involves combining single-stranded
PT   circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT   enzyme to yield desired RNA complementary to circular oligonucleotide
PT   template.
XX
PS   Example 18; SEQ ID NO 38; 78pp; English.
XX
CC   The invention relates to a method for synthesising an RNA
CC   oligonucleotide, comprising combining a single-stranded circular
CC   oligonucleotide template with at least two types of ribonucleotide
CC   triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC   oligonucleotide multimer complementary to the circular oligonucleotide
CC   template, where the RNA oligonucleotide multimer comprises multiple
CC   copies of the desired RNA oligonucleotide. The method is useful for
CC   synthesising an RNA oligonucleotide with well-defined ends. The circular
CC   oligonucleotide is introduced into the cell using direct injection,
CC   electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC   cation-mediated delivery. The method is useful for treating bacterial
CC   and/or viral infections in mammals, particularly drug resistant
CC   infections, and for producing double stranded DNA oligomers. The method
CC   is performed in the absence of an oligonucleotide primer, or without the
CC   addition of auxiliary proteins. This sequence represents an
CC   oligonucleotide used in the method of the invention.
XX
SQ   Sequence 34 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 6 Other;

  Query Match             0.8%;  Score 23.8;  DB 1;  Length 34;
  Best Local Similarity   78.1%;  Pred. No. 3.4e+02;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              || |||| ||  | |||| ||| |||||||||
Db          2 TTNTTTTNTCGATNTTTTNTTTNTTTTTTTT 33


RESULT 69
ABN83375/c
ID   ABN83375 standard; DNA; 32 BP.
XX
AC   ABN83375;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Mononucleotide repeat locus BAT26 probe #2.
XX
KW   Mononucleotide repeat locus; human; BAT26; probe; microsatellite; tumour;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Labelled with LightCycler fluorescent dye LC-Red-
FT                   640"
XX
PN   EP1207210-A1.
XX
PD   22-MAY-2002.
XX
PF   13-NOV-2001; 2001EP-00126930.
XX
PR   15-NOV-2000; 2000EP-00124897.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Dietmaier W;
XX
DR   WPI; 2002-437469/47.
XX
PT   Analyzing repeat sequences in DNA using a probe which hybridizes to
PT   adjacent repetitive and non-repetitive regions and determining hybrid
PT   melting point is useful to detect microsatellite instability such as in
PT   hereditary cancer.
XX
PS   Claim 16; Page 7; 19pp; English.
XX
CC   The present invention relates to a method for analysing a target nucleic
CC   acid consisting of repetitive and non-repetitive sequences. The method
CC   comprises hybridising a polynucleotide probe comprising a segment
CC   complementary to a non-repetitive region and a segment complementary to
CC   an adjacent repetitive region, where the second segment consists of a
CC   defined number of repeats, and determining the melting point temperature
CC   of the hybrid. The method is used to analyse microsatellites, especially
CC   microsatellite instability, particularly as a means for detecting
CC   hereditary tumours. Alternatively, the method is used to identify an
CC   individual in a population. The present sequence is a probe for
CC   Mononucleotide repeat locus BAT26, and was used to illustrate the
CC   invention
XX
SQ   Sequence 32 BP; 27 A; 1 C; 2 G; 2 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23.6;  DB 1;  Length 32;
  Best Local Similarity   86.7%;  Pred. No. 3.1e+02;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTTAACT 2190
              | |  |||||||||||||||||||||| ||
Db         32 TTTTTTTTTTTTTTTTTTTTTTTTTACCT 3


RESULT 70
AAD46356
ID   AAD46356 standard; DNA; 35 BP.
XX
AC   AAD46356;
XX
DT   29-AUG-2003  (revised)
DT   07-AUG-2003  (revised)
DT   27-JAN-2003  (first entry)
XX
```

```
DE   Vp3 oligonucleotide used to generate pox virus late promoter.
XX
KW   Recombinant leporipox virus; vector vaccine; treatment; prophylaxis;
KW   infectious disease; promoter; ss.
XX
OS   Viruses.
XX
PN   WO200272852-A2.
XX
PD   19-SEP-2002.
XX
PF   07-MAR-2002; 2002WO-EP002858.
XX
PR   08-MAR-2001; 2001EP-00200869.
XX
PA   (ALKU ) AKZO NOBEL NV.
XX
PI   Spibey N;
XX
DR   WPI; 2002-723365/78.
XX
PT   Use of a live, recombinant leporipox virus in the manufacture of a vector
PT   vaccine for the treatment and/or prophylaxis of infectious disease in non
PT   -lepori species.
XX
PS   Example 1; Page 9; 28pp; English.
XX
CC   The invention relates to the use of a live, recombinant leporipox virus
CC   (which comprises exogenous DNA that is operably linked to at least one
CC   expression control element and is incorporated in a non-essential region
CC   of the virus genome) in the manufacture of a vector vaccine for the
CC   treatment and/or prophylaxis of infectious disease in non-lepori species
CC   such as felines or canines. The present sequence is an oligonucleotide
CC   used to generate pox virus late promoter. This sequence is used in the
CC   exemplification of the invention. (Updated on 07-AUG-2003 to correct OS
CC   field.) (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 35 BP; 5 A; 4 C; 2 G; 24 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23.6;  DB 1;  Length 35;
  Best Local Similarity   86.7%;  Pred. No. 3.9e+02;
  Matches   26;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
             ||||||||||||||||||||||  | | |||
Db          2 TTTTTTTTTTTTTTTTTTTTTAGATCTTAAA 31


RESULT 71
AAS63441/c
ID   AAS63441 standard; DNA; 30 BP.
XX
AC   AAS63441;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Oligonucleotide-nanoparticle probe #63.
XX
KW   Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW   nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200173123-A2.
XX
PD   04-OCT-2001.
XX
PF   28-MAR-2001; 2001WO-US010071.
XX
PR   28-MAR-2000; 2000US-0192699P.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
PR   26-JUN-2000; 2000US-0213906P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Park S,  Li Z;
XX
DR   WPI; 2001-656926/75.
XX
PT   Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT   comprises reaction with nanoparticles that carry oligonucleotides
PT   complementary to parts of the target.
XX
PS   Example 24; Fig 44; 404pp; English.
XX
CC   The invention relates to a method for detection of nucleic acid (I)
CC   having at least 2 portions, comprising treatment with nanoparticles that
CC   carry oligonucleotides complementary to at least 2 parts of (I), where
CC   detectable change caused by hybridisation of the oligonucleotide to (I)
CC   is observed. The method is used to detect (or to separate) specific (I),
CC   e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC   analysis etc., and generally to detect analytes other than (I). The
CC   oligonucleotide-derivatised nanoparticles are also useful for preparing
CC   nanostructures useful, for example, as biochips, biofilters, mechanical
CC   devices, separation membranes, chemical sensors, in computers, and for
CC   drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
CC   produced, allowing their direct use (as probes) in polymerase chain
CC   reaction, i.e. they survive multiple heating/cooling cycles so do not
CC   need to be added after amplification. (I) are detected by simple colour
CC   change, without the need for special equipment, making possible rapid
CC   field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC   oligonucleotide-nanoparticle probes, and related sequences, used in the
CC   method of the invention
XX
SQ   Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23.4;  DB 1;  Length 30;
  Best Local Similarity   96.0%;  Pred. No. 2.9e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTT 2185
             ||| ||||||||||||||||||||||
Db         25 TCTGCTTTTTTTTTTTTTTTTTTTT 1


RESULT 72
AAS10385/c
ID   AAS10385 standard; DNA; 30 BP.
XX
AC   AAS10385;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Oligonucleotide-cyclic disulphide linker, c1 #2.
XX
KW   Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
KW   DNA isolation; genetic disease; bacterial disease; viral disease;
KW   forensic science; paternity testing; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "A is covalently linked to a cyclic-disulphide
FT                   moiety"
XX
PN   WO200151665-A2.
XX
```

PD 19-JUL-2001.
XX
PF 12-JAN-2001; 2001WO-US001190.
XX
PR 13-JAN-2000; 2000US-0176409P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 12-JAN-2001; 2001US-00760500.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Li Z;
XX
DR WPI; 2001-451868/48.
XX
PT Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
PT viral diseases, by contacting the nucleic acid with oligonucleotides
PT attached to nanoparticles and having sequences complementary a portion of
PT the nucleic acid.
XX
PS Example 24; Fig 44; 323pp; English.
XX
CC The sequence represents a cyclic disulphide linked oligonucleotide which
CC may be coupled with colloidal gold particles (nanoparticles) and used to
CC demonstrate the method of the invention. The invention relates to
CC isolating or detecting a nucleic acid of interest, in a mixture of
CC nucleic acids, by binding it to 2 or more complimentary nucleotides which
CC have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
CC colloidal gold) are used to both isolate and detect (e.g. by linking the
CC particle to a fluorescent probe) the resultant complex. The methods are
CC useful for detecting nucleic acids, natural or synthetic, and modified or
CC unmodified. The methods may also be applied in the diagnosis of genetic,
CC bacterial and viral diseases, in forensics, in DNA sequencing, for
CC paternity testing, for cell line authentication, and for monitoring gene
CC therapy. The methods are further useful in research and analytical
CC laboratories in DNA sequencing, in the field to detect the presence of
CC specific pathogens, for quick identification of an infection to assist in
CC drug prescription, and in homes and health centres for inexpensive first-
CC line screening. The methods, which are based on observing colour change
CC with the naked eye, are cheap, fast, simple, robust (reagents are
CC stable), do not require specialised or expensive equipment, and little or
CC no instrumentation is required
XX
SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 23.4; DB 1; Length 30;
Best Local Similarity 96.0%; Pred. No. 2.9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
||| ||||||||||||||||||||||
Db 25 TCTGCTTTTTTTTTTTTTTTTTTT 1

RESULT 73
ABK65048/c
ID ABK65048 standard; DNA; 30 BP.
XX
AC ABK65048;
XX
DT 02-JUL-2002 (first entry)
XX
DE Nanoparticle-oligonucleotide #68.
XX
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW ss.
XX
OS Synthetic.
XX
PN WO200218643-A2.
XX
PD 07-MAR-2002.
XX
PF 10-AUG-2001; 2001WO-US025237.
XX
PR 11-AUG-2000; 2000US-0224631P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-258024/30.
XX
PT Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX
PS Example 24; Fig 44; 412pp; English.
XX
CC The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA; and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroid residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX
SQ Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 23.4; DB 1; Length 30;
Best Local Similarity 96.0%; Pred. No. 2.9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
||| ||||||||||||||||||||||
Db 25 TCTGCTTTTTTTTTTTTTTTTTTT 1

RESULT 74
ABS64686/c
ID ABS64686 standard; DNA; 30 BP.
XX
AC ABS64686;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polynucleotide #68.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.

```
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US046418.
XX
PR   08-DEC-2000; 2000US-0254392P.
PR   08-DEC-2000; 2000US-0254418P.
PR   11-DEC-2000; 2000US-0255235P.
PR   11-DEC-2000; 2000US-0255236P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
PR   09-APR-2001; 2001US-0282640P.
PR   10-AUG-2001; 2001US-00927777.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI   Taton TA, Garimella V, Li Z, Park S;
XX
DR   WPI; 2002-608256/65.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 24; Fig 44; 442pp; English.
XX
CC   The invention describes a method of detecting (M1) a nucleic acid having
CC   two portions, involving providing nanoparticles having oligonucleotides
CC   attached to it, which has a sequence complementary to sequence of two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC   allow hybridisation of oligonucleotides with two or more portions of
CC   nucleic acid, and observing a detectable change brought about by
CC   hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC   conjugates (II) and the aggregate probe are useful for detecting two or
CC   more nucleic acids (from a biological source) having at least two
CC   portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC   with a disease, synthetic, or structurally-modified natural or synthetic
CC   RNA or DNA, or a product of a polymerase chain reaction amplification.
CC   (II) is useful for preparing a nanoprobe conjugate for detecting an
CC   analyte, and for detecting a nucleic acid bound to an electrode surface.
CC   (I) and (II) are useful for fabrication, and for separating a selected
CC   nucleic acid having two portions from other nucleic acids. (I), (II) and
CC   the aggregate probe are useful for detecting an analyte (especially
CC   polyvalent analyte) in a sample. This sequence represents a
CC   polynucleotide used to demonstrate the method of the invention
XX
SQ   Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23.4;  DB 1;  Length 30;
  Best Local Similarity   96.0%;  Pred. No. 2.9e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
             ||| ||||||||||||||||||||
Db         25 TCTGCTTTTTTTTTTTTTTTTTTT 1


RESULT 75
AAL61658/c
ID   AAL61658 standard; DNA; 30 BP.
XX
AC   AAL61658;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Oligonucleotide #19 used in the nucleic acid detection method.
XX
KW   Nucleic acid detection; fabrication; ss.
XX
OS   Unidentified.
XX
PN   WO2003035829-A2.
XX
PD   01-MAY-2003.
XX
PF   08-OCT-2002; 2002WO-US032088.
XX
PR   09-OCT-2001; 2001US-0327864P.
PR   07-DEC-2001; 2001US-00008978.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Park S,  Taton TA,  Mirkin CA;
XX
DR   WPI; 2003-430409/40.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 24; Fig 44; 467pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid having two
CC   portions. The method involves providing nanoparticles having
CC   oligonucleotides attached to it which has a sequence complementary to
CC   sequence of two portions of nucleic acid, contacting nucleic acid and
CC   nanoparticles to allow hybridisation of oligonucleotides with two or more
CC   portions of nucleic acid and observing a detectable change brought about
CC   by hybridisation. The method and aggregate probes are useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic or structurally modified natural or
CC   synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. The invention is useful for preparing a nanoprobe
CC   conjugate for detecting an analyte and for detecting a nucleic acid bound
CC   to an electrode surface. It is also useful for fabrication and for
CC   separating a selected nucleic acid having two portions from other nucleic
CC   acids. The present sequence is an oligo used to illustrate the method of
CC   the invention
XX
SQ   Sequence 30 BP; 23 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23.4;  DB 1;  Length 30;
  Best Local Similarity   96.0%;  Pred. No. 2.9e+02;
  Matches   24;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
             ||| ||||||||||||||||||||
Db         25 TCTGCTTTTTTTTTTTTTTTTTTT 1


RESULT 76
AAA94321
ID   AAA94321 standard; DNA; 36 BP.
XX
AC   AAA94321;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 37-P.
XX
KW   RNA-protein fusion; protein library; protein isolation; DNA-RNA hybrid;
KW   gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .13
FT                   /*tag=  a
FT                   /label= RNA
FT   modified_base   36
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
```

PN WO200047775-A1.
XX
PD 17-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US002589.
XX
PR 09-FEB-1999; 99US-00247190.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Szostak JW, Roberts RW, Liu R;
XX
DR WPI; 2000-533022/48.
XX
PT Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
XX
PS Disclosure; Page 44; 121pp; English.
XX
CC The present sequence is one of a number of oligonucleotides which were
CC used for the generation of RNA-protein fusions, including fusions having
CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC and in vitro or in situ translation of an mRNA molecule with a peptide
CC acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC under high salt conditions to produce a protein library. This method is
CC useful for improving or altering existing proteins, as well as for
CC isolating new proteins and nucleic acid or small molecule targets. It may
CC also be used to improve human or humanised single-chain antibodies for
CC the treatment of a number of diseases. The method is useful for the
CC isolation of proteins with specific binding properties, for screening
CC cDNA libraries and cloning new genes on the basis of protein-protein
CC interactions. Unlike prior art, the new method does not rely on
CC maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC complex, which is very fragile and is therefore of limited use. The
CC method does not rely on topological links between the protein and the
CC nucleic acid so that the information of the protein is retained and can
CC be recovered in readable, nucleic acid form
XX
SQ Sequence 36 BP; 25 A; 4 C; 6 G; 0 T; 1 U; 0 Other;

Query Match 0.8%; Score 23.4; DB 1; Length 36;
Best Local Similarity 92.0%; Pred. No. 4.6e+02;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
||| :||||||||||||||||||||
Db 8 GAACUGAAAAAAAAAAAAAAAAAAA 32

RESULT 77
ABK99274/c
ID ABK99274 standard; RNA; 36 BP.
XX
AC ABK99274;
XX
DT 21-OCT-2002 (first entry)
XX
DE Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #4.
XX
KW Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS Synthetic.
XX
PN US2002064771-A1.
XX
PD 30-MAY-2002.
XX
PF 06-APR-2001; 2001US-00828034.
XX
PR 07-APR-2000; 2000US-0195852P.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.
PA (FERR/) FERRARI E.
XX
PI Zhong W, Hong Z, Ferrari E;
XX
DR WPI; 2002-582330/62.
XX
PT Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT and template and primer which do not form a stable duplex in the absence
PT of HCV NS5B.
XX
PS Example; Page 6; 17pp; English.
XX
CC The invention relates to a replicase complex comprising a hepatitis C
CC virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC complementary nucleic acid primer which is annealed to the 3' terminus of
CC the template, where the template is at least three nucleotides and the
CC primer is two or three nucleotides, and the template and primer do not
CC form a stable duplex in solution in the absence of the HCV NS5B protein.
CC The complex is useful for detecting HCV replicase activity and permits
CC establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC and evaluate antiviral inhibitors and to improve the specificity and
CC efficacy of the inhibitors. The complex is also useful in the development
CC of a reliable system for determining kinetic and thermodynamic constants
CC of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC mechanistic inhibitors for mis-incorporation or chain termination.
CC Specifically, the short RNA template and primer pairs are useful in
CC screening assays which are used for determining kinetic, thermodynamic
CC and mechanistic properties of NS5B replication and ultimately in the
CC development of inhibitors of NS5B. Newly identified inhibitors of
CC replicase activity may be used for developing anti-HCV pharmaceuticals.
CC Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC templates
XX
SQ Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 23.4; DB 1; Length 36;
Best Local Similarity 81.8%; Pred. No. 4.6e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
|| | | | | ||||||||||||||||||||||
Db 36 ATATATATATTTTTTTTTTTTTTTTTTTT 4

RESULT 78
AAD27118/c
ID AAD27118 standard; RNA; 36 BP.
XX
AC AAD27118;
XX
DT 09-APR-2002 (first entry)
XX
DE RNA template, (AU)5 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW lead compound; RNA polymerase; ss.
XX
OS Unidentified.
XX
PN US6322966-B1.
XX
PD 27-NOV-2001.
XX
PF 11-MAY-1999; 99US-00309670.
XX
PR 11-MAY-1999; 99US-00309670.
XX
PA (ZHON/) ZHONG W.
PA (HONG/) HONG Z.

PA (LAUJ/) LAU J Y N.
XX
PI Zhong W, Hong Z, Lau JYN;
XX
DR WPI; 2002-096587/13.
XX
PT Assay system for hepatitis C virus replicase activity comprises RNA
PT template with unstable, small stemloop capable of forming copy-back
PT structure, viral non-structural protein 5B, nucleoside triphosphates,
PT buffer.
XX
PS Example 1; Fig 1A; 10pp; English.
XX
CC The present invention relates to an assay system for hepatitis C virus
CC (HCV) replicase activity. The assay system comprises an RNA template that
CC has an unstable, small stemloop at the 3' end capable of forming a copy-
CC back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC radiolabelled and an assay buffer that supports replication activity of
CC NS5B. The invention also relates to the identification of optimal
CC properties of an RNA template for copy-back self-priming RNA synthesis of
CC HCV. This activity can be used to screen for anti-HCV replicase compounds
CC or to characterise the biological relevance of lead compounds. The
CC optimal RNA templates can be used for developing a system to characterise
CC HCV NS5B polymerase mechanistically and kinetically and for designing
CC small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC system of the invention is useful for detecting HCV replicase activity.
CC The nucleic acid synthesised by NS5B is detected by evaluating an
CC autoradiograph of reaction products separated by gel electrophoresis. The
CC present sequence is RNA template, (AU)5 used to direct RNA synthesis by
CC RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used
CC in the exemplification of the invention
XX
SQ Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 23.4; DB 1; Length 36;
Best Local Similarity 81.8%; Pred. No. 4.6e+02;
Matches 27; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                || | | | | ||||||||||||||||||||
Db         36 ATATATATATTTTTTTTTTTTTTTTTTTTT 4
```

RESULT 79
AAV15487
ID AAV15487 standard; DNA; 29 BP.
XX
AC AAV15487;
XX
DT 20-JUL-1998 (first entry)
XX
DE PR-1 promoter primer P41+ for in vivo footprinting.
XX
KW Promoter PR-1; salicylic acid, 2,6-dichloroisonicotinic acid;
KW benzo(1,2,3)thiadiazole-7-carbothioic acid S-methyl ester;
KW transgenic plant; PCR; primer; ss.
XX
OS Synthetic.
OS Arabidopsis thaliana.
XX
PN WO9803536-A1.
XX
PD 29-JAN-1998.
XX
PF 18-JUL-1997; 97WO-US012626.
XX
PR 23-JUL-1996; 96US-0027228P.
XX
PA (NOVS) NOVARTIS CORP.
XX
PI Lebel EG, Ryals JA, Thorne L, Uknes SJ, Ward ER;
XX
DR WPI; 1998-120690/11.
XX
PT New chemically inducible promoter from Arabidopsis - used to regulate
PT gene expression in response to e.g. salicylic acid.
XX
PS Example 9; Page 32; 60pp; English.
XX
CC Primer P41+ corresponds to nucleotides -735 to -706 relative to the
CC transcription start site in the upstream region (see AAV15448) of the
CC Arabidopsis PR-1 gene (see AAV15448). It was used in non-coding strand
CC analysis of the PR-1 promoter region. In vivo footprinting analysis was
CC performed of the PR-1 promoter region. Inducible in vivo footprints are
CC located at positions -629 and -628 and at position -604 on the coding
CC strand and at position -641 on the non-coding strand. The use of PR-1
CC promoter fragments to regulate gene expression in plants in the presence
CC of chemical inducers is disclosed
XX
SQ Sequence 29 BP; 0 A; 2 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 0.8%; Score 23.2; DB 1; Length 29;
Best Local Similarity 89.3%; Pred. No. 2.9e+02;
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACTTT 2192
                ||||||||||||||||||||||   |||
Db          1 CTTTTTTTTTTTTTTTTTTTTTTTTTT 28
```

RESULT 80
ABN83378/c
ID ABN83378 standard; DNA; 29 BP.
XX
AC ABN83378;
XX
DT 15-AUG-2002 (first entry)
XX
DE Mononucleotide repeat locus BAT25 probe #1.
XX
KW Mononucleotide repeat locus; human; BAT25; probe; microsatellite; tumour;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 29
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Labelled with Fluorescein"
XX
PN EP1207210-A1.
XX
PD 22-MAY-2002.
XX
PF 13-NOV-2001; 2001EP-00126930.
XX
PR 15-NOV-2000; 2000EP-00124897.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Dietmaier W;
XX
DR WPI; 2002-437469/47.
XX
PT Analyzing repeat sequences in DNA using a probe which hybridizes to
PT adjacent repetitive and non-repetitive regions and determining hybrid
PT melting point is useful to detect microsatellite instability such as in
PT hereditary cancer.
XX
PS Claim 16; Page 7; 19pp; English.
XX
CC The present invention relates to a method for analysing a target nucleic
CC acid consisting of repetitive and non-repetitive sequences. The method

```
CC   comprises hybridising a polynucleotide probe comprising a segment
CC   complementary to a non-repetitive region and a segment complementary to
CC   an adjacent repetitive region, where the second segment consists of a
CC   defined number of repeats, and determining the melting point temperature
CC   of the hybrid. The method is used to analyse microsatellites, especially
CC   microsatellite instability, particularly as a means for detecting
CC   hereditary tumours. Alternatively, the method is used to identify an
CC   individual in a population. The present sequence is a probe for
CC   Mononucleotide repeat locus BAT25, and was used to illustrate the
CC   invention
XX
SQ   Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23.2;  DB 1;  Length 29;
  Best Local Similarity   89.3%;  Pred. No. 2.9e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2152 TGATTTTTTTCTCCTTTTTTTTTTTTT 2179
             ||||||||||  |  ||||||||||||||
Db         29 TGATTTTTTTTTTTTTTTTTTTTTTTT 2

RESULT 81
ADA26489/c
ID   ADA26489 standard; DNA; 32 BP.
XX
AC   ADA26489;
XX
DT   20-NOV-2003  (first entry)
XX
DE   DNA nanolithography method example oligonucleotide G1.
XX
KW   ss; direct-write nanolithography; nanoscopic tip; nanoscale pattern;
KW   patterning; scanning probe microscopic tip; nanoparticle; nanoarray.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   32
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "contains a thiol group (CH2)3SH) at the 5' end"
XX
PN   WO2003048314-A2.
XX
PD   12-JUN-2003.
XX
PF   02-DEC-2002; 2002WO-US038252.
XX
PR   30-NOV-2001; 2001US-0337598P.
PR   07-MAR-2002; 2002US-0362924P.
XX
PA   (UYNW-) UNIV NORTHWESTERN TECHNOLOGY TRANSFER PR.
XX
PI   Mirkin CA,  Demers ML,  Ginger DS;
XX
DR   WPI; 2003-671287/63.
XX
PT   Depositing nucleic acid on substrate by direct-write nanolithography, by
PT   positioning nanoscopic tip relative to substrate, to transfer nucleic
PT   acid to substrate and generate stable nucleic acid nanoscale pattern.
XX
PS   Disclosure; Page 38; 76pp; English.
XX
CC   The invention relates to a method of depositing nucleic acid onto a
CC   substrate by direct-write nanolithography, by positioning at least one
CC   nanoscopic tip relative to a substrate so that the tip and substrate
CC   approach each other, and the nucleic acid is transferred from the tip to
CC   the substrate to generate a stable nucleic acid nanoscale pattern on the
CC   substrate which is hybridizable with complementary nucleic acid. The
CC   method is useful for generating nanoscale patterns of nucleic acid on a
CC   substrate, in which before transfer the tip is modified to allow the
CC   nucleic acid to wet the tip and the nucleic acid is modified to chemisorb
CC   or covalently bond to the substrate upon transfer. The method is also
CC   useful for direct patterning of modified nucleic acid onto a substrate,
CC   by inking a scanning probe microscopic tip with a modified nucleic acid
CC   and positioning the inked tip close enough to the substrate to effect
CC   transfer of the nucleic acid to the substrate to form a nanoscale
CC   pattern. Another use for the method is for assembling nanoparticles (e.g.
CC   gold nanoparticles) to form nanoscale patterns, by depositing from a
CC   nanoscopic tip a first nucleic acid onto a substrate to form a deposit
CC   with lateral nanoscale features of 1000 mm or less by direct write
CC   nanolithography, hybridizing the nucleic acid deposit with the
CC   nanoparticle, where the nanoparticle is functionalized with a second
CC   nucleic acid which is either complementary to the first or complementary
CC   to the nucleic acid of a linking strand which links the second nucleic
CC   acid to the first. Deposition of nucleic acid on the substrate is
CC   repeated to form a nanoarray of the nucleic acid and the hybridization is
CC   carried out with the nanoarray. The method is suitable for writing
CC   preconceived nanoscale features directly, without use of expensive and
CC   potentially destructive methods such as electron beam and
CC   photolithographic methods. The structures can be built up, if desired,
CC   without degrading existing structures. Complicated stamps and resists are
CC   not needed. Improvements in the consistency and stability of the
CC   nanolithography can be observed. This sequence represents an example of a
CC   nucleic acid that can be used in the method of the invention.
XX
SQ   Sequence 32 BP; 23 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23.2;  DB 1;  Length 32;
  Best Local Similarity   89.3%;  Pred. No. 3.7e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACTTTGA 2194
             |||||||||||||||||||||    ||||
Db         32 TTTTTTTTTTTTTTTTTTTAGAGTTGA 5

RESULT 82
AAA94321/c
ID   AAA94321 standard; DNA; 36 BP.
XX
AC   AAA94321;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 37-P.
XX
KW   RNA-protein fusion; protein library; protein isolation; DNA-RNA hybrid;
KW   gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .13
FT                   /*tag=  a
FT                   /label= RNA
FT   modified_base   36
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US002589.
XX
PR   09-FEB-1999;   99US-00247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
```

```
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions.
XX
PS   Disclosure; Page 44; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides which were
CC   used for the generation of RNA-protein fusions, including fusions having
CC   a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form
XX
SQ   Sequence 36 BP; 25 A; 4 C; 6 G; 0 T; 1 U; 0 Other;

  Query Match             0.8%;  Score 23.2;  DB 1;  Length 36;
  Best Local Similarity   89.3%;  Pred. No. 5e+02;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
                ||||||||||||||||||||| | || |
Db         34 TTTTTTTTTTTTTTTTTTTTCAGTTCG 7


RESULT 83
AAQ30431
ID   AAQ30431 standard; DNA; 23 BP.
XX
AC   AAQ30431;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer IL6804 for forming triplex with HUMIL6 target duplex.
XX
KW   Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW   malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
FT   misc_feature     11. .12
FT                    /*tag=  d
FT                    /note= "o-xyloso dimer synthon linkage"
FT   misc_feature     12. .23
FT                    /*tag=  c
FT                    /label= inverted_polarity_region
FT                    /note= "see comments"
FT   modified_base    23
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 71; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC   concd. on one strand of the duplex. The oligomer, and others like it are
CC   useful in diagnosis and therapy of diseases characterised by specific DNA
CC   duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC   tumours and inflammation. The triple helices form under mild conditions
CC   thus assays may be carried out without subjecting the test specimen to
CC   harsh conditions. The oligomer contains an inverted polarity region
CC   formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC   (nucleotides have the 3'positions of xylose sugars linked via the o-
CC   xylene ring). Two nucleotides are coupled through a xylene residue to
CC   form the dimer synthon. This additional modifications may render the
CC   oligomer stable to nuclease activity. The oligomer is able to inhibit
CC   gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTTA 2187
                |||||||||||||||||||||||
Db          1 CTTTTTTTTTTTTTTTTTTTTTA 23


RESULT 84
AAI72268
ID   AAI72268 standard; DNA; 25 BP.
XX
AC   AAI72268;
XX
DT   15-APR-2002  (first entry)
XX
DE   P4 primer used in differential display s-AFLP analysis.
XX
KW   Lung; cancer; metastasis; solid tumour; blood; bone marrow; syndecan 1;
KW   collagen 1 alpha 2; 7013; 7018; amplification; mammal; human; dog; cat;
KW   bile duct; colon; breast; uterus; oesophagus; larynx; liver; brain; PCR;
KW   remission; relapse; polymerase chain reaction; amplify; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200198539-A2.
XX
PD   27-DEC-2001.
```

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XX
PF   21-JUN-2001; 2001WO-US019980.
XX
PR   21-JUN-2000; 2000US-0215727P.
PR   27-OCT-2000; 2000US-0243976P.
XX
PA   (HITB ) HITACHI CHEM CO LTD.
PA   (HITB ) HITACHI CHEM RES CENT INC.
PA   (HITA ) HITACHI LTD.
XX
PI   Mitsuhashi M,  Kambara H,  Matsunaga H,  Kawamura M;
XX
DR   WPI; 2002-098233/13.
XX
PT   Identifying lung cancer/metastasis of solid tumor in patient by isolating
PT   blood or non-lung tissue, or bone marrow from patient and identifying
PT   presence of marker e.g. syndecan 1, collagen 1 alpha 2, 7013, or 7018.
XX
PS   Example 1; Page 6; 29pp; English.
XX
CC   The sequences given in AAI72265-69 are oligonucleotides which were used
CC   in the method of the invention for identifying lung cancer or metastasis
CC   of a solid tumour. The method comprises isolating blood (or non-lung
CC   tissue in the case of identifying lung cancer, or bone marrow in case of
CC   identifying metastasis) from a patient, and identifying the presence of
CC   at least one marker (M) such as syndecan 1, collagen 1 alpha 2, 7013, or
CC   7018. These oligos lead to the amplification of cDNA's which were more
CC   abundant in lung cancer RNA than in normal blood. The method is useful
CC   for identifying lung cancer in a mammal e.g., human, dog or cat, and
CC   identifying metastasis of solid tumour in a patient, where the solid
CC   tumour is of bile duct, colon, breast, uterus, oesophagus or larynx. The
CC   method is useful for identifying presence of lung cancer cells in the
CC   blood or bone marrow, and also for identifying metastasis and thus for
CC   identifying lung cancer cells in an organ such as liver or brain. The
CC   method is useful to identify the presence of lung cancer cells at a very
CC   early stage in the disease, or after remission or to identify a relapse
XX
SQ   Sequence 25 BP; 0 A; 3 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.8%;  Score 23;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||||
Db          1 TCTCCTTTTTTTTTTTTTTTTT 23


RESULT 85
AAV71935
ID   AAV71935 standard; DNA; 27 BP.
XX
AC   AAV71935;
XX
DT   18-FEB-1999  (first entry)
XX
DE   Anchored poly T RT-PCR primer.
XX
KW   Normalised; cDNA library; mRNA cloning; reverse transcription;
KW   immobilise; screening; hybridisation; nucleic acid amplification;
KW   expression pattern; drug development; PCR primer; RT-PCR; ss.
XX
OS   Synthetic.
XX
PN   WO9851789-A2.
XX
PD   19-NOV-1998.
XX
PF   13-MAY-1998;   98WO-DK000186.
XX
PR   13-MAY-1997;   97DK-00000547.
PR   19-MAY-1997;   97US-00871030.
PR   27-MAR-1998;   98DK-00000432.
XX
PA   (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX
PI   Warthoe PR;
XX
DR   WPI; 1999-009772/01.
XX
PT   Preparation of normalised, subdivided cDNA libraries from mRNA - by
PT   reverse transcription and amplification, used to screen for new genes and
PT   interacting proteins, potential drugs, and for diagnosis.
XX
PS   Example 1; Page 29; 71pp; English.
XX
CC   The invention relates to preparation of a normalised, subdivided library
CC   of amplified cDNA from the coding regions of mRNA in a sample. The method
CC   involves reverse transcription, with at least one cDNA primer of formula
CC   5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence
CC   of 1-100 nucleotides; dT = deoxythymidinyl; n2 is at least 1; n3 and n4
CC   are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
CC   cDNA synthesis using the first strand as template and a second cDNA
CC   primer of a similar formula, in the presence of DNA polymerase I (or its
CC   Klenow fragment) and amplification of double-stranded cDNA with a set of
CC   amplification primers. Comparison of cDNA in the prepared library with a
CC   database (a computer-generated list of molecular weights of restricted
CC   DNA fragments of known sequence) is used to determine presence of an
CC   expressed protein in a cell, also to detect changes in such expression
CC   (particularly for diagnosis of disease). Surfaces (chip) having amplified
CC   cDNA stably immobilised on it, obtained by a similar method, are used to
CC   screen for genes of a particular family, by hybridisation with nucleic
CC   acid from the family (to identify new genes) and to detect differences in
CC   expression patterns between cells. The polypeptides expressed by the
CC   libraries can be used for drug development. Sequences AAV71935 to
CC   AAV71946 represent primers used to exemplify the method of the invention
XX
SQ   Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTAA 27


RESULT 86
AAA40362
ID   AAA40362 standard; DNA; 28 BP.
XX
AC   AAA40362;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 12.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
XX
DR   WPI; 2000-442381/38.
XX
```

PT Inserting a nucleic acid into a circular vector comprising joining their
PT ends, melting, and reannealing ends at two different concentrations,
PT useful for cloning small amounts of nucleic acids and forming genomic
PT libraries.
XX
PS Example 4; Page 68; 71pp; English.
XX
CC This invention describes a novel method (M1) for inserting a nucleic acid
CC (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC under a first nucleic acid concentration, melting hybridized cohesive
CC circularization ends, and reannealing the ends at a second concentration.
CC The methods are useful for the cloning small amounts of nucleic acids and
CC forming genomic libraries of complex populations of DNA or cDNA. The
CC methods allow the cloning of minute amounts of nucleic acids efficiently
CC and avoids the size selection problems of prior art systems. Larger
CC nucleic acid fragments are just as easily cloned, allowing highly
CC representative libraries to be made. Vector to vector ligation is avoided
CC using the methods. AAA40351-A40366 represents primers used to illustrate
CC the method of the invention
XX
SQ Sequence 28 BP; 0 A; 2 C; 2 G; 24 T; 0 U; 0 Other;

Query Match 0.8%; Score 23; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||||||
Db 3 CCTTTTTTTTTTTTTTTTTTTTT 25

RESULT 87
AAQ87894
ID AAQ87894 standard; DNA; 32 BP.
XX
AC AAQ87894;
XX
DT 25-MAR-2003 (revised)
DT 29-NOV-1995 (first entry)
XX
DE Normalised library first strand cDNA synthesis primer.
XX
KW Normalised cDNA library; directionally cloned cDNA library; screening;
KW hybridisation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 15. .18
FT /*tag= a
FT /note= "characteristic sequence identifier"
XX
PN WO9508647-A1.
XX
PD 30-MAR-1995.
XX
PF 23-SEP-1994; 94WO-US010821.
XX
PR 24-SEP-1993; 93US-00126594.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Soares MB, Efstratiadis A;
XX
DR WPI; 1995-139615/18.
XX
PT New normalised directional cDNA libraries - used for isolating novel
PT cDNA's, including tissue-specific and development-specific DNA.
XX
PS Disclosure; Page 45; 186pp; English.
XX
CC Human tissues were obtained for construction of a variety of cDNA
CC libraries, including infant brain, adult brain and adult hippocampus.
CC Each of the cDNA libraries had a characteristic sequence identifier,
CC provided by the oligonucleotide utilised to prime first strand cDNA
CC synthesis (see AAQ87894-Q87907 for these primer sequences; all these
CC primers have the PacI restriction site for directional cloning of cDNAs).
CC Each of the libraries was propagated in the form of single-stranded (ss)
CC circles and normalised separately by a novel method. The method
CC comprises: generating fragments complementary to the 3' non-coding
CC sequence of the ss circles in the library to produce partial duplexes;
CC purifying the partial duplexes; melting and reassociating them to
CC appropriate Cot; and purifying the unassociated ss circles to generate a
CC normalised cDNA library. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 32 BP; 4 A; 0 C; 0 G; 28 T; 0 U; 0 Other;

Query Match 0.8%; Score 23; DB 1; Length 32;
Best Local Similarity 83.9%; Pred. No. 4e+02;
Matches 26; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
|||||| | || ||||||||||||||||
Db 1 TTTTTTTAATTAATTTTTTTTTTTTTTTT 31

RESULT 88
AAF60568
ID AAF60568 standard; DNA; 32 BP.
XX
AC AAF60568;
XX
DT 27-APR-2001 (first entry)
XX
DE Neuraminidase PCR primer #6.
XX
KW PCR primer; virucide; vaccine; gene therapy; neuraminidase; vaccine;
KW immune response; ss.
XX
OS Influenza virus.
XX
PN WO200109291-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-2000; 2000WO-GB002933.
XX
PR 30-JUL-1999; 99GB-00017981.
PR 30-JUL-1999; 99US-0146145P.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Brownlee GG, Fodor E, Poon L;
XX
DR WPI; 2001-159859/16.
XX
PT New negative-sense single stranded RNA virus, e.g. influenza virus,
PT attenuated by replacing the poly U track with a poly A track, useful as a
PT vaccine and in gene therapy.
XX
PS Example 7; Page 28; 49pp; English.
XX
CC The present invention relates to an attenuated influenza virus. The virus
CC is attenuated by replacement of the poly U track in a genomic nucleic
CC acid by a poly A track capable of being copied to provide a poly U tail
CC for mRNA transcribed from the nucleic acid. The attenuated virus is
CC useful as a vaccine, for immunisation against diseases caused by the
CC equivalent wild type viruses. The present sequence is a PCR primer used
CC to generate the virus of the present invention
XX
SQ Sequence 32 BP; 1 A; 6 C; 4 G; 21 T; 0 U; 0 Other;

Query Match 0.8%; Score 23; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2163 TCCTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||||
Db         10 TCCTTTTTTTTTTTTTTTTTTT 32


RESULT 89
AAT93816
ID   AAT93816 standard; DNA; 35 BP.
XX
AC   AAT93816;
XX
DT   25-MAR-2003  (revised)
DT   24-FEB-1998  (first entry)
XX
DE   Antitumoural phosphodiester oligonucleotide 6 with cytotoxic activity.
XX
KW   Phosphodiester; selective binding; cell viability; growth;
KW   tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW   lymphoblastic tumour; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .35
FT                    /*tag=  a
FT                    /note= "phosphodiester oligonucleotide"
XX
PN   WO9720924-A1.
XX
PD   12-JUN-1997.
XX
PF   04-DEC-1996;   96WO-EP005388.
XX
PR   04-DEC-1995;   95IT-MI002539.
XX
PA   (SAIC-) SAICOM SRL.
XX
PI   Scaggiante B,  Quadrifoglio F;
XX
DR   WPI; 1997-319771/29.
XX
PT   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT   selective cytotoxic effect on tumour cells, for treating both solid and
PT   liquid tumours.
XX
PS   Claim 10; Page 5; 38pp; English.
XX
CC   Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC   generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-
CC   (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''- (G-gTg')g''-N', where: N and
CC   N' = T or G, equal or different from each other; x = 0-8, equal or
CC   different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC   different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC   or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC   16, equal or different from each other; The oligonucleotides are believed
CC   to selectively bind and sequester some proteins which are essential to
CC   the viability and growth of tumoural cell line. They have specific and
CC   selective cytotoxic activity against tumour cells, and can be used for
CC   treating tumours of the liquid type, in particular of lymphoblastic
CC   origin, and of solid type, in particular lymphomas. The present
CC   phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC   reduced growth of CCRF-CEM tumoural cells by 83%, which is detectable 48
CC   hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 35 BP; 0 A; 0 C; 5 G; 30 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 23;  DB 1;  Length 35;
  Best Local Similarity   83.9%;  Pred. No. 5e+02;
  Matches   26;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              ||||||| |  |||| ||||||| |||||||
Db          3 TTTTTTGTTTTTTGTTTTTTGTTTTTT 33


RESULT 90
ABX79828
ID   ABX79828 standard; cDNA; 27 BP.
XX
AC   ABX79828;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #153.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 717; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.8;  DB 1;  Length 27;
  Best Local Similarity   92.3%;  Pred. No. 2.8e+02;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTT 2191
              |||||||||||||||||||||| | ||
Db          2 TTTTTTTTTTTTTTTTTTTTTATTT 27


RESULT 91
AAQ52157
ID   AAQ52157 standard; RNA; 35 BP.
XX
```

```
AC   AAQ52157;
XX
DT   25-MAR-2003  (revised)
DT   26-MAY-1994  (first entry)
XX
DE   Breast cancer specific mRNA ribozyme cleavable nucleotide (4416).
XX
KW   Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW   resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW   actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW   adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW   human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW   B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW   neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW   hairpin; hepatitis delta virus; group I intron; RNaseP; leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO9323057-A1.
XX
PD   25-NOV-1993.
XX
PF   13-MAY-1993;   93WO-US004573.
XX
PR   14-MAY-1992;   92US-00882822.
PR   14-MAY-1992;   92US-00882885.
PR   26-AUG-1992;   92US-00936110.
PR   26-AUG-1992;   92US-00936421.
PR   26-AUG-1992;   92US-00936422.
PR   26-AUG-1992;   92US-00936531.
PR   26-AUG-1992;   92US-00936532.
PR   07-DEC-1992;   92US-00987131.
PR   19-JAN-1993;   93US-00006122.
PR   19-JAN-1993;   93US-00008910.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Draper KG;
XX
DR   WPI; 1993-386203/48.
XX
PT   New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
PT   with tumours or mRNA expressed from gene encoding multiple drug
PT   resistance.
XX
PS   Claim 3; Fig 8; 69pp; English.
XX
CC   The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC   associated with development or maintenance of chronic myelogenous
CC   leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
CC   lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
CC   leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
CC   The full length mRNAs containing these target sequences, encode aberant
CC   cellular proteins which are able to control cellular proliferation and
CC   are directly linked to a leukemic phenotype. These target sequences are
CC   identified by the ribozyme of the invention. The ribozymes is formed in a
CC   hammerhead motif, but may also be formed in the motif of a hairpin,
CC   hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
CC   may be used to inhibit the development or expression of a transformed
CC   phenotype in man and other animals by modulating expression of the
CC   corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
CC   and transformed cells elicits inhibition of the transformed state.
CC   Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the
CC   mechanism of drug resistance used by transformed cells and thus enhances
CC   drug therapies for tumours. The ribozymes may also be used to study
CC   genetic drift and mutations within cells. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 35 BP; 5 A; 1 C; 4 G; 0 T; 25 U; 0 Other;

 Query Match             0.8%;  Score 22.8;  DB 1;  Length 35;
 Best Local Similarity   8.8%;  Pred. No. 5.4e+02;
 Matches    3;  Conservative   24;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTAA 2188
              ::  ::: :. |::::::: :::: ::::::: ||
Db          1 UUAGUUUUUACUUUUUUUGUUUUGUUUUUUUAAA 34


RESULT 92
ABS64697
ID   ABS64697 standard; DNA; 35 BP.
XX
AC   ABS64697;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Nucleic acid detection method associated polynucleotide #79.
XX
KW   Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW   nanoparticle; viral RNA detection; bacterial DNA detection;
KW   fungal DNA detection; nanoprobe conjugate; ss.
XX
OS   Synthetic.
XX
PN   WO200246472-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US046418.
XX
PR   08-DEC-2000; 2000US-0254392P.
PR   08-DEC-2000; 2000US-0254418P.
PR   11-DEC-2000; 2000US-0255235P.
PR   11-DEC-2000; 2000US-0255236P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
PR   09-APR-2001; 2001US-0282640P.
PR   10-AUG-2001; 2001US-00927777.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-608256/65.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Disclosure; Page 57; 442pp; English.
XX
CC   The invention describes a method of detecting (M1) a nucleic acid having
CC   two portions, involving providing nanoparticles having oligonucleotides
CC   attached to it, which has a sequence complementary to sequence of two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC   allow hybridisation of oligonucleotides with two or more portions of
CC   nucleic acid, and observing a detectable change brought about by
CC   hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC   conjugates (II) and the aggregate probe are useful for detecting two or
CC   more nucleic acids (from a biological source) having at least two
CC   portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC   with a disease, synthetic, or structurally-modified natural or synthetic
CC   RNA or DNA, or a product of a polymerase chain reaction amplification.
CC   (II) is useful for preparing a nanoprobe conjugate for detecting an
CC   analyte, and for detecting a nucleic acid bound to an electrode surface.
CC   (I) and (II) are useful for fabrication, and for separating a selected
CC   nucleic acid having two portions from other nucleic acids. (I), (II) and
CC   the aggregate probe are useful for detecting an analyte (especially
CC   polyvalent analyte) in a sample. This sequence represents a
CC   polynucleotide used to demonstrate the method of the invention
XX
SQ   Sequence 35 BP; 24 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

 Query Match             0.8%;  Score 22.8;  DB 1;  Length 35;
```

```
  Best Local Similarity   79.4%;  Pred. No. 5.4e+02;
  Matches   27;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2767 AGTATTCTTGTTAGAATTGAAAAAAAAAAAAAAA 2800
              | ||| ||| ||| ||   ||||||||||||||||
Db          2 AATATCCTTCTTATAAAAAAAAAAAAAAAAAAAAA 35


RESULT 93
AAL61669
ID   AAL61669 standard; DNA; 35 BP.
XX
AC   AAL61669;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Oligonucleotide #28 used in the nucleic acid detection method.
XX
KW   Nucleic acid detection; fabrication; ss.
XX
OS   Unidentified.
XX
PN   WO2003035829-A2.
XX
PD   01-MAY-2003.
XX
PF   08-OCT-2002; 2002WO-US032088.
XX
PR   09-OCT-2001; 2001US-0327864P.
PR   07-DEC-2001; 2001US-00008978.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Park S,  Taton TA,  Mirkin CA;
XX
DR   WPI; 2003-430409/40.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Disclosure; Page 58-59; 467pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid having two
CC   portions. The method involves providing nanoparticles having
CC   oligonucleotides attached to it which has a sequence complementary to
CC   sequence of two portions of nucleic acid, contacting nucleic acid and
CC   nanoparticles to allow hybridisation of oligonucleotides with two or more
CC   portions of nucleic acid and observing a detectable change brought about
CC   by hybridisation. The method and aggregate probes are useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic or structurally modified natural or
CC   synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. The invention is useful for preparing a nanoprobe
CC   conjugate for detecting an analyte and for detecting a nucleic acid bound
CC   to an electrode surface. It is also useful for fabrication and for
CC   separating a selected nucleic acid having two portions from other nucleic
CC   acids. The present sequence is an oligo used to illustrate the method of
CC   the invention
XX
SQ   Sequence 35 BP; 24 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.8;  DB 1;  Length 35;
  Best Local Similarity   79.4%;  Pred. No. 5.4e+02;
  Matches   27;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2767 AGTATTCTTGTTAGAATTGAAAAAAAAAAAAAAA 2800
              | ||| ||| ||| ||   ||||||||||||||||
Db          2 AATATCCTTCTTATAAAAAAAAAAAAAAAAAAAAA 35


RESULT 94
ABQ80396/c
ID   ABQ80396 standard; DNA; 35 BP.
XX
AC   ABQ80396;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Probe APC 2.
XX
KW   Probe; target; nanoparticle; detection; DNA sequencing; pathogen;
KW   infection; screening; colour change; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Gold-S'-A"
XX
PN   WO2003048769-A1.
XX
PD   12-JUN-2003.
XX
PF   27-NOV-2002; 2002WO-US038069.
XX
PR   30-NOV-2001; 2001US-0334644P.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Storhoff JJ,  Fritz BM,  Herrmann M;
XX
DR   WPI; 2003-617993/58.
XX
PT   Detecting target polynucleotide in a sample, by amplifying target,
PT   hybridizing it to oligonucleotides bound to nanoparticles in nanoparticle
PT   detection system, and determining amount of signal generated due to
PT   binding.
XX
PS   Example 1; Page 35; 74pp; English.
XX
CC   The sequences given in ABQ80394-99 represent probes and targets which
CC   were used in the method of the invention for detecting a target
CC   polynucleotide in a sample. The method comprises amplifying the target,
CC   hybridizing the target to oligonucleotides bound to nanoparticles in a
CC   nanoparticle detection system, determining the amount of signal generated
CC   as a result of binding, optionally repeating the above steps, and
CC   detecting the presence of the target oligonucleotide by analysing for the
CC   amount of signal produced after at least one amplification cycle. The
CC   method is useful for detecting target polynucleotide in a sample, and for
CC   determining the quantity of target polynucleotide in a sample. The method
CC   is useful in research and analytical laboratories in DNA sequencing, in
CC   the field to detect the presence of specific pathogens, in the doctor's
CC   office for quick identification of an infection to assist in prescribing
CC   a drug for treatment, and in homes and health centres for inexpensive
CC   first-line screening. The method is based on observing colour change with
CC   the naked eye, hence the method is cheap, fast, simple, robust, do not
CC   require specialized or expensive equipment, and little or no
CC   instrumentation is required
XX
SQ   Sequence 35 BP; 28 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.8;  DB 1;  Length 35;
  Best Local Similarity   92.3%;  Pred. No. 5.4e+02;
  Matches   24;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTT 2186
              |||  ||||||||||||||||||||
Db         26 TCTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 95
AAQ79096
ID   AAQ79096 standard; DNA; 29 BP.
```

```
XX
AC   AAQ79096;
XX
DT   25-MAR-2003  (revised)
DT   07-AUG-1995  (first entry)
XX
DE   Tobacco PMT PCR primer P-23.
XX
KW   Tobacco; transgenic plant; putrescine-N-methyltransferase; PMT; alkaloid;
KW   nicotine; primer; polymerase chain reaction; PCR; Nicotiana tabacum; ss.
XX
OS   Synthetic.
XX
PN   WO9428142-A1.
XX
PD   08-DEC-1994.
XX
PF   01-JUN-1994;   94WO-US006106.
XX
PR   01-JUN-1993;   93US-00076681.
XX
PA   (PHIM ) PHILIP MORRIS PROD INC.
XX
PI   Wahab SZ,  Malik VS;
XX
DR   WPI; 1995-022814/03.
XX
PT   Recombinant DNA encoding tobacco protein, PMT - useful for producing
PT   transgenic tobacco plants with decreased alkaloid content.
XX
PS   Disclosure; Page 57; 69pp; English.
XX
CC   Forward primer P-18 (AAQ79095), based on an N-terminal methionine and
CC   amino acids 1-7 of a CNBr fragment (AAR67579) of tobacco putrescine-N-
CC   methyltransferase (PMT), and reverse primer P-23 (AAQ79096), were used to
CC   amplify RNA derived from tobacco var. Burley 21 root extract. Clone Q7
CC   was obtained. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 29 BP; 2 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.7e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
                 |||   | ||||||||||||||||||||||
Db          1 TTTGAATTCTTTTTTTTTTTTTTTTTTT 29


RESULT 96
AAA94315/c
ID   AAA94315 standard; DNA; 29 BP.
XX
AC   AAA94315;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 30-P.
XX
KW   RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   29
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US002589.
XX
PR   09-FEB-1999;   99US-00247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions.
XX
PS   Disclosure; Page 43; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides which were
CC   used for the generation of RNA-protein fusions, including fusions having
CC   a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.7e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                 | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 97
AAS00066/c
ID   AAS00066 standard; DNA; 29 BP.
XX
AC   AAS00066;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Synthetic branched encoding molecule sequence.
XX
KW   Addressing element; microarray; protein display;
KW   branched encoding molecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   9. .10
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "AXA, where X is a branching monomer, linked to
FT                   nucleotide 16 of sequence in AAS00065 via a (Hexaethylene
FT                   oxide)n linkage"
FT   modified_base   30
FT                   /*tag=  b
FT                   /mod_base= OTHER
```

```
FT                   /note= "Other= Covalently linked to puromycin"
XX
PN   WO200116352-A1.
XX
PD   08-MAR-2001.
XX
PF   25-AUG-2000; 2000WO-US023414.
XX
PR   27-AUG-1999;   99US-0151261P.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Kuimelis RG;
XX
DR   WPI; 2001-183261/18.
XX
PT   Encoding and sorting in vitro translated proteins, useful for the
PT   identification of desired binding partners, comprises attaching a nucleic
PT   acid linker to the protein and binding an encoding molecule to the
PT   linker.
XX
PS   Example 3; Fig 9B; 48pp; English.
XX
CC   The sequence represents part of a branched encoding molecule used in
CC   methods to hybridise a capture probe to the addressing element of a DNA
CC   linker attached to an in vitro translated protein, in order to immobilise
CC   the protein to a solid support. The new methods are useful for tagging or
CC   encoding in vitro translated proteins with unique and minimal encoding
CC   molecules and sorting these molecules onto solid supports. They are also
CC   useful for the identification of a desired binding partner. The method
CC   allows the use of pre-made sets of universal encoding molecules, such as
CC   nucleic acid(s) (analogues). These can be used in conjunction with
CC   corresponding universal microarrays or sets of microparticles to create
CC   new protein display systems which are flexible, modular, scalable and
CC   cost effective. The method allows the use of nucleic acid analogue which
CC   are not susceptible to enzymatic incorporation or polymerisation and are
CC   superior to conventional DNA/RNA. The proteins can also be labelled with
CC   fluorescent groups which can be used to monitor the protein in real time.
CC   The absence of RNA is advantageous as they can adopt secondary structures
CC   which are difficult to predict and can interfere with hybridisation steps
CC   and protein folding/function
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.7e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 98
AAH20990/c
ID   AAH20990 standard; DNA; 29 BP.
XX
AC   AAH20990;
XX
DT   31-AUG-2001  (first entry)
XX
DE   C-myc epitope puromycin linker primer #1.
XX
KW   C-myc; epitope; detection; amplification; biomedical diagnosis;
KW   environmental monitoring; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200142494-A2.
XX
PD   14-JUN-2001.
XX
PF   20-OCT-2000; 2000WO-EP010336.
XX
PR   10-DEC-1999;   99DE-01059857.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Burgstaller P,  Konz D;
XX
DR   WPI; 2001-381706/40.
XX
PT   System for detecting immobilized analyte, useful e.g. for biomedical
PT   diagnosis, has as detection agent specific polypeptide coupled to nucleic
PT   acid for signal amplification.
XX
PS   Example; Page 6; 12pp; German.
XX
CC   This invention describes a novel test system (A) which comprises at least
CC   one immobilized analyte (I) on an insoluble carrier and a polypeptide
CC   detection agent (II), specific for (I) and conjugated, via a linker, to
CC   an amplifier (III). (A) is used for direct, in vitro detection of (I)
CC   with amplification of the signal by polymerase chain reaction (PCR), or a
CC   related technique, applied to (III). The method is useful in biomedical
CC   diagnosis and environmental monitoring and can be used to detect a wide
CC   range of (I), e.g. diagnostic or pharmaceutical agents, secondary
CC   metabolites, herbicides or pesticides. (A) allow simultaneous, parallel
CC   detection of many different analytes (high throughput capacity),
CC   relatively simply (only a few incubation and washing steps are required)
CC   and with high sensitivity and selectivity. This sequence represents
CC   primer used in the ampification of the c-myc DNA fragment which encodes
CC   an epitope used to illustrate the method of the invention
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.7e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 99
AAK98637/c
ID   AAK98637 standard; DNA; 29 BP.
XX
AC   AAK98637;
XX
DT   19-APR-2002  (first entry)
XX
DE   S cerevisiae alpha factor receptor STE2 vector linker.
XX
KW   Biological material detection; electrophoresis; bioprobe isolation;
KW   alpha factor receptor; STE2; linker; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   29
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "modified by puromycin"
XX
PN   WO200204656-A2.
XX
PD   17-JAN-2002.
XX
PF   26-JUN-2001; 2001WO-EP007259.
XX
PR   07-JUL-2000; 2000DE-01033194.
XX
PA   (XZIL-) XZILLION GMBH & CO KG.
XX
PI   Wagner P,  Polakowski T;
```

```
XX
DR   WPI; 2002-154934/20.
XX
PT   Detecting and purifying biological material by (di)electrophoresis,
PT   useful e.g. for separating tissues and viruses, comprises using a probe
PT   that alters (di)electrophoretic properties.
XX
PS   Example 1; Page 12; 20pp; German.
XX
CC   The present invention relates to a method for the detection or
CC   purification of biological material by electrophoresis, which comprises
CC   (i) treating the biological material containing different species with a
CC   bioprobe and (ii) establishing an electric field for detection or
CC   purification of at least one complex formed between the biological
CC   material being tested and a specifically bound bioprobe. The method is
CC   used for detection and purification of tissue, cells, cell organelles,
CC   viruses, proteins, nucleic acids, lipids and/or other organic compounds.
CC   It can also be used for the isolation of specific bioprobes from a
CC   library of bioprobes. The present sequence is a linker described in the
CC   exemplification of the invention
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 29;
  Best Local Similarity   86.2%;  Pred. No. 3.7e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
             | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 100
AAV48087/c
ID   AAV48087 standard; DNA; 30 BP.
XX
AC   AAV48087;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Oligonucleotide 30-P.
XX
KW   In situ translation; RNA-protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   30
FT                   /*tag=  a
FT                   /note= "Puromycin"
XX
PN   WO9831700-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;   98WO-US000807.
XX
PR   21-JAN-1997;   97US-0035963P.
PR   06-NOV-1997;   97US-0064491P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 1998-414032/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions generated
PT   in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
PT   with altered properties, potentially useful as catalysts or for therapy
PT   or diagnosis.
XX
PS   Disclosure; Page 39; 94pp; English.
XX
CC   The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
CC   variations were used to generate RNA-protein fusions. These were used in
CC   the selection of a specific protein or RNA, by in vitro or in situ
CC   translation of candidate RNA molecules to produce RNA-protein fusions,
CC   then selecting specific RNA protein fusions. The method is used to select
CC   proteins (or DNA encoding them) having altered properties, e.g. for
CC   identification of new binding reagents, to identify improved human
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The methods allow many
CC   rounds of selection and amplification to be performed, resulting in
CC   enrichment of even very rare molecules and allowing isolation of proteins
CC   that bind specifically to almost any compound or catalyse almost any
CC   reaction
XX
SQ   Sequence 30 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 22.6;  DB 1;  Length 30;
  Best Local Similarity   86.2%;  Pred. No. 4e+02;
  Matches   25;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2153 GATTTTTTTCTCCTTTTTTTTTTTTTTT 2181
             | ||||||| |  ||||||||||||||||
Db         29 GGTTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 101
ABL35101/c
ID   ABL35101 standard; DNA; 30 BP.
XX
AC   ABL35101;
XX
DT   04-APR-2002  (first entry)
XX
DE   Phosphorothioate substituted RNA/DNA hybrid oligonucleotide SEQ ID NO: 7.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .14
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
FT   misc_RNA        1. .14
FT                   /*tag=  b
FT   misc_RNA        17. .30
FT                   /*tag=  c
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
```

PS Example 1; Page 30; 68pp; English.
XX
CC The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention
XX
SQ Sequence 30 BP; 28 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 22.6; DB 1; Length 30;
Best Local Similarity 86.2%; Pred. No. 4e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2151 TTGATTTTTTTCTCCTTTTTTTTTTTTT 2179
|| ||||||| || ||||||||||||||
Db 29 TTTTTTTTTTTTCGTTTTTTTTTTTTT 1

RESULT 102
ABK86169/c
ID ABK86169 standard; DNA; 24 BP.
XX
AC ABK86169;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #2 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
PN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045401.
XX
PR 01-NOV-2000; 2000US-0244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
DR WPI; 2002-508123/54.
XX
PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identimer having a oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end.
XX
PS Disclosure; Page 11; 45pp; English.
XX
CC The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identimer having
CC a specific oligo-dT primer sequence, where the identimer comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level, to determine mRNA expression level and mRNA identification
CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence in formation. The present
CC sequence represents an oligo dT primer used in the method of the
CC invention
XX
SQ Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 2.4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTAAC 2189
|||||||||||||||||||| |||
Db 24 TTTTTTTTTTTTTTTTTTTTAAAC 1

RESULT 103
ABK86168
ID ABK86168 standard; DNA; 24 BP.
XX
AC ABK86168;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #1 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
PN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045401.
XX
PR 01-NOV-2000; 2000US-0244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
DR WPI; 2002-508123/54.
XX
PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identimer having a oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end.
XX
PS Disclosure; Page 11; 45pp; English.
XX
CC The invention relates to systems for identification and characterisation
CC of gene expression in one or more samples, comprising an identimer having
CC a specific oligo-dT primer sequence, where the identimer comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing

```
CC   methods: (a) prior sequence information or clone library construction is
CC   not needed to enable the assay; (b) provides immediate sequence
CC   information in addition to information concerning changes or differences
CC   in mRNA level, to determine mRNA expression level and mRNA identification
CC   in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC   sample for subsequent investigation by common molecular biology
CC   techniques; and (d) does not require prior knowledge of the sequence of
CC   the genome of the organism under investigation and can be employed in
CC   organisms lacking significant genomic sequence in formation. The present
CC   sequence represents an oligo dT primer used in the method of the
CC   invention
XX
SQ   Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 24;
  Best Local Similarity   95.8%;  Pred. No. 2.4e+02;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTTTTAAAC 24


RESULT 104
AAV42215
ID   AAV42215 standard; DNA; 25 BP.
XX
AC   AAV42215;
XX
DT   16-OCT-1998  (first entry)
XX
DE   Sequencing primer used to exemplify the invention.
XX
KW   Incyte clone 1; fluorescent label; probe; primer; DNA sequencing; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "labelled with the donor carboxyfluoscein"
FT   modified_base   7
FT                   /*tag=  b
FT                   /note= "optionally laballed with the acceptor 6-
FT                   carboxyrhodamine"
FT   modified_base   14
FT                   /*tag=  b
FT                   /note= "optionally laballed with the acceptor 6-
FT                   carboxyrhodamine"
FT   modified_base   17
FT                   /*tag=  a
FT                   /note= "optionally labelled with the donor
FT                   carboxyfluoscein"
FT   modified_base   17
FT                   /*tag=  b
FT                   /note= "optionally laballed with the acceptor 6-
FT                   carboxyrhodamine"
XX
PN   WO9831834-A1.
XX
PD   23-JUL-1998.
XX
PF   12-DEC-1997;   97WO-US022914.
XX
PR   15-JAN-1997;   97US-00784162.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Ju J;
XX
DR   WPI; 1998-414127/35.
XX
PT   Set of energy-transfer fluorescent labels with donor and acceptor at
PT   different separations - useful for DNA sequencing allows use of fewer
PT   analysing wavelengths or an increased throughput.
XX
PS   Example 1; Page 14; 30pp; English.
XX
CC   The present sequence exxemplified the primer of the invention, and is
CC   used to sequence Incyte clone 1 (AAV42737). The primer of the invention
CC   is labelled with a set of at least 2 different fluorescent labels. The
CC   set comprises an energy-transfer fluorescent label with at least 1 each
CC   of a donor fluorophore and an acceptor fluorophore capable of energy
CC   transfer, and separated by a distance x, and a second similar fluorescent
CC   label in which the separation distance is y, x and y being sufficiently
CC   different for the two fluorescent labels to produce distinct fluorescent
CC   signals. Fluorescent labels are useful in multicomponent analyses, e.g.
CC   as probes for fluorescent in situ hybridisation or especially as primers
CC   for DNA sequencing
XX
SQ   Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 25;
  Best Local Similarity   95.8%;  Pred. No. 2.7e+02;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||||||||| ||
Db          2 TTTTTTTTTTTTTTTTTTTTTTAC 25


RESULT 105
ADC16682
ID   ADC16682 standard; DNA; 30 BP.
XX
AC   ADC16682;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Aminoacylation RNA molecule related DNA oligo, P3-2.
XX
KW   ribozyme; aminoacylate; tRNA; non-cognate; catalytic RNA molecule; cis;
KW   aminoacylation; trans; proteomic; ds.
XX
OS   Unidentified.
XX
PN   WO2003070740-A1.
XX
PD   28-AUG-2003.
XX
PF   18-FEB-2003; 2003WO-US005007.
XX
PR   15-FEB-2002; 2002US-0357424P.
XX
PA   (UYNY ) UNIV NEW YORK STATE RES FOUND.
XX
PI   Suga H,  Murakami H,  Saito H;
XX
DR   WPI; 2003-748198/70.
XX
PT   New polynucleotide, useful for preparing peptides containing non-cognate
PT   amino acids, encodes ribozyme that can aminoacylate tRNA with such amino
PT   acids.
XX
PS   Example 3; SEQ ID NO 42; 85pp; English.
XX
CC   The invention relates to a novel polynucleotide comprising a sequence
CC   encoding a ribozyme that can aminoacylate tRNA with a non-cognate amino
CC   acid. Ribozymes encoded by the polynucleotide of the invention are used
CC   to prepare polypeptides that contain non-cognate, including non-natural,
CC   amino acids. The invention more specifically provides catalytic RNA
CC   molecules having cis aminoacylation activity with a catalytic and
CC   aminoacylation domain, or an RNA molecule with trans aminoacylation
CC   activity with only a catalytic domain. The products of the invention are
CC   potentially useful for biomedical and therapeutic use, e.g. for probing
CC   the structure and function of proteins; preparation of peptide libraries
```

```
CC   and in proteomics. This polynucleotide sequence represents a DNA oligo
CC   relating to the RNA molecule with aminoacylation activity of the
CC   invention.
XX
SQ   Sequence 30 BP; 3 A; 5 C; 1 G; 21 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 30;
  Best Local Similarity   95.8%;  Pred. No. 4.3e+02;
  Matches   23;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTTTTACCT 24


RESULT 106
AAA94322
ID   AAA94322 standard; DNA; 33 BP.
XX
AC   AAA94322;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 34-P.
XX
KW   RNA-protein fusion; protein library; protein isolation; DNA-RNA hybrid;
KW   gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .13
FT                   /*tag=  a
FT                   /label= RNA
FT   modified_base   33
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US002589.
XX
PR   09-FEB-1999;   99US-00247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions.
XX
PS   Disclosure; Page 44; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides which were
CC   used for the generation of RNA-protein fusions, including fusions having
CC   a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form
XX
SQ   Sequence 33 BP; 22 A; 4 C; 6 G; 0 T; 1 U; 0 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 33;
  Best Local Similarity   91.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAA 2803
              ||| :||||||||||||||||||
Db          8 GAACUGAAAAAAAAAAAAAAAAAA 31


RESULT 107
AAV12929
ID   AAV12929 standard; DNA; 34 BP.
XX
AC   AAV12929;
XX
DT   15-MAY-1998  (first entry)
XX
DE   Oligonucleotide SEQ ID NO:38 from US5174320 Example 18.
XX
KW   Synthesis; selection; amplification; circular oligonucleotide;
KW   rolling circle synthesis; diagnosis; therapeutic agent; ss.
XX
OS   Synthetic.
XX
PN   US5714320-A.
XX
PD   03-FEB-1998.
XX
PF   23-FEB-1995;   95US-00393439.
XX
PR   15-APR-1993;   93US-00047860.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-144278/13.
XX
PT   Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
PT   template to produce oligonucleotide multimer for cleavage.
XX
PS   Example 18; Col 57; 38pp; English.
XX
CC   The present sequence represents an oligonucleotide used in an example of
CC   the present invention. The present invention describes a method for
CC   synthesising a selected oligonucleotide (I) having well defined ends. The
CC   method comprises: (a) annealing a primer to a single-stranded (ss)
CC   circular template to yield a primed circular template, where the template
CC   comprises: (i) at least one nucleotide sequence complementary to (I); and
CC   (ii) at least one nucleotide effective to produce a cleavage site in the
CC   oligonucleotide multimer; (b) combining the primed circular template with
CC   at least two types of nucleotide triphosphates and a polymerase enzyme
CC   without the addition of auxiliary proteins to yield a ss oligonucleotide
CC   multimer complementary to the circular oligonucleotide template,
CC   comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC   multimer at the cleavage site to produce (I) having well defined ends.
CC   The method is used for the large-scale synthesis of DNA and RNA oligomers
CC   for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX
SQ   Sequence 34 BP; 1 A; 7 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 34;
  Best Local Similarity   81.2%;  Pred. No. 6e+02;
  Matches   26;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
```

```
Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              || ||||||| | |||| ||| |||||||||
Db          2 TTCTTTTCTCGATCTTTTCTTTCTTTTTTTT 33


RESULT 108
AAV59243
ID   AAV59243 standard; DNA; 34 BP.
XX
AC   AAV59243;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Small synthetic DNA circle sequence ID No.38.
XX
KW   ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent;
KW   circular; cyclic.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1
FT                   /*tag=  a
FT                   /note= "Bound to position 34"
FT   modified_base   4
FT                   /*tag=  c
FT                   /note= "5-methyl-C residue"
FT   modified_base   9
FT                   /*tag=  d
FT                   /note= "5-methyl-C residue"
FT   modified_base   15
FT                   /*tag=  e
FT                   /note= "5-methyl-C residue"
FT   modified_base   20
FT                   /*tag=  f
FT                   /note= "5-methyl-C residue"
FT   modified_base   24
FT                   /*tag=  g
FT                   /note= "5-methyl-C residue"
FT   modified_base   34
FT                   /*tag=  h
FT                   /note= "5-methyl-C residue"
FT   misc_binding    34
FT                   /*tag=  b
FT                   /note= "Bound to position 1"
XX
PN   WO9838300-A1.
XX
PD   03-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US003784.
XX
PR   26-FEB-1997;   97US-00805631.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-481202/41.
XX
PT   Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT   oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
PT   polymerase to form multimer(s) which can be cleaved.
XX
PS   Example 18; Page 59; 100pp; English.
XX
CC   The oligomer sequence ID No.38 was used in an example of the invention
CC   for synthesising an RNA oligonucleotide, comprising combining a single-
CC   stranded circular oligonucleotide template comprising at least one copy
CC   of a nucleotide sequence complementary to the sequence of the desired RNA
CC   oligonucleotide with at least 2 types of ribonucleotide triphosphate and
CC   a polymerase enzyme to yield a single-stranded RNA oligonucleotide
CC   multimer complementary to the circular oligonucleotide template, where
CC   the RNA oligonucleotide multimer comprises multiple copies of the desired
CC   RNA oligonucleotide. The methods can be used for producing RNA
CC   oligonucleotides having a specific sequence and well defined ends. The
CC   RNA oligonucleotides produced can be used as probes, standards and
CC   diagnostic or therapeutic agents. They can be used for modifying the
CC   structure or function of a target molecule. They can also be used to
CC   cleave disease-associated RNA, DNA or protein
XX
SQ   Sequence 34 BP; 1 A; 7 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 34;
  Best Local Similarity   81.2%;  Pred. No. 6e+02;
  Matches   26;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              || ||||||| | |||| ||| |||||||||
Db          2 TTCTTTTCTCGATCTTTTCTTTCTTTTTTTT 33


RESULT 109
AAV48094
ID   AAV48094 standard; DNA; 34 BP.
XX
AC   AAV48094;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Oligonucleotide 34-P.
XX
KW   In situ translation; RNA-protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss; rRNA/DNA hybrid.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   34
FT                   /*tag=  a
FT                   /note= "Puromycin"
XX
PN   WO9831700-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;   98WO-US000807.
XX
PR   21-JAN-1997;   97US-0035963P.
PR   06-NOV-1997;   97US-0064491P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 1998-414032/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions generated
PT   in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
PT   with altered properties, potentially useful as catalysts or for therapy
PT   or diagnosis.
XX
PS   Disclosure; Page 40; 94pp; English.
XX
CC   The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
CC   variations were used to generate RNA-protein fusions. These were used in
CC   the selection of a specific protein or RNA, by in vitro or in situ
CC   translation of candidate RNA molecules to produce RNA-protein fusions,
CC   then selecting specific RNA protein fusions. The method is used to select
CC   proteins (or DNA encoding them) having altered properties, e.g. for
CC   identification of new binding reagents, to identify improved human
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The methods allow many
CC   rounds of selection and amplification to be performed, resulting in
CC   enrichment of even very rare molecules and allowing isolation of proteins
```

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CC   that bind specifically to almost any compound or catalyse almost any
CC   reaction
XX
SQ   Sequence 34 BP; 22 A; 4 C; 6 G; 0 T; 1 U; 1 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 34;
  Best Local Similarity   91.7%;  Pred. No. 6e+02;
  Matches   22;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAA 2803
              ||| :||||||||||||||||||||
Db          8 GAACUGAAAAAAAAAAAAAAAAAA 31


RESULT 110
AAC90605
ID   AAC90605 standard; RNA; 34 BP.
XX
AC   AAC90605;
XX
DT   20-MAR-2001  (first entry)
XX
DE   Tomato spotted wilt virus S RNA partial sequence #9.
XX
KW   Tospovirus resistance; transgenic plant; tomato spotted wilt virus;
KW   Impatiens necrotic spot virus; TSWV; ss.
XX
OS   Tomato spotted wilt virus.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1
FT                   /*tag=  a
FT                   /bound_moiety= "binds nucleotide 32 of AAC89654"
FT   misc_binding    2. .10
FT                   /*tag=  b
FT                   /bound_moiety= "binds nucleotides 30-22 of AAC89654"
FT   misc_binding    17. .32
FT                   /*tag=  c
FT                   /bound_moiety= "binds nucleotides 30-5 of AAC89564"
FT   misc_binding    33. .34
FT                   /*tag=  d
FT                   /bound_moiety= "binds nucleotides 1-2 of AAC89654"
XX
PN   US6150585-A.
XX
PD   21-NOV-2000.
XX
PF   26-NOV-1996;   96US-00757011.
XX
PR   03-NOV-1989;   89US-00431259.
PR   05-DEC-1989;   89US-00446024.
PR   02-MAY-1991;   91US-00694734.
PR   14-APR-1993;   93US-00047346.
PR   26-OCT-1993;   93US-00143397.
PR   27-JUL-1994;   94US-00280903.
XX
PA   (NOVS ) NOVARTIS FINANCE CORP.
XX
PI   Peters D,  Gielen JJL,  De Haan PT,  Van Grinsven MQJM,  Kool AJ;
PI   Goldbach RW;
XX
DR   WPI; 2001-060031/07.
XX
PT   Recombinant DNA construct comprising a DNA sequence encoding an RNA
PT   sequence that codes for a tospovirus protein, useful for producing plants
PT   with reduced susceptibility to tospovirus infection.
XX
PS   Example 9; Fig 16B; 49pp; English.
XX
CC   The present invention provides DNA constructs encoding RNA sequences from
CC   a tospovirus which can be used to produce transgenic plants with immunity
CC   to tospoviruses. Examples of tospoviruses include the tomato spotted wilt
CC   virus and the Impatiens necrotic spot virus
XX
SQ   Sequence 34 BP; 4 A; 0 C; 2 G; 0 T; 28 U; 0 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 34;
  Best Local Similarity   3.1%;  Pred. No. 6e+02;
  Matches    1;  Conservative   25;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTTTA 2187
              ::::::  :  ::: ::::::: :::: ::::::|
Db          2 UUUUUUGUUUUUUAUUUUUUAUUUUAUUUUUA 33


RESULT 111
AAD46356/c
ID   AAD46356 standard; DNA; 35 BP.
XX
AC   AAD46356;
XX
DT   29-AUG-2003  (revised)
DT   07-AUG-2003  (revised)
DT   27-JAN-2003  (first entry)
XX
DE   Vp3 oligonucleotide used to generate pox virus late promoter.
XX
KW   Recombinant leporipox virus; vector vaccine; treatment; prophylaxis;
KW   infectious disease; promoter; ss.
XX
OS   Viruses.
XX
PN   WO200272852-A2.
XX
PD   19-SEP-2002.
XX
PF   07-MAR-2002; 2002WO-EP002858.
XX
PR   08-MAR-2001; 2001EP-00200869.
XX
PA   (ALKU ) AKZO NOBEL NV.
XX
PI   Spibey N;
XX
DR   WPI; 2002-723365/78.
XX
PT   Use of a live, recombinant leporipox virus in the manufacture of a vector
PT   vaccine for the treatment and/or prophylaxis of infectious disease in non
PT   -lepori species.
XX
PS   Example 1; Page 9; 28pp; English.
XX
CC   The invention relates to the use of a live, recombinant leporipox virus
CC   (which comprises exogenous DNA that is operably linked to at least one
CC   expression control element and is incorporated in a non-essential region
CC   of the virus genome) in the manufacture of a vector vaccine for the
CC   treatment and/or prophylaxis of infectious disease in non-lepori species
CC   such as felines or canines. The present sequence is an oligonucleotide
CC   used to generate pox virus late promoter. This sequence is used in the
CC   exemplification of the invention. (Updated on 07-AUG-2003 to correct OS
CC   field.) (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ   Sequence 35 BP; 5 A; 4 C; 2 G; 24 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.4;  DB 1;  Length 35;
  Best Local Similarity   81.2%;  Pred. No. 6.4e+02;
  Matches   26;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2773 CTTGTTAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | | | |||  | ||||||||||||||||||
Db         33 CATTTAAGATCTAAAAAAAAAAAAAAAAAAA 2

RESULT 112
AAN70281
ID   AAN70281 standard; DNA; 27 BP.
```

```
XX
AC   AAN70281;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC071 (HL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   81.5%;  Pred. No. 3.6e+02;
  Matches   22;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||::|||||||||||
Db          1 TTTTTTTTTTTTTTTTUUTTTTTTTTT 27


RESULT 113
AAN70274
ID   AAN70274 standard; DNA; 27 BP.
XX
AC   AAN70274;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC046 (PL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   70.4%;  Pred. No. 3.6e+02;
  Matches   19;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  :::::|||||||||||
Db          1 TTTTTTTTTTUUUUUUTTTTTTTTTT 27


RESULT 114
AAN92240
ID   AAN92240 standard; DNA; 27 BP.
XX
AC   AAN92240;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRC046.
XX
KW   Probe MRC046; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .10
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    11. .16
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    17. .27
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
```

```
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO46 is bound by a permanent linkage to a solid support at its 3'
CC   end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   70.4%;  Pred. No. 3.6e+02;
  Matches   19;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                 ||||||| |  :::::|||||||||||
Db          1 TTTTTTTTTTUUUUUUTTTTTTTTTT 27


RESULT 115
AAN92247
ID   AAN92247 standard; DNA; 27 BP.
XX
AC   AAN92247;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRCO71.
XX
KW   Probe MRCO71; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    16. .17
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    18. .27
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO71 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   81.5%;  Pred. No. 3.6e+02;
  Matches   22;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                 ||||||| |  ||||::||||||||||
Db          1 TTTTTTTTTTTTTTTUUTTTTTTTTTT 27


RESULT 116
AAQ40854/c
ID   AAQ40854 standard; DNA; 27 BP.
XX
AC   AAQ40854;
XX
DT   23-SEP-1993  (first entry)
XX
DE   DNA sequence used in DNA replication method.
XX
KW   ss.
XX
OS   Synthetic.
XX
PN   JP05103673-A.
XX
PD   27-APR-1993.
XX
PF   26-AUG-1991;   91JP-00240525.
XX
PR   26-AUG-1991;   91JP-00240525.
XX
PA   (UYAR-) UNIV ARIZONA.
XX
DR   WPI; 1993-171830/21.
XX
PT   Replication of DNA - useful in genetic engineering and medical
PT   applications.
XX
PS   Disclosure; Page 20; 20pp; Japanese.
XX
CC   The sequence is given in the disclosure to illustrate the invention
XX
SQ   Sequence 27 BP; 27 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3.6e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
                 ||||||| |  ||||||||||||||||
Db         27 TTTTTTTTTTTTTTTTTTTTTTTTTT 1


RESULT 117
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```
AAF99706
ID   AAF99706 standard; DNA; 27 BP.
XX
AC   AAF99706;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #822.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3.6e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTT 27


RESULT 118
ABS78427
ID   ABS78427 standard; DNA; 27 BP.
XX
AC   ABS78427;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #911.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 35; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3.6e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTT 27


RESULT 119
ABL39406
ID   ABL39406 standard; DNA; 27 BP.
XX
AC   ABL39406;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 842.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
```

```
FT   modified_base   1. .27
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 310; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3.6e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTT 27


RESULT 120
ACH03245
ID   ACH03245 standard; DNA; 27 BP.
XX
AC   ACH03245;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #880.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 32; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3.6e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTT 27


RESULT 121
ADB37208
ID   ADB37208 standard; DNA; 27 BP.
XX
AC   ADB37208;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #822.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 17; 221pp; English.
XX
```

```
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 27;
  Best Local Similarity   88.9%;  Pred. No. 3.6e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTT 2181
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTTT 27


RESULT 122
ADC60749
ID   ADC60749 standard; DNA; 33 BP.
XX
AC   ADC60749;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Termitomyces albuminosus acidic peroxidase-related RT-PCR primer.
XX
KW   acidic peroxidase; TAP; organochlorine compound;
KW   waste water purification; Western blotting; ss; PCR; RT-PCR; primer.
XX
OS   Termitomyces albuminosus.
XX
PN   JP2003070473-A.
XX
PD   11-MAR-2003.
XX
PF   03-SEP-2001; 2001JP-00266069.
XX
PR   03-SEP-2001; 2001JP-00266069.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
PA   (RIKA ) RIKAGAKU KENKYUSHO.
XX
DR   WPI; 2003-590855/56.
XX
PT   New protein with acidic peroxidase activity, derived from Termitomyces
PT   albuminosus ATTC42010, useful in the analysis of organochlorine compounds
PT   during waste water purification processes.
XX
PS   Example 2; SEQ ID NO 3; 12pp; Japanese.
XX
CC   The invention relates to a novel acidic peroxidase protein (TAP) obtained
CC   from Termitomyces albuminosus ATTC42010. The polypeptide of the invention
CC   may be useful in the analysis of organochlorine compounds during waste
CC   water purification processes and in Western blotting techniques. The
CC   polypeptide has enhanced activity under acidic pH relative to
CC   conventional peroxidases. The current sequence is that of the
CC   Termitomyces albuminosus acidic peroxidase-related RT-PCR primer of the
CC   invention.
XX
SQ   Sequence 33 BP; 2 A; 5 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 33;
  Best Local Similarity   88.9%;  Pred. No. 6e+02;
  Matches   24;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2158 TTTCTCCTTTTTTTTTTTTTTTTTT 2184
              | |||  ||||||||||||||||||
Db          7 TCTTCAGCTTTTTTTTTTTTTTTTT 33


RESULT 123
AAL31948
ID   AAL31948 standard; DNA; 43 BP.
XX
AC   AAL31948;
XX
DT   24-JAN-2002  (first entry)
XX
DE   Human SNP oligonucleotide #5156.
XX
KW   Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW   neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW   amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW   cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW   complement related protein; cytochrome; kinesin; cytokine; interferon;
KW   interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW   multifactorial disease; autoimmune disease; infection;
KW   nervous system disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO200147944-A2.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035498.
XX
PR   28-DEC-1999;   99US-0173419P.
PR   27-DEC-2000; 2000US-00173419.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach M;
XX
DR   WPI; 2001-465210/50.
XX
PT   Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT   oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT   autoimmune diseases and infections.
XX
PS   Claim 1; Page 2871; 4143pp; English.
XX
CC   The present invention relates to oligonucleotides encoding polymorphic
CC   variants of proteins related to amylases, amyloid proteins, angiopoietin,
CC   apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC   histones, kinases, colony stimulating factors, complement related
CC   proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
CC   protein coupled receptors and thioesterases. The present sequence is one
CC   such oligonucleotide. The oligonucleotides and the peptides encoded by
CC   them may be used in the prevention, diagnosis and treatment of diseases
CC   associated with inappropriate expression of the proteins listed above.
CC   Disorders that may be prevented, diagnosed and/or treated include
CC   multifactorial diseases with a genetic component, such as autoimmune
CC   diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC   systemic lupus erythromatosus and Grave's disease), inflammation, cancer
CC   (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC   leukaemia), diseases of the nervous system and an infection of pathogenic
CC   organisms
XX
SQ   Sequence 43 BP; 9 A; 4 C; 2 G; 28 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22.2;  DB 1;  Length 43;
  Best Local Similarity   69.8%;  Pred. No. 1.1e+03;
  Matches   30;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTGAAAGTTAACTCTTCAAAT 2211
              ||||||||||||||||||    ||   |||  ||  |||   ||
Db          1 TTTTTTTTTTTTTTTTTTCCTTTCTGAAGAAAAAACTTTTTAT 43


RESULT 124
AAQ30432
ID   AAQ30432 standard; DNA; 23 BP.
XX
```

```
AC   AAQ30432;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer IL6805 for forming triplex with HUMIL6 target duplex.
XX
KW   Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW   malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
FT   misc_feature     11. .12
FT                    /*tag=  d
FT                    /note= "o-xyloso dimer synthon linkage"
FT   misc_feature     12. .23
FT                    /*tag=  c
FT                    /label= inverted_polarity_region
FT                    /note= "see comments"
FT   modified_base    23
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 71; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC   concd. on one strand of the duplex. The oligomer, and others like it are
CC   useful in diagnosis and therapy of diseases characterised by specific DNA
CC   duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC   tumours and inflammation. The triple helices form under mild conditions
CC   thus assays may be carried out without subjecting the test specimen to
CC   harsh conditions. The oligomer contains an inverted polarity region
CC   formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC   (nucleotides have the 3'positions of xylose sugars linked via the o-
CC   xylene ring). Two nucleotides are coupled through a xylene residue to
CC   form the dimer synthon. This additional modifications may render the
CC   oligomer stable to nuclease activity. The oligomer is able to inhibit
CC   gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||||
Db          1 CTTTTTTTTTTTTTTTTTTTTT 22


RESULT 125
AAQ30430
ID   AAQ30430 standard; DNA; 23 BP.
XX
AC   AAQ30430;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer IL6803 for forming triplex with HUMIL6 target duplex.
XX
KW   Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW   malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
FT   misc_feature     11. .12
FT                    /*tag=  d
FT                    /note= "o-xyloso dimer synthon linkage"
FT   misc_feature     12. .23
FT                    /*tag=  c
FT                    /label= inverted_polarity_region
FT                    /note= "see comments"
FT   modified_base    23
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 71; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
```

CC interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC concd. on one strand of the duplex. The oligomer, and others like it are
CC useful in diagnosis and therapy of diseases characterised by specific DNA
CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC tumours and inflammation. The triple helices form under mild conditions
CC thus assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer contains an inverted polarity region
CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC (nucleotides have the 3'positions of xylose sugars linked via the o-
CC xylene ring). Two nucleotides are coupled through a xylene residue to
CC form the dimer synthon. This additional modifications may render the
CC oligomer stable to nuclease activity. The oligomer is able to inhibit
CC gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||||
Db 2 TTTTTTTTTTTTTTTTTTTTTA 23

RESULT 126
ABL01773/c
ID ABL01773 standard; DNA; 23 BP.
XX
AC ABL01773;
XX
DT 18-MAR-2002 (first entry)
XX
DE Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.
XX
KW Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;
KW hereditary non-polyposis colorectal cancer; ds.
XX
OS Homo sapiens.
XX
PN US2001044936-A1.
XX
PD 22-NOV-2001.
XX
PF 22-OCT-1999; 99US-00426548.
XX
PR 22-OCT-1998; 98US-0105180P.
XX
PA (ROBB/) ROBBINS D.
PA (LING/) LIN-GOERKE J L.
PA (LING/) LING J C.
XX
PI Robbins D, Lin-Goerke JL, Ling JC;
XX
DR WPI; 2002-105577/14.
XX
PT New variants of the human MLH1 and MSH2 genes for diagnosing or
PT determining a predisposition for hereditary non-polyposis colorectal
PT cancer.
XX
PS Disclosure; Page 4; 38pp; English.
XX
CC The present invention describes a variant human MLH1 or MSH2 gene. Also
CC described are: (1) a method for diagnosing or predicting susceptibility
CC to hereditary non-polyposis colorectal cancer (HNPCC), comprising
CC screening a DNA sample for the variant MLH1 or MSH2 gene where presence
CC of the variant indicates presence of, or susceptibility to HNPCC; (2) a
CC method of identifying mutants in splice donor or acceptor sites of a
CC human MLH1 gene, comprising sequencing splice donor or acceptor sites of
CC the gene with intronic primers for the human MLH1 gene and analysing the
CC sequence to identify any mutants; (3) a method of identifying mutants in
CC splice donor or acceptor sites of a human MSH2 gene, comprising
CC sequencing splice donor or acceptor sites of the gene with intronic
CC primers for the human MSH2 gene and analysing the sequence to identify
CC any mutants; and (4) a transgenic model system for colorectal cancer
CC comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and
CC hMSH2 variants are used to diagnose or determine a patients
CC susceptibility to hereditary non-polyposis colorectal cancer. ABL01648 to
CC ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene
CC fragments from the present invention. ABL01832 to ABL01839 represent
CC mutagenic primers used in the exemplification of the present invention
XX
SQ Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||||
Db 23 TTTTTTTTTTTTTTTTTTTTTA 2

RESULT 127
AAI66361
ID AAI66361 standard; DNA; 24 BP.
XX
AC AAI66361;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX
KW Human; phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer;
KW haemopathy; development disorder; HIV infection; immunological disease;
KW inflammation; gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200175014-A2.
XX
PD 11-OCT-2001.
XX
PF 16-MAR-2001; 2001WO-CN000328.
XX
PR 17-MAR-2000; 2000CN-00114973.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-025836/03.
XX
PT New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and
PT treating malignant tumor, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations.
XX
PS Example 2; Page 12; 34pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in
CC the treatment of cancer, haemopathy, HIV infection, development
CC disorders, immunological diseases and inflammation. The present sequence
CC is a PCR primer for the coding sequence of the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2167 TTTTTTTTTTTTTTTTTTTTAA 2188
||||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTTAA 22

```
RESULT 128
AAX84259
ID   AAX84259 standard; DNA; 25 BP.
XX
AC   AAX84259;
XX
DT   08-SEP-1999  (first entry)
XX
DE   PCR primer for human Nck associated protein 1 coding sequence.
XX
KW   Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW   therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931239-A1.
XX
PD   24-JUN-1999.
XX
PF   14-DEC-1998;   98WO-JP005646.
XX
PR   15-DEC-1997;   97JP-00363183.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SAKA/) SAKAKI Y.
XX
PI   Sakaki Y;
XX
DR   WPI; 1999-395181/33.
XX
PT   Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT   Alzheimer's disease.
XX
PS   Disclosure; Page 76; 90pp; Japanese.
XX
CC   This sequence represents a PCR primer used to isolate DNA encoding the
CC   human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC   apoptosis. The protein can be used in the investigation, diagnosis and
CC   treatment (e.g. by gene therapy) of Alzheimer's disease
XX
SQ   Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||
Db          4 TTTTTTTTTTTTTTTTTTTTA 25


RESULT 129
AAD34264/c
ID   AAD34264 standard; DNA; 25 BP.
XX
AC   AAD34264;
XX
DT   16-JUL-2002  (first entry)
XX
DE   Human CYP2D6 gene polymorphic site 385 detecting sense 5' oligo.
XX
KW   Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
KW   ligase-based sequenced determination; drug metabolism; chromosome 22; ss.
XX
OS   Homo sapiens.
XX
PN   WO200218638-A2.
XX
PD   07-MAR-2002.
XX
PF   27-AUG-2001; 2001WO-IB001544.
XX
PR   30-AUG-2000; 2000GB-00021286.
XX
PA   (GEMI-) GEMINI GENOMICS PLC.
XX
PI   Risinger C,  Andersson MK,  Lewander T,  Oliasson E;
XX
DR   WPI; 2002-329785/36.
XX
PT   New sequence determination oligonucleotides, useful for detecting
PT   polymorphic sites in a 5' flanking region of a CYP2D6 gene, as
PT   hybridization probes, as components of diagnostic assays, or in ligase-
PT   based sequence determination.
XX
PS   Claim 2; Page 23; 63pp; English.
XX
CC   The invention relates to sequence determination oligonucleotides for
CC   detecting polymorphic sites in a 5' flanking region of cytochrome P450
CC   2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many
CC   different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The
CC   oligonucleotides may be used as in situ hybridisation probes, in ligase-
CC   based sequenced determination, as components of diagnostic assays, as
CC   probes in sequence determination methods based on mismatches, as
CC   hybridisation-based diagnostic assays, and as components of diagnostic
CC   microarray. CYP2D6 is useful to predict variations in an individual's
CC   ability to metabolise certain drugs. The present sequence is a sense
CC   oligonucleotide used for detecting of human CYP2D6 gene 5' flanking
CC   region single nucleotide polymorphism (SNP)
XX
SQ   Sequence 25 BP; 22 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.2e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db         25 CTTTTTTTTTTTTTTTTTTTT 4


RESULT 130
AAD03682
ID   AAD03682 standard; DNA; 26 BP.
XX
AC   AAD03682;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Human full length zcytor13 cDNA isolating polyA PCR primer, ZC7764b.
XX
KW   Human; phosphodiesterase; PDE; zcytor13; antiasthmatic; antiarthritic;
KW   antipsoriatic; cytostatic; antiatherosclerotic; antiinfertility;
KW   cardiant; antiinflammatory; dermatological; wound healing; antiviral;
KW   antibacterial; therapy; inflammatory bowel disease; diverticulitis;
KW   spermatogenesis; sperm capacitation; immunocontraceptive; vaccine;
KW   cancer; reperfusion ischaemia; psoriasis; melanoma; myocarditis; PID;
KW   pelvic inflammatory disease; eczema; scleroderma; vasoconstriction;
KW   heart arrhythmia; congestive heart disease; muscle spasm; fatigue;
KW   chromosomal abnormality; gene therapy; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200125444-A2.
XX
PD   12-APR-2001.
XX
PF   06-OCT-2000; 2000WO-US027734.
XX
PR   07-OCT-1999;   99US-00414025.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Novak JE,  Gao Z;
```

XX
DR WPI; 2001-266312/27.
XX
PT Novel human phosphodiesterase polypeptide, zcytor13 and polynucleotide
PT encoding it, for detecting human chromosomal abnormalities, identifying
PT modulators and treating inflammatory and cardiovascular diseases.
XX
PS Example 1C; Page 118; 122pp; English.
XX
CC The patent discloses novel human phosphodiesterase (PDE), zcytor13 cDNA
CC and its corresponding protein. Zcytor13 protein is used to promote wound
CC healing in tissues, to exhibit anti-bacterial and anti-viral effects and
CC to identify modulators (e.g. agonists or antagonists). Zcytor13, its
CC agonists or antagonists are useful in the treatment of inflammatory heart
CC or cardiovascular conditions, muscle inflammation, inflammation during
CC and after surgery, arthritis, asthma, inflammatory bowel disease or
CC diverticulitis, for modulating spermatogenesis, sperm capacitation, as
CC immunocontraceptive or anti-fertility vaccine and for treating male
CC infertility. Zcytor13 protein and its antibodies are used to diagnose
CC cancer, reperfusion ischaemia, asthma, psoriasis and melanoma. Zcytor13
CC proteins are used to enhance fertilisation. Zcytor13 antagonists are used
CC to treat myocarditis, atherosclerosis, pelvic inflammatory disease (PID),
CC psoriasis, eczema, scleroderma and other inflammatory diseases. Zcytor13
CC sequences and/or its antibodies are useful for treatment of disorders
CC associated with vasoconstriction, heart arrhythmia, congestive heart
CC disease, muscle spasms and fatigue. They are used for detecting human
CC chromosomal abnormalities. Zcytor13 cDNAs are used in gene therapy.
CC Zcytor13-cytokine fusion proteins or antibody-cytokine fusion proteins
CC are useful for enhancing in vivo killing of target tissue. The present
CC sequence is a polyA PCR primer, ZC7764b which is used to isolate full
CC length zcytor13 cDNA by screening human placental cDNA library
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||||
Db 5 TTTTTTTTTTTTTTTTTTTTTA 26

RESULT 131
AAS20596
ID AAS20596 standard; DNA; 26 BP.
XX
AC AAS20596;
XX
DT 23-APR-2002 (first entry)
XX
DE Human zsig63 cDNA sequencing primer ZC7764a.
XX
KW Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KW gastrointestinal disease; urinary tract infection; vaginal infection;
KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
KW chronic bronchitis; gene therapy; protein therapy; primer; ZC7764a.
XX
OS Homo sapiens.
XX
PN US6331413-B1.
XX
PD 18-DEC-2001.
XX
PF 17-MAR-2000; 2000US-00527345.
XX
PR 17-MAR-1999; 99US-0124820P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2002-096707/13.
XX
PT Polynucleotides encoding salivary proteins useful as anti-microbial
PT agents.
XX
PS Example 1; Col 53; 29pp; English.
XX
CC The invention relates to a polynucleotide derived from the 4q12-4q13
CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC secreted salivary protein with anti-microbial activity. Due to their
CC microbial activity, the sequences can be used in the study of microbial
CC infections, e.g. for recombinant production of anti-microbial proteins.
CC The sequences can be used in the treatment of tooth decay, periodontal
CC disease, thrush, gastrointestinal disease, urinary tract infections,
CC vaginal infections, skin infections, epithelial wounds, chronic tissue
CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC represents a sequencing primer for cDNA encoding human zsig63
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||||
Db 5 TTTTTTTTTTTTTTTTTTTTTA 26

RESULT 132
ABS52638
ID ABS52638 standard; DNA; 26 BP.
XX
AC ABS52638;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human secreted salivary protein zsig63 PCR primer ZC7764a.
XX
KW Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
KW antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KW fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KW tooth decay; periodontal disease; thrush; gastrointestinal disease;
KW urinary tract infection; vaginal infection; skin infection; microflora;
KW epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KW chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KW incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KW chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KW digestion; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002081701-A1.
XX
PD 27-JUN-2002.
XX
PF 03-AUG-2001; 2001US-00922480.
XX
PR 17-MAR-1999; 99US-0124820P.
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLE/) ADLER D A.
PA (SHEP/) SHEPPARD P O.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2002-635468/68.
XX
PT Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT useful for treating microbial infections, inflammatory conditions, dental
PT caries and lung infections associated with cystic fibrosis.

```
XX
PS   Example 1; Page 29; 33pp; English.
XX
CC   The present invention relates to a new secreted salivary protein, zsig63.
CC   The invention is useful for detecting in a test sample, the presence of
CC   an antagonist or agonist of zsig63 protein activity. The invention is
CC   also useful as an immunogen for producing an antibody to zsig63
CC   polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC   protein are useful for enhancing in vivo killing of target tissues.
CC   Pharmaceutical composition comprising purified zsig63 polypeptide are
CC   useful in the treatment of conditions associated with pathological
CC   microbes, including bacterial, fungal and viral infections. High
CC   expression of zsig63 in salivary gland suggests that anti-microbial
CC   polypeptides are useful for treatment of dental caries (tooth decay),
CC   periodontal disease, thrush and gastrointestinal disease. Other
CC   applications can be used in urinary tract infections, vaginal infections,
CC   prevention of infection in skin and other epithelial wounds. The
CC   polypeptides can be used to establish normal microflora and protect
CC   against pathogenic colonisation and invasion. The invention is useful
CC   when pro-inflammatory activity is desired. Applications for such pro-
CC   inflammatory activity include the treatment of chronic tissue damage,
CC   particularly in areas having a limited or damaged vascular system e.g.,
CC   damage in extremities associated with diabetes. Antagonists to zsig63
CC   polypeptides may be useful as anti-inflammatory agents. The invention is
CC   useful for the treatment of patients having incompetent immune system,
CC   such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC   that have undergone chemotherapy, radiation treatment. The invention is
CC   also useful for the treatment of lung infections associated with cystic
CC   fibrosis and its agonists or antagonists are useful for aiding digestion.
CC   The present nucleic acid sequence represents a PCR primer that was used
CC   in the methods of the invention for identification of zsig63
XX
SQ   Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTTA 26


RESULT 133
AAD45055
ID   AAD45055 standard; DNA; 26 BP.
XX
AC   AAD45055;
XX
DT   27-DEC-2002  (first entry)
XX
DE   ZC7764a primer used in the identification of human zsig63 DNA.
XX
KW   Human; secreted salivary protein; zsig63 protein; host defense protein;
KW   immune modulating factor; antipathogenic; cell-cell signalling molecule;
KW   growth factor; cytokine; growth factor hormone activity; dental carries;
KW   infection; tooth decay; periodontal disease; gastrointestinal disease;
KW   thrush; urinary tract infection; vaginal infection; diabetes; obesity;
KW   anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
KW   gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KW   forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002090677-A1.
XX
PD   11-JUL-2002.
XX
PF   03-AUG-2001; 2001US-00923236.
XX
PR   17-MAR-1999;   99US-0124820P.
PR   17-MAR-2000; 2000US-00527345.
XX
PA   (ADLE/) ADLER D A.
PA   (SHEP/) SHEPPARD P O.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2002-642378/69.
XX
PT   Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
PT   agent for treating microbial infection, dental carries, periodontal
PT   disease, thrush gastrointestinal disease, and for aiding digestion.
XX
PS   Example 1; Page 30; 33pp; English.
XX
CC   The invention relates to human secreted salivary polypeptide designated
CC   as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
CC   can be used in detecting agonists and antagonists of its activity, and is
CC   also useful as a host defense polypeptide, immune modulating factor,
CC   antipathogenic polypeptide, cell-cell signalling molecule, growth factor,
CC   cytokine, or as secreted extracellular matrix associated proteins with
CC   growth factor hormone activity. It is useful for treating conditions
CC   associated with pathological microbes, including bacterial, fungal and
CC   viral infections, for treating dental carries (tooth decay), periodontal
CC   disease, thrush and gastrointestinal disease, for treating urinary tract
CC   infection, vaginal infection and for preventing infection in skin and
CC   other epithelial wounds. zsig63 is useful for establishing normal
CC   microflora and protect against pathogenic colonisation and invasion, for
CC   treating chronic tissue damage e.g. damage in extremities associated with
CC   diabetes and useful as anti-inflammatory agents. It is useful as a marker
CC   of lung dysfunction, salivary gland dysfunction, or dysfunction of
CC   prostate gland. It is also therapeutically useful for aiding digestion.
CC   Polynucleotides of the invention are used in gene therapy for increasing
CC   or inhibiting zsig63 activity, for detecting abnormalities on human
CC   chromosome 4 associated with disease or other human traits and as
CC   diagnostics in forensic DNA profiling. Sequences of the invention are
CC   useful for stimulating proliferation or differentiation of cardiac
CC   myocytes, for proliferation or differentiation of adipocytes and for
CC   inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The
CC   present sequence is a primer used in the identification of human zsig63
CC   DNA
XX
SQ   Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||||
Db          5 TTTTTTTTTTTTTTTTTTTTTA 26


RESULT 134
AAS20671
ID   AAS20671 standard; DNA; 26 BP.
XX
AC   AAS20671;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human zalpha11 Ligand sequencing primer ZC7764a.
XX
KW   Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW   natural killer cell proliferation; T-cell proliferation;
KW   B-cell proliferation; anti-tumour response; immune system;
KW   immunostimulant; cytostatic; human; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6307024-B1.
XX
PD   23-OCT-2001.
XX
PF   09-MAR-2000; 2000US-00522217.
```

XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI; 2002-040208/05.
XX
PT New zalpha11 ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
PS Example 7; Col 139; 105pp; English.
XX
CC The present invention relates to the isolation of a novel cytokine,
CC zalpha11 Ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalpha11 receptor and the polynucleotide
CC encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC zalpha11 Ligand polypeptide is also useful in preparing antibodies that
CC bind to zalpha11 Ligand epitopes. The zalpha11 Ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalpha11 Ligand gene,
CC and in gene therapy. Zalpha11 Ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC a sequencing primer used to sequence cDNA clones in the isolation of
CC human zalpha11 Ligand
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||||
Db 5 TTTTTTTTTTTTTTTTTTTTTA 26

RESULT 135
ABX93599
ID ABX93599 standard; DNA; 26 BP.
XX
AC ABX93599;
XX
DT 28-MAY-2003 (first entry)
XX
DE Human zsig63 PCR/sequencing primer ZC7764a.
XX
KW ss; PCR; zsig63; adhesin; salivary gland; dental carries;
KW periodontal disease; thrush; gastrointestinal disease; epithelial wound;
KW urinary tract infection; vaginal infection; skin infection; primer;
KW pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
KW lung infection; cystic fibrosis; lung dysfunction; digestive;
KW salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
KW chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
KW cell culture media; gene therapy; human chromosome 4q12-4q13;
KW dentinogenesis imperfecta; dentin dysplasia type II.
XX
OS Synthetic.
XX
PN US2002173027-A1.
XX
PD 21-NOV-2002.
XX
PF 03-AUG-2001; 2001US-00922469.
XX
PR 17-MAR-1999; 99US-0124820P.
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLE/) ADLER D A.
PA (SHEP/) SHEPPARD P O.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2003-328428/31.
XX
PT Novel isolated zsig63 polypeptide, member of the adhesin family, useful
PT for treating dental carries, periodontal disease, thrush,
PT gastrointestinal disease, urinary tract infections, vaginal infections,
PT skin infections.
XX
PS Example 1; Page 29; 32pp; English.
XX
CC The invention relates to an isolated zsig63 polypeptide comprising at
CC least 90% identity to an amino acid sequence which comprises domain 1 of
CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also
CC included are the polynucleotide encoding zsig63, a zsig63 expression
CC vector, a cultured cell comprising the vector and expressing the protein,
CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a
CC zsig63 reporter gene construct to identify zsig63 agonists, and producing
CC an anti-zsig63 antibody using zsig63 immunogenic peptides, Zsig63 is
CC useful for detecting in a test sample, the presence of antagonist of
CC zsig63 protein activity. Zsig63 has antimicrobial activity and since
CC exhibits high expression in salivary gland, can be used for treating
CC dental carries, periodontal disease, thrush, and gastrointestinal
CC disease, urinary tract infections, vaginal infections, skin infections
CC and other epithelial wounds. The polypeptides can be used to establish
CC normal microflora and protect against pathogenic colonization and
CC invasion. Zsig63 can also be used for providing pro-inflammatory activity
CC for treating chronic, tissue damage particularly in areas having limited
CC or damaged vascular system, e.g. in diabetes, and for treating
CC immunocompromised AIDS patients or in individuals that have undergone
CC chemotherapy, radiation treatment, for treating lung infections e.g. in
CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high
CC levels in the trachea may indicate that such polypeptides may serve as a
CC marker of lung dysfunction. Zsig63 is also useful in diagnosing
CC conditions associated with salivary gland or lung dysfunction including
CC salivary gland carcinoma, Pneumocystis carinii infection, emphysema,
CC chronic bronchitis, prostate dysfunctions such as prostate
CC adenocarcinoma, aiding digestion, and as components of defined cell
CC culture media and may be used to replace serum that is commonly used in
CC culture. The DNA is useful in gene therapy applications to increase or
CC inhibit zsig63 activity, and for detecting abnormalities on human
CC chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta,
CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The
CC present sequence is a primer used to isolate and sequence nucleic acdis
CC encoding human zsig63
XX
SQ Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||||
Db 5 TTTTTTTTTTTTTTTTTTTTTA 26

RESULT 136
AAX77343
ID AAX77343 standard; DNA; 30 BP.
XX
AC AAX77343;
XX

```
DT   09-AUG-1999  (first entry)
XX
DE   Sindbis virus mRNA amplifying RT-PCR 3' primer.
XX
KW   Nucleic acid identification; exogenous protein; gene sorting;
KW   growth factor; membrane receptor; sindbis virus; RT-PCR; primer; ss.
XX
OS   Synthetic.
OS   Sindbis virus.
XX
PN   WO9925876-A1.
XX
PD   27-MAY-1999.
XX
PF   17-NOV-1998;   98WO-US024520.
XX
PR   17-NOV-1997;   97US-00972218.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
PI   Bailey JE,  Renner WA,  Orberger GH,  Koller D;
XX
DR   WPI; 1999-357620/30.
XX
PT   Isolating genes encoding proteins with selected properties, useful for
PT   identifying therapeutic agents or targets.
XX
PS   Disclosure; Page 66; 136pp; English.
XX
CC   The invention relates to the identification of a recombinant nucleic acid
CC   encoding an exogenous protein having a selected property. The method
CC   comprises preparing a population of eukaryotic host cells, culturing the
CC   cells under suitable conditions and identifying cells that contain the
CC   recombinant nucleic acid. The method is used to sort genes according to
CC   the type of proteins they express, and also to identify new ligand/
CC   receptor interactions. Typical applications of the nucleic acid and the
CC   exogenous protein are in isolation of new growth factors, cytokines,
CC   membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC   which may be useful as therapeutic agents or therapeutic targets, e.g.
CC   apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC   proliferation or metabolic processes etc. The protein can also be used to
CC   screen for specific modulators. The nucleic acid can also be used as
CC   sources of therapeutic antisense or ribozyme sequences. The method allows
CC   the protein (rather than a partial DNA sequence) to be isolated and,
CC   since a wide range of cells can be used, they can be expressed with the
CC   correct glycosylation pattern
XX
SQ   Sequence 30 BP; 0 A; 5 C; 5 G; 20 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||||
Db          9 CCTTTTTTTTTTTTTTTTTTTT 30


RESULT 137
AAA90394
ID   AAA90394 standard; DNA; 30 BP.
XX
AC   AAA90394;
XX
DT   10-JAN-2001  (first entry)
XX
DE   Sindbis virus 3' RT-PCR primer.
XX
KW   Nucleic acid identification; exogenous protein; drug screening;
KW   recombinant expression; pSinRep5 vector; mammalian expression system;
KW   reverse transcription-PCR; RT-PCR primer; ss.
XX
OS   Sindbis virus.
OS   Synthetic.
XX
PN   JP2000189173-A.
XX
PD   11-JUL-2000.
XX
PF   23-AUG-1999;   99JP-00236220.
XX
PR   17-NOV-1998;   98US-00193707.
PR   17-NOV-1998;   98WO-US024520.
XX
PA   (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
XX
DR   WPI; 2000-551637/51.
XX
PT   Identifying a recombinant nucleic acid to identify and isolate various
PT   cellular proteins, comprises culturing a composition comprising
PT   eukaryotic host cells and identifying a cell comprising recombinant
PT   nucleic acid.
XX
PS   Example; Page 35; 56pp; Japanese.
XX
CC   The invention relates to the identification of a recombinant nucleic acid
CC   encoding an exogenous protein having a selected property.The method
CC   comprises preparing populations of eukaryotic host cells, where each cell
CC   comprises an expression vector encoding a different exogenous protein.
CC   The host cells are cultured under suitable conditions and the nucleic
CC   acid which encodes the exogenous protein is identified. The method is
CC   useful for the identification and isolation of proteins with a selected
CC   property. Typical applications of the nucleic acid and the exogenous
CC   protein are in isolation of new growth factors, cytokines, membrane
CC   receptors, cytoplasmic, organelle or nuclear proteins, all of which may
CC   be useful as therapeutic agents or therapeutic targets, e.g., pro-
CC   apoptotic or tumour suppressing proteins, regulators of cell
CC   proliferation or of metabolic processes. The protein can also be used to
CC   screen for ligands and specific modulators of activity. The method of the
CC   invention allows the direct cloning of full length cDNAs in one step. It
CC   facilitates direct expression of the protein without the need to perform
CC   further procedures such as subcloning and establishment of a cell line
CC   for protein production. The method allows a protein of interest (rather
CC   than a partial DNA sequence) to be isolated and, since a wide range of
CC   cell types can be used, they can be expressed in a correctly folded and
CC   glycosylated form. Sequences AAA90394-A90395 represent Sindbis virus
CC   reverse transcription-PCR (RT-PCR) primers used in the exemplifications
CC   of the invention. This patent is related to WO9925876
XX
SQ   Sequence 30 BP; 0 A; 5 C; 5 G; 20 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 5.1e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||||
Db          9 CCTTTTTTTTTTTTTTTTTTTT 30


RESULT 138
ABL56893
ID   ABL56893 standard; DNA; 30 BP.
XX
AC   ABL56893;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly f.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
```

XX
PD 25-OCT-2000.
XX
PF 20-APR-2000; 2000EP-00108643.
XX
PR 20-APR-1999; 99JP-00111601.
XX
PA (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Kurata S, Yamada K, Yokomaku T;
PI Koyama O, Furusho K;
XX
DR WPI; 2000-657765/64.
XX
PT Determining the concentration of a target nucleic acid, useful e.g. for
PT detecting genetic mutations, comprises using a fluorescently labeled
PT probe in which emission is reduced by binding to the target nucleic acid.
XX
PS Example 5; Page 21; 55pp; English.
XX
CC The invention relates to the determination of the concentration of a
CC nucleic acid target, using a fluorescently labeled probe which produces
CC reduced fluorescence emission when hybridised to the target nucleic acid.
CC The method comprises measuring the reduction in emission caused by
CC hybridisation. The new method is particularly used to quantify target
CC nucleic acids by a real-time polymerase chain reaction, e.g. for
CC quantifying microbial cells in co-cultures or symbiotic systems, for
CC detecting gene mutations or polymorphisms, and for analysing melting
CC curves of target nucleic acids to determine a Tm value. Methods of the
CC invention allow target nucleic acids to be quantified quickly, easily and
CC accurately. Particularly there is no need to remove unbound probe, and no
CC materials are introduced that inhibit amplification by Taq polymerase (so
CC conventional PCR conditions can be used). The specificity of PCR is kept
CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 30;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
|| || ||||| | ||||||||||||||||
Db 1 ATATATATTTTTTTTCTTTTTTTTTTTTTT 30

RESULT 139
AAF26221/c
ID AAF26221 standard; DNA; 30 BP.
XX
AC AAF26221;
XX
DT 26-APR-2001 (first entry)
XX
DE APC binding protein associated primer ON-AT+ SEQ ID 6.
XX
KW APC binding protein; cell proliferation; adenomatous polyposis coli;
KW tumor cell detection; primer; ss.
XX
OS Unidentified.
XX
PN DE19933237-A1.
XX
PD 18-JAN-2001.
XX
PF 15-JUL-1999; 99DE-01033237.
XX
PR 15-JUL-1999; 99DE-01033237.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Mueller O;
XX
DR WPI; 2001-148321/16.
XX
PT Determining proliferative capacity of cells, useful e.g. for detecting
PT tumor cells, by measuring concentration and subcellular localization of
PT adenomatous polyposis coli protein.
XX
PS Claim 10; Page 12; 26pp; German.
XX
CC This invention describes a novel method for determining the proliferative
CC activity of cells, comprising detecting, in a sample, the concentration
CC and/or subcellular localization of APC (adenomatous polyposis coli)
CC protein (I). The invention also describes (1) determining function of (I)
CC in a sample by detecting presence of the C-terminal, DNA-binding domain
CC of (I); (2) detecting mutations in (I)-encoding nucleic acid by detecting
CC the DNA-binding domain of (I); (3) purifying, enriching and/or detecting
CC (I) or its fragments by reaction with a probe; (4) double-stranded DNA
CC (II) that contains the sequence GGCCGCA_2_3G (S1) and/or GATCCT_2_3GC
CC (S2); (5) peptide fragment of (I) containing at least the DNA-binding
CC domain; (6) antibodies (Ab) directed against an epitope of positions 1340
CC -1901, 2219-2580 or 2581-2843 of (I); (7) set of two or more antibodies,
CC one of which is Ab and the other directed against the N-terminal region
CC (1-1299) of (I); and (8) kit for detecting DNA-binding capacity of (I) or
CC its fragments in a sample consisting of (II), Ab or the set of (7). The
CC method is used to detect proliferative, especially tumor (precursor),
CC cells, to detect function of (I) and mutations in (I), and to purify
CC and/or enrich (I), or its fragments, from a sample. The method allows
CC simple, rapid and reliable detection of proliferation, without the need
CC for polymerase chain reaction or sequencing
XX
SQ Sequence 30 BP; 23 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 22; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||||
Db 30 CTTTTTTTTTTTTTTTTTTTTT 9

RESULT 140
ABA97617
ID ABA97617 standard; DNA; 30 BP.
XX
AC ABA97617;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly f nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.

```
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 5.1e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || ||||| | ||||||||||||||||
Db          1 ATATATATTTTTTTTCTTTTTTTTTTTTTT 30


RESULT 141
ABL95890
ID   ABL95890 standard; DNA; 30 BP.
XX
AC   ABL95890;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly f for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 30;
  Best Local Similarity   83.3%;  Pred. No. 5.1e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || ||||| | ||||||||||||||||
Db          1 ATATATATTTTTTTTCTTTTTTTTTTTTTT 30


RESULT 142
ABS55182
ID   ABS55182 standard; DNA; 31 BP.
XX
AC   ABS55182;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Tumour-suppressor gene associated oligonucleotide.
XX
KW   Tumour-suppressor; cancer; ss.
XX
OS   Unidentified.
XX
PN   KR2001061173-A.
XX
PD   07-JUL-2001.
XX
PF   28-DEC-1999;   99KR-00063661.
XX
PR   28-DEC-1999;   99KR-00063661.
XX
PA   (CHAE/) CHAE J H.
PA   (CHOI/) CHOI W H.
PA   (CHUN/) CHUNG T J.
PA   (JUNG/) JUNG H J.
PA   (KIMC/) KIM C G.
PA   (KIMH/) KIM H G.
PA   (PARK/) PARK C I.
PA   (PARK/) PARK J H.
XX
PI   Chae JH,  Choi WH,  Chung TJ,  Jung HJ,  Kim CG,  Kim HG,  Park CI;
PI   Park JH;
XX
DR   WPI; 2002-016333/02.
XX
PT   Vector containing polymerase chain reaction primers of tumor-suppressor
PT   gene, useful for diagnosis of cancer.
XX
PS   Disclosure; Page 11; 19pp; Korean.
XX
CC   The present invention relates to a new vector comprising polymerase chain
CC   reaction (PCR) primers of tumour-suppressor gene. The invention can be
CC   useful for the diagnosis of cancer. The present nucleic acid sequence
CC   represents an oligonucleotide as described in the invention
XX
SQ   Sequence 31 BP; 22 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 31;
  Best Local Similarity   83.3%;  Pred. No. 5.6e+02;
  Matches   25;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAAAAAAA 2803
              | |||  |  ||||||||||||||||||||
Db          2 TGGTTGAATATGAAAAAAAAAAAAAAAAAA 31
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RESULT 143
ACC42844/c
ID   ACC42844 standard; DNA; 33 BP.
XX
AC   ACC42844;
XX
DT   01-SEP-2003  (first entry)
XX
DE   Nuclear transition protein I-9.57 PCR primer #4.
XX
KW   Nuclear transition protein I-9.57; tumour; cytostatic; haemopathy; PCR;
KW   HIV infection; anti-HIV; immunological disease; inflammation; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1380328-A.
XX
PD   20-NOV-2002.
XX
PF   10-APR-2001; 2001CN-00105924.
XX
PR   10-APR-2001; 2001CN-00105924.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-222560/22.
XX
PT   Polypeptide-nuclear transformation protein -9.57 and polynucleotide for
PT   coding this polypeptide.
XX
PS   Example 5; Page 27; 29pp; Chinese.
XX
CC   The present invention relates to nuclear transition protein I-9.57 and
CC   its coding sequence. The protein can be used for treating several
CC   diseases, such as malignant tumours, haemopathy, HIV infection,
CC   immunological disease and various inflammations. The present sequence is
CC   a PCR primer, which was used in an example from the invention. Note: The
CC   present sequence is SEQ ID 6 from the sequence listing. This sequence
CC   differs from the SEQ ID 6 shown in the disclosure (see ACC42932)
XX
SQ   Sequence 33 BP; 24 A; 4 C; 2 G; 3 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 22;  DB 1;  Length 33;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||||
Db         32 TTTTTTTTTTTTTTTTTTTTTA 11


RESULT 144
AAF16616/c
ID   AAF16616 standard; DNA; 26 BP.
XX
AC   AAF16616;
XX
DT   13-MAR-2001  (first entry)
XX
DE   Gastric acid production inhibiting oligonucleotide SEQ ID NO: 103.
XX
KW   Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW   stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW   DNA-RNA hybrid; ss.
XX
OS   Homo sapiens.
XX
PN   WO200071164-A1.
XX
PD   30-NOV-2000.
XX
PF   24-MAY-2000; 2000WO-AU000498.
XX
PR   24-MAY-1999;   99AU-00000510.
XX
PA   (TACH/) TACHAS G.
XX
PI   Tachas G;
XX
DR   WPI; 2001-025093/03.
XX
PT   Treating gastric acid disturbance by administering an oligonucleotide
PT   which modulates the activity of a polypeptide involved in gastric acid
PT   production or secretion.
XX
PS   Example 3; Page 150; 164pp; English.
XX
CC   The present invention provides oligonucleotides, and methods for their
CC   use, which are useful in modulating the action of proteins involved in
CC   gastric acid production. The target protein is preferably the histamine
CC   H2 receptor or one of the proteins which form part of the gastric proton
CC   pump. The sequences and methods of the invention are useful in the
CC   treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC   duodenal ulcers and other gastric acid disturbances, most of which are
CC   caused by Helicobacter pylori
XX
SQ   Sequence 26 BP; 23 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 26;
  Best Local Similarity   92.0%;  Pred. No. 3.9e+02;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||| |||||||||| ||||||||||
Db         26 CTCTTTTTTTTTTCTTTTTTTTT 2


RESULT 145
AAZ43904
ID   AAZ43904 standard; DNA; 27 BP.
XX
AC   AAZ43904;
XX
DT   10-MAR-2000  (first entry)
XX
DE   M. tuberculosis rpo-beta primer 17.
XX
KW   RNA polymerase; rpo-beta; detection; diagnostic; trap probe; primer; ss.
XX
OS   Mycobacterium tuberculosis.
XX
PN   EP962536-A1.
XX
PD   08-DEC-1999.
XX
PF   29-MAY-1999;   99EP-00110458.
XX
PR   04-JUN-1998;   98DE-01024900.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Weindel K,  Brand J;
XX
DR   WPI; 2000-055287/05.
XX
PT   Selective detection of nucleic acids by amplification with labeled
PT   primers and detection with a trap probe.
XX
PS   Example 1c; Page 19; 27pp; German.
XX
CC   This invention describes a novel method for the selective detection of
CC   nucleic acids which comprises amplification of the nucleic acid with the
```

```
CC   help of labeled primers and detection with a trap probe. The methods and
CC   reagents are used for the detection of a marker primer and at least 2
CC   immobilized (or immobilizable) trap probes with the corresponding nucleic
CC   acid sequence of interest for mutation analysis. The method can be used
CC   to detect a specific sequence in a sample of one or more nucleic acids by
CC   using several sets of primers and trap probes (i.e. in an array). The
CC   methods are useful in molecular biology and diagnostic applications,
CC   especially for simultaneous detection of multi-pathogens, typing of
CC   organisms, analyzing genetic diversity and sequencing of genes or
CC   genomes. This sequence represents a primer used in the method of the
CC   invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 27;
  Best Local Similarity   85.2%;  Pred. No. 4.3e+02;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2181
              ||||||| |  |||||||||||||:|
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTYT 27


RESULT 146
AAA57856
ID   AAA57856 standard; DNA; 28 BP.
XX
AC   AAA57856;
XX
DT   11-OCT-2000  (first entry)
XX
DE   Deoxy-T22-tagged substrate oligonucleotide.
XX
KW   Ribozyme; catalytic RNA; analyte detection; effector molecule;
KW   nucleic acid substrate; in vitro selection; ribozyme ligase;
KW   conformation dependent activity; allosteric activation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        23. .28
FT                   /*tag=  a
FT   misc_binding    24. .28
FT                   /*tag=  b
FT                   /bound_moiety= "Bases 13-17 of N90 RNA pool (AAA57851)"
XX
PN   WO200024931-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-IL000557.
XX
PR   23-OCT-1998;   98IL-00126731.
XX
PA   (INTE-) INTELLIGENE LTD.
XX
PI   Nathan A,  Ellington A;
XX
DR   WPI; 2000-350763/30.
XX
PT   Detecting an analyte in a sample comprises providing nucleic acid
PT   sequence which is catalytically active in presence of analyte, contacting
PT   catalytic nucleic acid with substrate and amplifying catalytic product.
XX
PS   Disclosure; Page; 36pp; English.
XX
CC   The invention relates to a method of detecting an analyte in a sample.
CC   The method comprises providing a nucleic acid sequence which is initially
CC   catalytically inactive, but which becomes catalytically active in the
CC   presence of an analyte (the effector); providing a nucleic acid substrate
CC   for the catalytic activity of the nucleic acid sequence; and contacting
CC   the nucleic acid sequence and the substrate with the sample under
CC   conditions allowing catalytic activity of nucleic acid sequences. The
CC   catalytic nucleic acid sequence will be able to convert the nucleic acid
CC   substrate into a nucleic acid product only if the analyte of interest is
CC   present. The nucleic acid catalytic product is then amplified, and a
CC   significant increase in the amount of product indicates the presence of
CC   the analyte in the sample. The method is useful for the qualitative or
CC   quantitative determination of an analyte in a sample in diagnostic
CC   assays. The invention describes the in vitro selection of a ribozyme
CC   ligase (L1; AAA57859, AAA57860) which is catalytically active only in the
CC   presence of an oligonucleotide effector (AAA57854). The L1 ribozyme
CC   ligase was selected from a pool of RNA molecules comprising a central
CC   randomised region 90 nucleotides in length flanked on both sides by
CC   constant sequence regions (the N90 RNA pool; AAA57851). In the presence
CC   of the effector, selection was performed using one of the tagged
CC   substrate molecules AAA57855-A57857. RNAs with ligase activity (i.e.,
CC   those which have become ligated to the substrate molecule) were reverse
CC   transcribed using the effector oligo, and then PCR amplified using the
CC   effector and a DNA primer identical in sequence to the substrate used for
CC   the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC   can only adopt its active conformation (AAA57859) in the presence of the
CC   effector oligo (analyte). In the absence of the effector, L1 adopts an
CC   inactive conformation (AAA57860). The present sequence represents the
CC   deoxy-T22-tagged substrate oligonucleotide. The dT22 tag enables
CC   successfully ligated products to be isolated using oligo(dA) cellulose
CC   Type 7. Note: The present sequence is not given in the specification, but
CC   is created from the inforamtion given on page 11
XX
SQ   Sequence 28 BP; 1 A; 2 C; 1 G; 22 T; 2 U; 0 Other;

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 28;
  Best Local Similarity   84.0%;  Pred. No. 4.7e+02;
  Matches   21;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||||:  ||:
Db          4 TTTTTTTTTTTTTTTTTTTTGCACU 28


RESULT 147
AAA40358
ID   AAA40358 standard; DNA; 28 BP.
XX
AC   AAA40358;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 8.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
XX
DR   WPI; 2000-442381/38.
XX
PT   Inserting a nucleic acid into a circular vector comprising joining their
PT   ends, melting, and reannealing ends at two different concentrations,
PT   useful for cloning small amounts of nucleic acids and forming genomic
PT   libraries.
XX
PS   Example 3; Page 67; 71pp; English.
XX
CC   This invention describes a novel method (M1) for inserting a nucleic acid
```

```
CC   (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC   under a first nucleic acid concentration, melting hybridized cohesive
CC   circularization ends, and reannealing the ends at a second concentration.
CC   The methods are useful for the cloning small amounts of nucleic acids and
CC   forming genomic libraries of complex populations of DNA or cDNA. The
CC   methods allow the cloning of minute amounts of nucleic acids efficiently
CC   and avoids the size selection problems of prior art systems. Larger
CC   nucleic acid fragments are just as easily cloned, allowing highly
CC   representative libraries to be made. Vector to vector ligation is avoided
CC   using the methods. AAA40351-A40366 represents primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 28 BP; 1 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 28;
  Best Local Similarity   92.0%;  Pred. No. 4.7e+02;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTTT 2186
              ||  ||||||||||||||||||||
Db          1 CTAGTTTTTTTTTTTTTTTTTTTT 25


RESULT 148
AAQ43410
ID   AAQ43410 standard; DNA; 31 BP.
XX
AC   AAQ43410;
XX
DT   25-MAR-2003  (revised)
DT   29-OCT-1993  (first entry)
XX
DE   Structural production oligonucleotide S-Strand-1.
XX
KW   Molecular scaffolding; molecule orientation; orient; juxtaposition;
KW   functional artificial components; one; two; three; dimensional;
KW   structure formation; therapeutic; analytical; industrial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "exposed/exposable sticky end"
FT   misc_feature    1
FT                   /*tag=  b
FT                   /note= "PO4-Cytosine"
FT   misc_feature    31
FT                   /*tag=  c
FT                   /note= "Thymine - Teflon based solid support"
XX
PN   WO9312244-A1.
XX
PD   24-JUN-1993.
XX
PF   03-DEC-1992;   92WO-US010431.
XX
PR   12-DEC-1991;   91US-00805564.
XX
PA   (UYNY ) UNIV NEW YORK STATE.
XX
PI   Seeman NC,  Zhang Y;
XX
DR   WPI; 1993-214185/26.
XX
PT   Prodn. of structure including double stranded polynucleotide - comprises
PT   cleavage of loop in core structure of 1st polynucleotide with restriction
PT   enzyme and ligation to 2nd polynucleotide, used to orient mols., etc.
XX
PS   Example; Page 34; 58pp; English.
XX
CC   The sequence is that of the oligonucleotide S-Strand-1 which can be used
CC   in the formation or modification of one-, two- and three- dimensional
CC   structures. It may be used as molecular scaffolding to orient and
CC   juxtapose other molecules. It has analytical, industrial or therapeutical
CC   potential. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 31 BP; 2 A; 4 C; 2 G; 23 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 31;
  Best Local Similarity   92.0%;  Pred. No. 6e+02;
  Matches   23;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||
Db          6 CGCGTTTTTTTTTTTTTTTTTTTT 30


RESULT 149
ABS64697/c
ID   ABS64697 standard; DNA; 35 BP.
XX
AC   ABS64697;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Nucleic acid detection method associated polynucleotide #79.
XX
KW   Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW   nanoparticle; viral RNA detection; bacterial DNA detection;
KW   fungal DNA detection; nanoprobe conjugate; ss.
XX
OS   Synthetic.
XX
PN   WO200246472-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US046418.
XX
PR   08-DEC-2000; 2000US-0254392P.
PR   08-DEC-2000; 2000US-0254418P.
PR   11-DEC-2000; 2000US-0255235P.
PR   11-DEC-2000; 2000US-0255236P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
PR   09-APR-2001; 2001US-0282640P.
PR   10-AUG-2001; 2001US-00927777.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-608256/65.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Disclosure; Page 57; 442pp; English.
XX
CC   The invention describes a method of detecting (M1) a nucleic acid having
CC   two portions, involving providing nanoparticles having oligonucleotides
CC   attached to it, which has a sequence complementary to sequence of two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC   allow hybridisation of oligonucleotides with two or more portions of
CC   nucleic acid, and observing a detectable change brought about by
CC   hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC   conjugates (II) and the aggregate probe are useful for detecting two or
CC   more nucleic acids (from a biological source) having at least two
CC   portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC   with a disease, synthetic, or structurally-modified natural or synthetic
CC   RNA or DNA, or a product of a polymerase chain reaction amplification.
CC   (II) is useful for preparing a nanoprobe conjugate for detecting an
CC   analyte, and for detecting a nucleic acid bound to an electrode surface.
```

```
CC   (I) and (II) are useful for fabrication, and for separating a selected
CC   nucleic acid having two portions from other nucleic acids. (I), (II) and
CC   the aggregate probe are useful for detecting an analyte (especially
CC   polyvalent analyte) in a sample. This sequence represents a
CC   polynucleotide used to demonstrate the method of the invention
XX
SQ   Sequence 35 BP; 24 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 35;
  Best Local Similarity   78.8%;  Pred. No. 8.1e+02;
  Matches   26;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||||||||||||| |||    || | |
Db         34 TTTTTTTTTTTTTTTTTTTTATAAGAAGGATATT 2

RESULT 150
AAL61669/c
ID   AAL61669 standard; DNA; 35 BP.
XX
AC   AAL61669;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Oligonucleotide #28 used in the nucleic acid detection method.
XX
KW   Nucleic acid detection; fabrication; ss.
XX
OS   Unidentified.
XX
PN   WO2003035829-A2.
XX
PD   01-MAY-2003.
XX
PF   08-OCT-2002; 2002WO-US032088.
XX
PR   09-OCT-2001; 2001US-0327864P.
PR   07-DEC-2001; 2001US-00008978.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Park S,  Taton TA,  Mirkin CA;
XX
DR   WPI; 2003-430409/40.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Disclosure; Page 58-59; 467pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid having two
CC   portions. The method involves providing nanoparticles having
CC   oligonucleotides attached to it which has a sequence complementary to
CC   sequence of two portions of nucleic acid, contacting nucleic acid and
CC   nanoparticles to allow hybridisation of oligonucleotides with two or more
CC   portions of nucleic acid and observing a detectable change brought about
CC   by hybridisation. The method and aggregate probes are useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic or structurally modified natural or
CC   synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. The invention is useful for preparing a nanoprobe
CC   conjugate for detecting an analyte and for detecting a nucleic acid bound
CC   to an electrode surface. It is also useful for fabrication and for
CC   separating a selected nucleic acid having two portions from other nucleic
CC   acids. The present sequence is an oligo used to illustrate the method of
CC   the invention
XX
SQ   Sequence 35 BP; 24 A; 3 C; 0 G; 8 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.8;  DB 1;  Length 35;
  Best Local Similarity   78.8%;  Pred. No. 8.1e+02;
  Matches   26;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTGAAAGT 2198
              ||||||||||||||||||||| |||    || | |
Db         34 TTTTTTTTTTTTTTTTTTTTATAAGAAGGATATT 2

RESULT 151
AAV59216
ID   AAV59216 standard; DNA; 29 BP.
XX
AC   AAV59216;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Linear multimer produced by rolling circle synthesis.
XX
KW   ss; RNA oligonucleotide; probe; standard; diagnostic; therapeutic agent.
XX
OS   Synthetic.
XX
PN   WO9838300-A1.
XX
PD   03-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US003784.
XX
PR   26-FEB-1997;   97US-00805631.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-481202/41.
XX
PT   Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT   oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
PT   polymerase to form multimer(s) which can be cleaved.
XX
PS   Example 2; Page 36; 100pp; English.
XX
CC   The linear multimer was produced by rolling circle synthesis in an
CC   example of the method of the invention for synthesising an RNA
CC   oligonucleotide, comprising combining a single-stranded circular
CC   oligonucleotide template comprising at least one copy of a nucleotide
CC   sequence complementary to the sequence of the desired RNA oligonucleotide
CC   with at least 2 types of ribonucleotide triphosphate and a polymerase
CC   enzyme to yield a single-stranded RNA oligonucleotide multimer
CC   complementary to the circular oligonucleotide template, where the RNA
CC   oligonucleotide multimer comprises multiple copies of the desired RNA
CC   oligonucleotide. The methods can be used for producing RNA
CC   oligonucleotides having a specific sequence and well defined ends. The
CC   RNA oligonucleotides produced can be used as probes, standards and
CC   diagnostic or therapeutic agents. They can be used for modifying the
CC   structure or function of a target molecule. They can also be used to
CC   cleave disease-associated RNA, DNA or protein
XX
SQ   Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 29;
  Best Local Similarity   85.7%;  Pred. No. 5.5e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              ||| |  ||||||||| ||||||||||
Db          1 TTTGTTTTTTTTTTTTGTTTTTTTTTT 28

RESULT 152
AAL44903
ID   AAL44903 standard; DNA; 29 BP.
XX
```

```
AC   AAL44903;
XX
DT   05-AUG-2002  (first entry)
XX
DE   Triplex forming oligonucleotide #4.
XX
KW   Cancer; cytostatic; gene therapy; triplex forming oligonucleotide; ds.
XX
OS   Unidentified.
XX
PN   KR2001086830-A.
XX
PD   15-SEP-2001.
XX
PF   03-MAR-2000; 2000KR-00010744.
XX
PR   03-MAR-2000; 2000KR-00010744.
XX
PA   (KOCH-) KOREA CHUNGANG EDUCATIONAL FOUND.
XX
PI   Choi JG,  Lee DH,  Lee GY,  Park GH,  Park MG,  Son JW;
XX
DR   WPI; 2002-233771/29.
XX
PT   Novel triplex forming synthetic oligonucleotide, useful for gene therapy
PT   of tumor.
XX
PS   Claim 4; Page 11; 13pp; Korean.
XX
CC   The present invention relates to a triplex forming oligonucleotide which
CC   specifically binds to a specific gene. This is useful for the gene
CC   therapy of cancer by binding itself to Auger electron emitters. The
CC   present sequence is a triplex forming oligonucleotide of the invention
XX
SQ   Sequence 29 BP; 0 A; 1 C; 3 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 29;
  Best Local Similarity   85.7%;  Pred. No. 5.5e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAACTTTG 2193
             ||||||||||||||| |||||   ||||
Db          2 TTTTTTTTTTTTTTTGTTTTCTTTTTG 29


RESULT 153
ADC65873
ID   ADC65873 standard; DNA; 29 BP.
XX
AC   ADC65873;
XX
DT   18-DEC-2003  (first entry)
XX
DE   DNA oligonucleotide #6.
XX
KW   RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW   electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW   cation-mediated delivery; bacterial infection; viral infection;
KW   drug resistant infection; double stranded DNA oligomer; ss.
XX
OS   Synthetic.
XX
PN   US2003087241-A1.
XX
PD   08-MAY-2003.
XX
PF   30-NOV-2001; 2001US-00997931.
XX
PR   15-APR-1993;   93US-00047860.
PR   23-FEB-1995;   95US-00393439.
PR   26-FEB-1997;   97US-00805631.
PR   11-MAY-2000; 2000US-00569344.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 2003-755141/71.
XX
PT   Synthesizing RNA oligonucleotide involves combining single-stranded
PT   circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT   enzyme to yield desired RNA complementary to circular oligonucleotide
PT   template.
XX
PS   Example 2; SEQ ID NO 6; 78pp; English.
XX
CC   The invention relates to a method for synthesising an RNA
CC   oligonucleotide, comprising combining a single-stranded circular
CC   oligonucleotide template with at least two types of ribonucleotide
CC   triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC   oligonucleotide multimer complementary to the circular oligonucleotide
CC   template, where the RNA oligonucleotide multimer comprises multiple
CC   copies of the desired RNA oligonucleotide. The method is useful for
CC   synthesising an RNA oligonucleotide with well-defined ends. The circular
CC   oligonucleotide is introduced into the cell using direct injection,
CC   electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC   cation-mediated delivery. The method is useful for treating bacterial
CC   and/or viral infections in mammals, particularly drug resistant
CC   infections, and for producing double stranded DNA oligomers. The method
CC   is performed in the absence of an oligonucleotide primer, or without the
CC   addition of auxiliary proteins. This sequence represents an
CC   oligonucleotide used in the method of the invention.
XX
SQ   Sequence 29 BP; 0 A; 0 C; 2 G; 27 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 29;
  Best Local Similarity   85.7%;  Pred. No. 5.5e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
             ||| |  |||||||| ||||||||||||
Db          1 TTTGTTTTTTTTTTTGTTTTTTTTTTT 28


RESULT 154
AAQ83940/c
ID   AAQ83940 standard; DNA; 30 BP.
XX
AC   AAQ83940;
XX
DT   25-MAR-2003  (revised)
DT   04-OCT-1995  (first entry)
XX
DE   Oligonucleotide clamp o, for producing comb-type brached polymer.
XX
KW   HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Modified with SP(O-)(=O)-"
XX
PN   WO9501365-A1.
XX
PD   12-JAN-1995.
XX
PF   05-JUL-1994;   94WO-US007557.
XX
PR   02-JUL-1993;   93US-00087386.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM;
XX
```

```
DR   WPI; 1995-060944/08.
XX
PT   Synthesis of branched polymers and novel branched polymeric structures -
PT   used as molecular probes esp. for detecting poly-nucleotide(s).
XX
PS   Example 8; Page 33; 52pp; English.
XX
CC   The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the
CC   construction of an oligonucleotide clamp. The clamp is a comb-type
CC   branched polymer which has 3' termini and was used to bind a target
CC   sequence comprising a segment of the HIV pol and nef genes in single
CC   stranded or double stranded forms. An oligonucleotide clamp is a compound
CC   capable of forming a covalently closed macromolecule or a stable circular
CC   complex after specifically binding to the target polynucleotide.
CC   Oligonucleotide clamps generally comprise one or more oligonucleotide
CC   moieties capable of specific binding to the target molecule and one or
CC   more pairs of binding moieties covalently linked to the oligonucleotide
CC   moieties. Upon annealing of the oligonucleotides moieties to the target
CC   polynucleotide, the binding moieties of a pair are bought into
CC   juxtaposition so that they form a stable covalent or non-covalent linkage
CC   or complex. The interaction of the binding moieties effectively clamps
CC   the specifically annealed oligonucleotide moieties to the target
CC   polynucleotide. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
             |||||||||||||||||||||   | ||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTGTG 3


RESULT 155
ABL56894
ID   ABL56894 standard; DNA; 30 BP.
XX
AC   ABL56894;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly g.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| || ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTTT 30


RESULT 156
ABL56895
ID   ABL56895 standard; DNA; 30 BP.
XX
AC   ABL56895;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly h.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
```

```
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
                ||  |||||||| | ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 157
AAF60462/c
ID   AAF60462 standard; DNA; 30 BP.
XX
AC   AAF60462;
XX
DT   27-APR-2001  (first entry)
XX
DE   Oligonucleotide clamp #22.
XX
KW   Oligonucleotide clamp; ds.
XX
OS   Unidentified.
XX
PN   US6180777-B1.
XX
PD   30-JAN-2001.
XX
PF   03-JAN-1997;   97US-00787321.
XX
PR   12-JAN-1996;   96US-0009918P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Horn T;
XX
DR   WPI; 2001-201911/20.
XX
PT   Synthesizing branched nucleic acids useful as diagnostic and molecular
PT   probes, involves combining first units having haloalkylamino groups and
PT   second units having thiol or phosphorothioate groups.
XX
PS   Example 8; Col 19; 20pp; English.
XX
CC   The present invention relates to a method for synthesising a branched or
CC   multiply connected macromolecular structure, comprising oligonucleotide
CC   clamps (OC). The macromolecular structure is capable of specifically
CC   binding to a target molecule, and can therefore be used as probes. At
CC   least one OC comprises a target binding sequence that binds specifically
CC   and stably with the target molecule, and at least two OCs comprise signal
CC   generation moieties capable of generating a detectable signal in the
CC   presence of the target molecule. In addition the OCs are connected to one
CC   another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC   present sequence is an OC used in the present invention
XX
SQ   Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTTAACTTTG 2193
                ||||||||||||||||||||||   | ||
Db         30 TTTTTTTTTTTTTTTTTTTTTTTTTGTG 3


RESULT 158
AAD25661
ID   AAD25661 standard; DNA; 30 BP.
XX
AC   AAD25661;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Oligonucleotide #7 related to method for production of RNA viruses.
XX
KW   Cytostatic; replication defective gene transfer; encapsidated RNA virus;
KW   gene therapy; cancer therapy; ss.
XX
OS   Unidentified.
XX
PN   WO200190302-A2.
XX
PD   29-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US015449.
XX
PR   24-MAY-2000; 2000US-0206997P.
XX
PA   (FENG/) FENG Y.
PA   (TANG/) TANG H.
XX
PI   Feng Y,  Tang H;
XX
DR   WPI; 2002-066766/09.
XX
PT   Producing encapsidated RNA virus by coexpressing RNA virus genomic
PT   sequence linked to bacteriophage promoter, and coding sequence for
PT   bacteriophage polymerase linked to poxvirus promoter in eukaryotic cell
PT   cytoplasm.
XX
PS   Disclosure; Page 38; 49pp; English.
XX
CC   The patent discloses methods to produce RNA viral sequences, recombinant
CC   RNA viruses, mutants of RNA viruses and RNA virus-derived vectors in cell
CC   culture and in vitro using non-viable, replication defective helper
CC   vaccinia recombinants. These methods generate RNA viral genomes and viral
CC   particles in cell culture and in vitro independent of their natural
CC   replication pathways, bypassing the limitation of any cellular barriers.
CC   The invention also relates to a method for producing encapsidated RNA
CC   virus comprising coexpressing polypeptide coding sequences capable of
CC   forming capsid and packaging RNA viral genomic sequence in eukaryotic
CC   cell, a construct comprising RNA viral genomic sequence linked to
CC   bacteriophage promoter and transcription terminator and bacteriophage
CC   polymerase coding sequence, which is operably compatible with the
CC   promoter and is linked to poxvirus promoter. The methods are useful for
CC   producing infectious or non-infectious, replication-defective,
CC   encapsidated RNA viruses such as hepatitis virus comprising an RNA genome
CC   e.g. hepatitis C virus (HCV), immature hepatitis B virus or hepatitis A
CC   virus, lentivirus, rhinovirus, influenza virus, LCMV, arenavirus,
CC   parainfluenza virus, reovirus, rotavirus, astrovirus, filovirus, or
CC   coronavirus. They are preferably useful for producing encapsidated human
CC   immunodeficiency virus (HIV)-1, where the HIV-1 lacks a Rev-response
CC   element (RRE) or an envelope sequence. Methods of the invention are also
CC   useful for producing replication defective gene transfer and gene therapy
```

```
CC   vectors, particularly to transfer nucleic acids to human cells in vivo
CC   and in vitro. The methods can be used for packaging therapeutic sequences
CC   as gene therapy vector preparations that are substantially free of helper
CC   virus and used as pharmaceuticals in e.g. gene replacement therapy, or
CC   cancer therapy. The present sequence is an oligonucleotide which is
CC   related to a method for production of RNA viruses
XX
SQ   Sequence 30 BP; 6 A; 0 C; 2 G; 22 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              ||||||||||||||||||   || |||
Db          1 TTTTTTTTTTTTTTTTTTAGGATTTAAA 28


RESULT 159
ABA97619
ID   ABA97619 standard; DNA; 30 BP.
XX
AC   ABA97619;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly h nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| | ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 160
ABA97618
ID   ABA97618 standard; DNA; 30 BP.
XX
AC   ABA97618;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly g nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 30;
  Best Local Similarity   85.7%;  Pred. No. 6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
              ||  |||||||| || ||||||||||||
Db          3 ATATATTTTTTTTTCTTTTTTTTTTTT 30


RESULT 161
ABL95891
ID   ABL95891 standard; DNA; 30 BP.
XX
AC   ABL95891;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly g for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
```

PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
|| |||||||| || ||||||||||||
Db 3 ATATATTTTTTTTTCTTTTTTTTTTTT 30

RESULT 162
ABL95892
ID ABL95892 standard; DNA; 30 BP.
XX
AC ABL95892;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly h for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.8%; Score 21.6; DB 1; Length 30;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2150 ATTGATTTTTTTCTCCTTTTTTTTTTTT 2177
|| |||||||| | ||||||||||||
Db 3 ATATATTTTTTTTTCTTTTTTTTTTTT 30

RESULT 163
AAV06769
ID AAV06769 standard; DNA; 33 BP.
XX
AC AAV06769;
XX
DT 02-JUN-1998 (first entry)
XX
DE Oligonucleotide containing a pentanucleotide loop.
XX
KW Thiol-substituted oligonucleotide; covalent cross-link; disulphide;
KW circular; bridged; hairpin; detection; pentanucleotide loop; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT repeat_region 1. .14
FT /*tag= a
FT misc_structure 15. .19
FT /*tag= b
FT /note= "pentanucleotide loop"
XX
PN WO9714708-A1.
XX
PD 24-APR-1997.
XX
PF 29-MAR-1996; 96WO-US004525.
XX
PR 04-OCT-1995; 95US-0004778P.
XX
PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
XX
PI Kool ET;
XX
DR WPI; 1997-245044/22.
XX
PT New C-5 thiol-substituted nucleoside derivatives - whose presence in
PT oligo:nucleotide(s) allows formation of covalent cross-links between non-
PT complementary DNA domains.
XX
PS Example 7; Page 89; 122pp; English.
XX
CC This sequence represents an oligonucleotide containing a pentanucleotide
CC loop. The invention relates to C-5 thiol-substituted nucleoside

```
CC   derivatives which can be incorporated into an RNA or DNA strand during
CC   synthesis of oligonucleotides. These compounds can be in the form of
CC   cross-linked linear, cross-linked hairpin or bridged circular oligo-
CC   nucleotides. The oligonucleotides may be used for detection and isolation
CC   of target nucleic acids, or for targeting drugs to specific cell types
CC   (e.g. for treatment of Alzheimer's disease, beta-thalassemia,
CC   osteogenesis imperfecta, arthritis, sickle cell anaemia or viral
CC   infections). The presence of the nucleoside derivatives in a linear
CC   oligonucleotide allows the formation of covalent crosslinks between non-
CC   complementary DNA domains
XX
SQ   Sequence 33 BP; 0 A; 8 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 33;
  Best Local Similarity   85.7%;  Pred. No. 7.6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTTTT 2183
              |||||||| |||||| || |||||| ||
Db          5 TTTTTTCTTCTTTTTCTTCTTTTTCTT 32


RESULT 164
ABK15694
ID   ABK15694 standard; DNA; 33 BP.
XX
AC   ABK15694;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Human activating GTPase negative regulator 11.66 PCR primer #1.
XX
KW   Human; ss; activating GTPase negative regulator 11.66; PCR; primer;
KW   malignant tumour; haemopathy; human immunodeficiency virus infection;
KW   HIV; immunological disease; inflammation; cytostatic; haemostatic;
KW   virucide; immunomodulatory; antiinflammatory.
XX
OS   Homo sapiens.
XX
PN   WO200211511-A1.
XX
PD   14-FEB-2002.
XX
PF   19-JUN-2001; 2001WO-CN001008.
XX
PR   21-JUN-2000; 2000CN-00116684.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-172120/22.
XX
PT   GTPase negative regulator 11.66 polypeptide and encoding polynucleotide,
PT   used in diagnosis and treatment of malignant tumors, hemopathy, human
PT   immunodeficiency virus infection, immunological diseases and
PT   inflammation.
XX
PS   Example 4; Page 13; 36pp; Chinese.
XX
CC   The invention relates to an isolated polypeptide of activating GTPase
CC   negative regulator 11.66, its fragment, analogue or derivative and the
CC   nucleic acid encoding it. Also included are vectors expressing the
CC   protein, a host cell comprising the vector, the isolation of modulators
CC   of the protein and an antibody which recognises the protein. The protein
CC   and nucleic acid are used in diagnosis and treatment of a malignant
CC   tumour, haemopathy, human immunodeficiency virus (HIV) infection,
CC   immunological diseases and various inflammations. The present sequence is
CC   a PCR primer used to clone the cDNA encoding activating GTPase negative
CC   regulator 11.66
XX
SQ   Sequence 33 BP; 3 A; 5 C; 2 G; 23 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 33;
  Best Local Similarity   85.7%;  Pred. No. 7.6e+02;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2158 TTTTCTCCTTTTTTTTTTTTTTTTTT 2185
              | |  | ||||||||||||||||||||||
Db          6 TATGATGCTTTTTTTTTTTTTTTTTT 33


RESULT 165
AAQ25023/c
ID   AAQ25023 standard; DNA; 40 BP.
XX
AC   AAQ25023;
XX
DT   13-JUL-1992  (first entry)
XX
DE   Anti-sense oligonucleotide specific for tRNA_Lys anti-codon region.
XX
KW   HIV; thiolation; reverse transcriptase; primer; inhibition; homooligomer;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9203127-A.
XX
PD   05-MAR-1992.
XX
PF   15-AUG-1991;   91WO-US005919.
XX
PR   16-AUG-1990;   90US-00568131.
XX
PA   (UYNY-) RES FOUND UNIV NEW.
XX
PI   Bardos TJ,  Ho YK,  Aradi J,  Schinazi RF;
XX
DR   WPI; 1992-096567/12.
XX
PT   Compsn. contg. 5-thiolated (oligo-poly-)-nucleotide(s) - for treating HIV
PT   infection, AIDS and for preventing HIV-1 infection.
XX
PS   Disclosure; Page 12; 42pp; English.
XX
CC   The oligomer comprises an 18-mer regional oligonucleotide corrre-
CC   sponding to the anti-codon region of the reverse transcriptase (RT)
CC   primer tRNA_Lys, with a 5' terminal thiolated 22-mer homooligomer. The
CC   homooligomer may be absent and the regional oligo may itself be thiolated
CC   (e.g. 5-Mercapto-), as in Claim 19. The oligos are used to inhibit
CC   reverse transcription in the treatment of HIV. See also AAQ22624-27 and
CC   AAQ25017-Q25032
XX
SQ   Sequence 40 BP; 7 A; 2 C; 3 G; 6 T; 22 U; 0 Other;

  Query Match             0.8%;  Score 21.6;  DB 1;  Length 40;
  Best Local Similarity   85.7%;  Pred. No. 1.2e+03;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              ||  |  ||||||||||||||||||||||
Db         32 TTTAATCTGAAAAAAAAAAAAAAAAAAA 5


RESULT 166
AAH38515
ID   AAH38515 standard; DNA; 25 BP.
XX
AC   AAH38515;
XX
DT   14-AUG-2001  (first entry)
XX
DE   SNP specific SNPE primer SEQ ID 1311.
XX
KW   Single nucleotide polymorphism; SNP; single nucleotide primer extension;
```

KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 56; 83pp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a single nucleotide
CC primer extension (SNPE) primer specific for a human SNP containing DNA
CC sequence
XX
SQ Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

Query Match 0.8%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 4.1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTTTTT 2186
|||||||||||||||||||||||
Db 1 CATTTTTTTTTTTTTTTTTTTTT 23

RESULT 167
AAH43080
ID AAH43080 standard; DNA; 27 BP.
XX
AC AAH43080;
XX
DT 15-OCT-2001 (first entry)
XX
DE Nucleotide sequence of a synthetic oligonucleotide.
XX
KW Nucleic acid immobilisation; ss.
XX
OS Synthetic.
XX
PN WO200155365-A1.
XX
PD 02-AUG-2001.
XX
PF 24-JAN-2001; 2001WO-JP000443.
XX
PR 27-JAN-2000; 2000JP-00019301.
XX
PA (TOJO) TOYO KOHAN CO LTD.
XX
PI Tanga M, Okamura H, Takagi K, Takahashi K;
XX
DR WPI; 2001-488794/53.
XX
PT Support for immobilizing nucleotides.
XX
PS Example 1; Page 8; 18pp; Japanese.
XX
CC The specification describes a support for immobilizing nucleotides which
CC contributes to the efficient clarification of DNA without damaging the
CC terminal parts of the DNA. The support is a chemically treated modified
CC substrate on which oligonucleotides with restriction enzyme cleavage
CC sites are immobilised. The support is useful for immobilizing nucleic
CC acids such as DNA. The present sequence represents a synthetic
CC oligonucleotide used in the course of the invention
XX
SQ Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 21.4; DB 1; Length 27;
Best Local Similarity 95.7%; Pred. No. 5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAA 2803
|||| ||||||||||||||||||
Db 1 AATTCAAAAAAAAAAAAAAAAAA 23

RESULT 168
ABQ79879
ID ABQ79879 standard; DNA; 27 BP.
XX
AC ABQ79879;
XX
DT 23-DEC-2002 (first entry)
XX
DE Nucleotide sequence of a PCR primer #9.
XX
KW Polymerase chain reaction; thermal cycle; immobilisation;
KW genetic engineering; PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2002191369-A.
XX
PD 09-JUL-2002.
XX
PF 27-DEC-2000; 2000JP-00399573.
XX
PR 27-DEC-2000; 2000JP-00399573.
XX
PA (TOJO) TOYO KOHAN CO LTD.
PA (TAKA/) TAKAHASHI K.
XX
DR WPI; 2002-630904/68.
XX
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT a substrate on which a DNA is immobilized used in medical, biochemical,
PT molecular biological and gene engineering fields.

```
XX
PS   Example; Page 10; 13pp; Japanese.
XX
CC   The invention relates to performing a thermal cycle of PCR by using a
CC   substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC   method is useful in the medical, biochemical, molecular biological and
CC   genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC   used in the method of the invention
XX
SQ   Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 27;
  Best Local Similarity   95.7%;  Pred. No. 5e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAA 2803
              |||| ||||||||||||||||||
Db          1 AATTCAAAAAAAAAAAAAAAAA 23


RESULT 169
ABX12469
ID   ABX12469 standard; DNA; 27 BP.
XX
AC   ABX12469;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Coxsackie B virus 4 (CBV-4) strain VD2921, PCR primer dT26V.
XX
KW   Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW   strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW   diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW   renal failure; leg amputation; PCR; primer; ss.
XX
OS   Coxsackievirus.
XX
PN   WO2002103060-A2.
XX
PD   27-DEC-2002.
XX
PF   19-JUN-2002; 2002WO-IB003278.
XX
PR   20-JUN-2001; 2001SE-00002198.
XX
PA   (INNO-) INNOVENTUS PROJECT AB.
XX
PI   Tuvemo HT,  Frisk GE,  Yin H;
XX
DR   WPI; 2003-278229/27.
XX
PT   Polymerase chain reaction and primers for detecting nucleic acids from
PT   the diabetogenic coxsackie B virus-4 strain VD2921.
XX
PS   Example 5; Page 44; 79pp; English.
XX
CC   The invention describes a polymerase chain reaction (PCR) and primers for
CC   detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC   strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC   P3C and P3D nucleic acids). The methods and primers are used for the
CC   detection of CBV-4 strain VD2921 which is associated with diabetes
CC   (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC   detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC   cells, can improve prognosis by allowing treatment e.g. with antiviral
CC   drugs, to prevent further loss of beta cells and severe long term
CC   consequences of diabetes including blindness, renal failure and leg
CC   amputations. This sequence represents a primer used to determine the
CC   genomic structure of diabetogenic coxsackie B virus 4 (CBV-4) strain
CC   VD2921
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 27;
  Best Local Similarity   85.2%;  Pred. No. 5e+02;
  Matches   23;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTTTA 2187
              | |  |||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTV 27


RESULT 170
ADC75074
ID   ADC75074 standard; DNA; 27 BP.
XX
AC   ADC75074;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Biosensor related oligonucleotide of the invention SEQ ID NO:2.
XX
KW   ss; biosensor; hybridisation.
XX
OS   Synthetic.
XX
PN   JP2003172737-A.
XX
PD   20-JUN-2003.
XX
PF   07-DEC-2001; 2001JP-00374764.
XX
PR   07-DEC-2001; 2001JP-00374764.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
XX
DR   WPI; 2003-819164/77.
XX
PT   Solid support body comprising crystal resonator on which a surface
PT   treatment layer is formed, and a substrate whose surface treatment layer
PT   is chemically modified, useful as biosensor.
XX
PS   Disclosure; SEQ ID NO 2; 7pp; Japanese.
XX
CC   The invention relates to a novel solid support body comprising a crystal
CC   resonator on which a surface treatment layer is formed. The biosensor is
CC   useful for analysing biological samples e.g., gene, a protein, and a
CC   peptide, and for analysing bioactive substances. Preferably, the
CC   biosensor is useful for analysing base sequences by carrying out
CC   hybridisation. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 27;
  Best Local Similarity   95.7%;  Pred. No. 5e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAA 2803
              |||| ||||||||||||||||||
Db          1 AATTCAAAAAAAAAAAAAAAAA 23


RESULT 171
AAA57855/c
ID   AAA57855 standard; DNA; 28 BP.
XX
AC   AAA57855;
XX
DT   11-OCT-2000  (first entry)
XX
DE   Deoxy-A22-tagged substrate oligonucleotide.
XX
KW   Ribozyme; catalytic RNA; analyte detection; effector molecule;
KW   nucleic acid substrate; in vitro selection; ribozyme ligase;
KW   conformation dependent activity; allosteric activation; ss.
XX
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        23. .28
FT                   /*tag=  a
FT   misc_binding    24. .28
FT                   /*tag=  b
FT                   /bound_moiety= "Bases 13-17 of N90 RNA pool (AAA57851)"
XX
PN   WO200024931-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-IL000557.
XX
PR   23-OCT-1998;   98IL-00126731.
XX
PA   (INTE-) INTELLIGENE LTD.
XX
PI   Nathan A,  Ellington A;
XX
DR   WPI; 2000-350763/30.
XX
PT   Detecting an analyte in a sample comprises providing nucleic acid
PT   sequence which is catalytically active in presence of analyte, contacting
PT   catalytic nucleic acid with substrate and amplifying catalytic product.
XX
PS   Disclosure; Page; 36pp; English.
XX
CC   The invention relates to a method of detecting an analyte in a sample.
CC   The method comprises providing a nucleic acid sequence which is initially
CC   catalytically inactive, but which becomes catalytically active in the
CC   presence of an analyte (the effector); providing a nucleic acid substrate
CC   for the catalytic activity of the nucleic acid sequence; and contacting
CC   the nucleic acid sequence and the substrate with the sample under
CC   conditions allowing catalytic activity of nucleic acid sequences. The
CC   catalytic nucleic acid sequence will be able to convert the nucleic acid
CC   substrate into a nucleic acid product only if the analyte of interest is
CC   present. The nucleic acid catalytic product is then amplified, and a
CC   significant increase in the amount of product indicates the presence of
CC   the analyte in the sample. The method is useful for the qualitative or
CC   quantitative determination of an analyte in a sample in diagnostic
CC   assays. The invention describes the in vitro selection of a ribozyme
CC   ligase (L1; AAA57859, AAA57860) which is catalytically active only in the
CC   presence of an oligonucleotide effector (AAA57854). The L1 ribozyme
CC   ligase was selected from a pool of RNA molecules comprising a central
CC   randomised region 90 nucleotides in length flanked on both sides by
CC   constant sequence regions (the N90 RNA pool; AAA57851). In the presence
CC   of the effector, selection was performed using one of the tagged
CC   substrate molecules AAA57855-A57857. RNAs with ligase activity (i.e.,
CC   those which have become ligated to the substrate molecule) were reverse
CC   transcribed using the effector oligo, and then PCR amplified using the
CC   effector and a DNA primer identical in sequence to the substrate used for
CC   the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC   can only adopt its active conformation (AAA57859) in the presence of the
CC   effector oligo (analyte). In the absence of the effector, L1 adopts an
CC   inactive conformation (AAA57860). The present sequence represents the
CC   deoxy-A22-tagged substrate oligonucleotide. The dA22 tag enables
CC   successfully ligated products to be isolated using oligo(dT)12-18
CC   cellulose. Note: The present sequence is not given in the specification,
CC   but is created from the inforamtion given on page 11
XX
SQ   Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 28;
  Best Local Similarity   95.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              | ||||||||||||||||||||
Db         24 CATTTTTTTTTTTTTTTTTTTT 2


RESULT 172
AAL43065/c
ID   AAL43065 standard; RNA; 28 BP.
XX
AC   AAL43065;
XX
DT   25-SEP-2002  (first entry)
XX
DE   Regulatable, catalytically active nucleic acid substrate #1.
XX
KW   Regulatable catalytically active nucleic acid; RCANA; ribozyme;
KW   gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "5' biotinylated"
XX
PN   WO200196559-A2.
XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-US019302.
XX
PR   15-JUN-2000; 2000US-0212097P.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Ellington AD,  Hesselberth J,  Marshall K,  Robertson M,  Sooter L;
PI   Davidson E,  Cox JC,  Reidel T;
XX
DR   WPI; 2002-122216/16.
XX
PT   New regulatable, catalytically active nucleic acids (RCANA), useful in
PT   gene therapy (particularly for regulating gene expression), or in assays
PT   for detecting the presence of ligands or activation of an effector of
PT   RCANA.
XX
PS   Example 6; Page 75; 126pp; English.
XX
CC   The present invention relates to regulatable, catalytically active
CC   nucleic acids (RCANAs) which are regulated by polypeptides. These are
CC   useful for regulating gene expression, in assays for detecting the
CC   presence of ligands, for activation of an effector of RCANA, and in gene
CC   therapy. The present sequence is an oligonucleotide substrate used in the
CC   construction of an RCANA
XX
SQ   Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 28;
  Best Local Similarity   95.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              | ||||||||||||||||||||
Db         24 CATTTTTTTTTTTTTTTTTTTT 2


RESULT 173
ADA39569/c
ID   ADA39569 standard; RNA; 28 BP.
XX
AC   ADA39569;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Substrate RNA related oligonucleotide SEQ ID NO:25.
XX
KW   regulatable catalytically active nucleic acid; RCANA; catalytic domain;
KW   regulation; screening; gene therapy; biological pathway regulation;
```

```
KW   regulatory element; metabolic pathway; ribozyme; ss.
XX
OS   Synthetic.
XX
PN   WO2003027310-A2.
XX
PD   03-APR-2003.
XX
PF   24-SEP-2002; 2002WO-US030458.
XX
PR   24-SEP-2001; 2001US-0324715P.
XX
PA   (ARCH-) ARCHEMIX CORP.
XX
PI   Wilson C,  Cload ST,  Keefe AD;
XX
DR   WPI; 2003-354657/33.
XX
PT   Regulating production of a product in a cell, comprises inserting a
PT   regulatable catalytically active nucleic acid into a gene that produces
PT   the product or regulates the production of the product in the cell.
XX
PS   Example 6; Page 76; 128pp; English.
XX
CC   The present invention describes a method for regulating production of a
CC   product in a cell. The method comprises inserting a regulatable
CC   catalytically active nucleic acid (RCANA) into a gene that produces the
CC   product or regulates the production of the product in the cell, where the
CC   RCANA comprises a catalytic domain which modifies a transcript to alter
CC   its coding potential and a regulatory domain that recognises an effector
CC   that alters the function of the catalytic domain, and contacting the
CC   regulatory domain with an effector to regulate production of the product.
CC   Also described: (1) regulating a biological pathway in cell; and (2)
CC   screening a population of cells for a cell that produces a bioproduct.
CC   The methods are useful for regulating a biological pathway in cell, or
CC   regulating production of a product in a cell. The RCANAs are useful as
CC   regulatory elements to control the expression of genes in a metabolic
CC   pathway, or as regulated selectable markers to increase a selective
CC   pressure favouring or disfavouring production of a targeted bioproduct.
CC   The RCANAs are also useful for in vitro or in vivo sensing or detection,
CC   and in gene therapy. The present sequence represents an RNA substrate
CC   oligonucleotide, which is used in an example from the present invention.
XX
SQ   Sequence 28 BP; 23 A; 2 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 28;
  Best Local Similarity   95.7%;  Pred. No. 5.5e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTTTT 2186
              | ||||||||||||||||||||
Db         24 CATTTTTTTTTTTTTTTTTTTT 2


RESULT 174
AAQ68614/c
ID   AAQ68614 standard; cDNA; 29 BP.
XX
AC   AAQ68614;
XX
DT   25-MAR-2003  (revised)
DT   19-JAN-1995  (first entry)
XX
DE   tRNAPolyU reverse tRNA primer.
XX
KW   cDNA; RNA template; reverse-transcriptase; primer; tRNAPolyU;
KW   tRNA template; pUC18; ss.
XX
OS   Synthetic.
XX
PN   WO9413689-A1.
XX
PD   23-JUN-1994.
XX
PF   09-DEC-1993;   93WO-US012029.
XX
PR   09-DEC-1992;   92US-00989851.
XX
PA   (MILL/) MILLER J E.
XX
PI   Miller JE;
XX
DR   WPI; 1994-217796/26.
XX
PT   In vivo cDNA synthesis - by using synthetic polynucleotide(s) which bind
PT   in vivo to RNA templates as primers for reverse transcriptase.
XX
PS   Example 1; Page 33; 102pp; English.
XX
CC   DNA encoding the modified tRNA primer, tRNAPolyU (AAQ68616), was obtained
CC   using the primer pair given in AAQ68612-13. The DNA was cloned in pUC18.
CC   PCR was used to amplify a promoter-tRNA-polyU fragment and to define the
CC   end of the tRNAPolyU coding template. A reverse tRNA primer (AAQ68614)
CC   was used. The 5' base of this primer was also the last 3' base of the
CC   encoded tRNAPolyU template, as shown in AAQ68617. For in vitro production
CC   of tRNAPolyU, a DraI-sensitive T7-tRNAPolyU cassette was linearized and
CC   used as template for in vitro transcription using oligomers AAQ68612 and
CC   AAQ68515. The tRNA primer is used for in vivo cDNA synthesis. (Updated on
CC   25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 29 BP; 22 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 29;
  Best Local Similarity   95.7%;  Pred. No. 6e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTT 2185
              | ||||||||||||||||||||
Db         23 TTCTTTTTTTTTTTTTTTTTT 1


RESULT 175
AAT09934/c
ID   AAT09934 standard; cDNA; 29 BP.
XX
AC   AAT09934;
XX
DT   07-AUG-1996  (first entry)
XX
DE   Reverse tRNA primer #5.
XX
KW   Polymerase chain reaction: PCR; primer; amplify; murine; tRNAproGGG; RT;
KW   DNA polymerase I; bacteriophage T7; RNA polymerase promoter; synthesis;
KW   Moloney Murine Leukaemia Virus; MoMuMLV; reverse transcriptase; analysis;
KW   covalently-linked cDNA; subtractive cDNA library; light sensitive cDNA;
KW   cytotoxic sensitive cDNA; cDNA probe; diagnosis; DNA sequencing; ss.
XX
OS   Synthetic.
XX
PN   WO9535369-A1.
XX
PD   28-DEC-1995.
XX
PF   22-JUN-1995;   95WO-US007968.
XX
PR   22-JUN-1994;   94US-00264038.
XX
PA   (MILL/) MILLER J E.
XX
PI   Miller JE;
XX
DR   WPI; 1996-058406/06.
XX
PT   Method for synthesising covalently linked complementary DNA - uses
PT   primers which can bind reverse transcriptase and anneal to a distinct
PT   template, allowing synthesis to occur.
```

```
XX
PS   Example 1; Page 43; 140pp; English.
XX
CC   This sequence represents a reverse tRNA primer and is used to amplify the
CC   sequence represented by AAT09937. The amplified sequence is used in the
CC   method of the invention, along with the sequence amplified by AAT09930
CC   and AAT09931. The sequence amplified by AAT09930 and AAT09931 is a
CC   recombinant tRNAproGGG primer operatively linked to the bacteriophage T7
CC   RNA polymerase promoter which is capable of binding to the Moloney Murine
CC   Leukaemia Virus (MoMuMLV) reverse transcriptase (RT) and can then be used
CC   in the method of the invention. The method is for synthesising a
CC   covalently-linked cDNA copy of a plurality of polynucleotide template
CC   molecules. In this method, a polynucleotide template primer molecule
CC   (such as the amplified sequence) is used in a mixture with a RT enzyme or
CC   complex. The mixture is then incubated under conditions which permit the
CC   synthesis of a DNA molecule which comprises regions complementary to the
CC   polynucleotide template molecule. The primers and DNA molecules can be
CC   used in the construction of subtractive cDNA libraries, production of
CC   specific cytotoxic or light sensitive cDNA products, and cDNA probes for
CC   analytical, diagnostic or preparative use. Also, they can be used in in
CC   vivo DNA sequencing. The method of cDNA synthesis utilises structure-
CC   specific analogues to the natural target site of the RT enzyme or complex
XX
SQ   Sequence 29 BP; 22 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 29;
  Best Local Similarity   95.7%;  Pred. No. 6e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTT 2185
              | ||||||||||||||||||||||
Db         23 TTCTTTTTTTTTTTTTTTTTTT 1


RESULT 176
AAD33519/c
ID   AAD33519 standard; DNA; 31 BP.
XX
AC   AAD33519;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS4-31-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 31 BP; 25 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 31;
  Best Local Similarity   80.6%;  Pred. No. 7.1e+02;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||||||       ||||||||||||||||||
Db         31 TTTTTTTGGGAGATTTTTTTTTTTTTTTTTT 1


RESULT 177
AAD33521/c
ID   AAD33521 standard; DNA; 32 BP.
XX
AC   AAD33521;
XX
DT   01-JUL-2002  (first entry)
XX
DE   T7T18Apad_PS3-32-0001 probe for calibration of molecular array data.
XX
KW   Molecular array; probe; ss.
XX
OS   Unidentified.
XX
PN   EP1186673-A2.
XX
PD   13-MAR-2002.
XX
PF   10-SEP-2001; 2001EP-00307665.
XX
PR   11-SEP-2000; 2000US-00659173.
XX
PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Wobler PK,  Delenstarr GC;
XX
DR   WPI; 2002-282886/33.
XX
PT   Calibration of molecular array data by employing calibration probes that
PT   generate signals proportional to total concentrations of labeled target
PT   molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS   Disclosure; Page 14; 32pp; English.
XX
CC   The invention relates to a method for calibrating data scanned from a
CC   molecular array. The method involves employing calibration probes that
CC   generate signals proportional to the total concentrations of labelled
CC   target molecules to which the molecular array probes are directed over an
CC   entire range of sample solutions and molecular arrays incorporating sets
CC   of calibration probes. Method is useful for calibrating different types
CC   of signals scanned from a molecular array, or calibrating signals scanned
CC   from different molecular arrays. The present sequence is poly (A)
CC   normalisation probe used in calibration of molecular array data
XX
SQ   Sequence 32 BP; 26 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 32;
  Best Local Similarity   80.6%;  Pred. No. 7.7e+02;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              |||||||       ||||||||||||||||||
Db         31 TTTTTTTGGGAGATTTTTTTTTTTTTTTTTT 1


RESULT 178
ABS53433
```

```
ID   ABS53433 standard; DNA; 32 BP.
XX
AC   ABS53433;
XX
DT   29-NOV-2002  (first entry)
XX
DE   First strand synthesis - first primer.
XX
KW   Terminal continuation; TC; ss; second strand cDNA synthesis; primer.
XX
OS   Synthetic.
XX
PN   WO200265093-A2.
XX
PD   22-AUG-2002.
XX
PF   14-FEB-2002; 2002WO-US005713.
XX
PR   14-FEB-2001; 2001US-0268645P.
PR   14-FEB-2001; 2001US-0268664P.
PR   18-JUL-2001; 2001US-0306216P.
PR   07-NOV-2001; 2001US-0344557P.
PR   07-NOV-2001; 2001US-0348242P.
PR   09-NOV-2001; 2001US-0350176P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (REME-) RES FOUND MENTAL HYGIENE INC.
XX
PI   Ginsberg SD,  Che S;
XX
DR   WPI; 2002-567050/60.
XX
PT   Increasing efficiency of second strand cDNA synthesis using terminal
PT   continuation model before performing further RNA amplification by RNA
PT   transcription.
XX
PS   Example 4; Page 78; 128pp; English.
XX
CC   This invention relates to a novel method for increasing the efficiency of
CC   second strand cDNA synthesis through a mechanism of terminal
CC   continuation. In the method an RNA molecule is obtained and a first
CC   primer is added that comprises a region that hybridises to a
CC   complementary region of the molecule before a second primer is added
CC   comprising at least one riboguanine at the 3' end of the primer. A first
CC   complementary nucleic acid molecule is synthesised, the RNA molecule and
CC   second primer are removed and a second complementary nucleic acid
CC   molecule is synthesised to form a second hybrid with an extension product
CC   of the third primer bound to the first complementary molecule. The method
CC   of the invention is useful for increasing the efficiency of second strand
CC   cDNA synthesis and may be used for linear amplification of genetic
CC   signals from histologically stained tissue. The present sequence
CC   represents a first strand synthesis - first primer used in the method of
CC   the invention
XX
SQ   Sequence 32 BP; 3 A; 4 C; 1 G; 22 T; 0 U; 2 Other;

  Query Match             0.8%;  Score 21.4;  DB 1;  Length 32;
  Best Local Similarity   95.7%;  Pred. No. 7.7e+02;
  Matches   22;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTT 2185
              | ||||||||||||||||||||
Db          8 TTCTTTTTTTTTTTTTTTTTTT 30


RESULT 179
ABK48140
ID   ABK48140 standard; DNA; 24 BP.
XX
AC   ABK48140;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Aspergillus niger aminopeptidase RT-PCR primer poly-T.
XX
KW   Aminopeptidase; primer; ss; food composition; dough; flavour enhancer;
KW   baked product; cheese; poly-T; reverse transcriptase PCR.
XX
OS   Synthetic.
XX
PN   WO200216618-A1.
XX
PD   28-FEB-2002.
XX
PF   22-AUG-2001; 2001WO-EP009925.
XX
PR   23-AUG-2000; 2000EP-00202995.
XX
PA   (STAM ) DSM NV.
XX
PI   Basten D,  Dekker PJT,  Schuurhuizen PW,  Schaap PJ,  Visser J;
XX
DR   WPI; 2002-257917/30.
XX
PT   An isolated polypeptide with aminopeptidase activity, for preparing food
PT   compositions, such as bread and cheese, with enhanced flavoring.
XX
PS   Example 5; Page 40; 94pp; English.
XX
CC   The invention relates to an isolated polypeptide with aminopeptidase
CC   activity and the gene encoding it (including sequences complimentary to
CC   the gene and which hybridise to it at high stringency), from Aspergillus
CC   niger. Also included are a nucleic acid construct comprising the above
CC   polynucleotide operably linked to one or more control sequences that
CC   direct the production of the polypeptide in a suitable expression host, a
CC   recombinant expression vector comprising the above nucleic acid
CC   construct, a recombinant host cell comprising the above construct or
CC   vector, and producing the protein comprising cultivating an above strain/
CC   recombinant host cell to produce a supernatant and/or cells comprising
CC   the polypeptide and recovering the polypeptide. The aminopeptidase is
CC   used to prepare a food composition such as dough to enhance the flavour
CC   of a baked product from the dough and for preparing a cheese to enhance
CC   the flavour. The invention provides a bacterial enzyme for protein
CC   hydrolysis i.e. with aminopeptidase activity, to produce flavouring
CC   agents, and the enzyme has been isolated and characterised, compared to a
CC   previously observed weak aminopeptidase activity which was detected in an
CC   Aspergillus niger culture filtrate but the source was never isolated or
CC   identified. The use of enzymes to produce flavouring agents from
CC   proteinaceous material is better than use of strong acids which can
CC   severely degrade the amino acids obtained. The present sequence is a
CC   reverse transcriptase (RT)-PCR primer used to investigate the intron-exon
CC   structure of the aminopeptidase gene
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 24;
  Best Local Similarity   95.5%;  Pred. No. 4e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||:
Db          3 TTTTTTTTTTTTTTTTTTTTV 24


RESULT 180
AAN70276
ID   AAN70276 standard; DNA; 26 BP.
XX
AC   AAN70276;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC060 (HL).
XX
KW   Hybridisation; probe; ss.
```

```
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   73.1%;  Pred. No. 5e+02;
  Matches   19;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2180
             ||||||| |  |::::|||||||||||
Db          1 TTTTTTTTTTTTTUUUUTTTTTTTTTT 26


RESULT 181
AAN70275
ID   AAN70275 standard; DNA; 26 BP.
XX
AC   AAN70275;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC059 (HL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   76.9%;  Pred. No. 5e+02;
  Matches   20;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2180
             ||||||| |  |::::|||||||||||
Db          1 TTTTTTTTTTTTUUUUTTTTTTTTTT 26


RESULT 182
AAN92241
ID   AAN92241 standard; DNA; 26 BP.
XX
AC   AAN92241;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRC059.
XX
KW   Probe MRC059; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .10
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    11. .14
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    15. .26
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
```

```
CC   Probe MRC059 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   76.9%;  Pred. No. 5e+02;
  Matches   20;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTT 2180
              ||||||| |  :::|||||||||||||
Db          1 TTTTTTTTTTUUUUTTTTTTTTTTT 26


RESULT 183
AAN92242
ID   AAN92242 standard; DNA; 26 BP.
XX
AC   AAN92242;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRC060.
XX
KW   Probe MRC060; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .12
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    13. .16
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    17. .26
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRC060 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   73.1%;  Pred. No. 5e+02;
  Matches   19;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTT 2180
              ||||||| |  |::::|||||||||||
Db          1 TTTTTTTTTTTTUUUUTTTTTTTTT 26


RESULT 184
AAX07466
ID   AAX07466 standard; cDNA; 26 BP.
XX
AC   AAX07466;
XX
DT   08-JUN-1999  (first entry)
XX
DE   Human BS124 specific EST clone oligonucleotide.
XX
KW   BS124; breast; cancer; detection; diagnosis; prevention; treatment; EST;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9859049-A1.
XX
PD   30-DEC-1998.
XX
PF   19-JUN-1998;   98WO-US012862.
XX
PR   20-JUN-1997;   97US-00879354.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Billing-Medel PA,  Cohen M,  Colpitts TL,  Friedman PN,  Gordon J;
PI   Granados EN,  Hodges SC,  Klass MR,  Kratochvil JD,  Russell JC;
PI   Scheffel CP,  Stroupe SD,  Yu H;
XX
DR   WPI; 1999-105623/09.
XX
PT   New isolated BS124 polynucleotides and polypeptides - used for detecting,
PT   diagnosing, preventing or treating diseases or conditions of the breast,
PT   such as breast cancer.
XX
PS   Disclosure; Page 97; 125pp; English.
XX
CC   The sequence is that of an oligonucleotide used in the isolation of a
CC   BS124-specific EST clone. It is useful for detecting, diagnosing,
CC   staging, preventing or treating, or determining predisposition to
CC   diseases or conditions of the breast, such as breast cancer
XX
SQ   Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||||||||   ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTG 26


RESULT 185
```

```
AAX78723
ID   AAX78723 standard; DNA; 26 BP.
XX
AC   AAX78723;
XX
DT   03-SEP-1999  (first entry)
XX
DE   Human pancreatic PA153 EST-specific clone primer 12.
XX
KW   Pancreatic disease; PA153; human; cytostatic; detection; antigen;
KW   anti-PA153; antagonist; therapy; treatment; tumour; metastasis;
KW   gene therapy; EST; expressed sequence tag; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931274-A2.
XX
PD   24-JUN-1999.
XX
PF   11-DEC-1998;   98WO-US026441.
XX
PR   15-DEC-1997;   97US-00990568.
XX
PA   (ABBO ) ABBOTT LAB.
XX
PI   Billing-Medel PA,  Cohen M,  Colpitts TL,  Friedman PN,  Gordon J;
PI   Granados EN,  Hodges SC,  Klass MR,  Kratochvil JD,  Roberts-Rapp L;
PI   Russell JC,  Stroupe SD;
XX
DR   WPI; 1999-405041/34.
XX
PT   PA153 cDNA transcribed from pancreatic tissue.
XX
PS   Example 2; Page 121; 123pp; English.
XX
CC   This invention describes novel contiguous and partially overlapping cDNA
CC   sequences and their encoded polypeptides, designated PA153, transcribed
CC   from human pancreatic tissue and which have cytostatic activity. The
CC   PA153 polynucleotides, proteins and antibodies are all useful in methods
CC   of detection. Detection of PA153 polynucleotide, antigens or anti-PA153
CC   antibodies in a sample is indicative of pancreatic disease. PA153
CC   antibodies (antagonists) can also be used in vivo for therapeutic use,
CC   e.g. treatment of pancreatic disease, tumours or metastases. Antisense
CC   PA153 polynucleotides can be used in gene therapy of pancreatic diseases.
CC   AAX78712-X78725 represent primers used in the method of the invention
XX
SQ   Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTTTG 2193
             |||||||||||||||||||   ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTG 26


RESULT 186
AAF77536
ID   AAF77536 standard; DNA; 26 BP.
XX
AC   AAF77536;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CDNA library production method related oligonucleotide SEQ ID NO: 5.
XX
KW   cDNA library production; SCLA; gene chip technology;
KW   differential screening; pathological diagnosis; genetic identification;
KW   single-cell cDNA library amplification; ds.
XX
OS   Synthetic.
XX
PN   US6197554-B1.
XX
PD   06-MAR-2001.
XX
PF   20-NOV-1998;   98US-00197951.
XX
PR   20-NOV-1998;   98US-00197951.
XX
PA   (LINS/) LIN S.
PA   (CHUO/) CHUONG C.
PA   (YING/) YING S.
XX
PI   Lin S,  Chuong C,  Ying S;
XX
DR   WPI; 2001-243448/25.
XX
PT   Generating a complete full-length cDNA library from single cells for use
PT   in gene chip technology, involves reverse transcribing intracellular
PT   mRNAs, adding polynucleotide tail and amplifying formed cDNAs.
XX
PS   Disclosure; Col 11-12; 11pp; English.
XX
CC   The present invention describes a method of producing full-length cDNA
CC   libraries from single cells, designated single-cell cDNA library
CC   amplification (SCLA). The method is useful in gene chip technology,
CC   differential screening, pathological diagnosis, physiological prognosis
CC   and genetic identification. No further information about this sequence is
CC   given in the specification
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTT 2180
             ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTT 26


RESULT 187
AAF23526
ID   AAF23526 standard; DNA; 26 BP.
XX
AC   AAF23526;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Primer #4.
XX
KW   Primer; mRNA; amplification; ss.
XX
OS   Unidentified.
XX
PN   WO200075356-A1.
XX
PD   14-DEC-2000.
XX
PF   04-JUN-1999;   99WO-US012461.
XX
PR   04-JUN-1999;   99WO-US012461.
XX
PA   (LINS/) LIN S.
PA   (YING/) YING S.
PA   (CHUO/) CHUONG C.
PA   (WIDE/) WIDELITZ R B.
XX
PI   Lin S,  Ying S,  Chuong C,  Widelitz RB;
XX
DR   WPI; 2001-061734/07.
XX
PT   Generating amplified messenger RNA sequences from single cells, involves
```

```
PT   cycling steps of reverse transcription, denaturation, double-stranded DNA
PT   sequences and in vitro transcription.
XX
PS   Disclosure; Page 17; 31pp; English.
XX
CC   The present invention relates to generating amplified messenger RNAs with
CC   polymerase reaction activity, comprising cycling steps of reverse
CC   transcription, denaturation, double-stranded cDNA synthesis and in vitro
CC   transcription. The invention is used for generating amplified mRNAs from
CC   limited mRNAs from single cells
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTT 2180
              ||||||| |  ||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTT 26


RESULT 188
AAS20595
ID   AAS20595 standard; DNA; 26 BP.
XX
AC   AAS20595;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human zsig63 cDNA sequencing primer ZC7231.
XX
KW   Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KW   microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KW   gastrointestinal disease; urinary tract infection; vaginal infection;
KW   skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KW   acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
KW   chronic bronchitis; gene therapy; protein therapy; primer; ZC7231.
XX
OS   Homo sapiens.
XX
PN   US6331413-B1.
XX
PD   18-DEC-2001.
XX
PF   17-MAR-2000; 2000US-00527345.
XX
PR   17-MAR-1999;   99US-0124820P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2002-096707/13.
XX
PT   Polynucleotides encoding salivary proteins useful as anti-microbial
PT   agents.
XX
PS   Example 1; Col 53; 29pp; English.
XX
CC   The invention relates to a polynucleotide derived from the 4q12-4q13
CC   region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC   secreted salivary protein with anti-microbial activity. Due to their
CC   microbial activity, the sequences can be used in the study of microbial
CC   infections, e.g. for recombinant production of anti-microbial proteins.
CC   The sequences can be used in the treatment of tooth decay, periodontal
CC   disease, thrush, gastrointestinal disease, urinary tract infections,
CC   vaginal infections, skin infections, epithelial wounds, chronic tissue
CC   damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC   infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC   represents a sequencing primer for cDNA encoding human zsig63
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 5e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 189
ABS52637
ID   ABS52637 standard; DNA; 26 BP.
XX
AC   ABS52637;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human secreted salivary protein zsig63 PCR primer ZC7321.
XX
KW   Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
KW   antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KW   fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KW   tooth decay; periodontal disease; thrush; gastrointestinal disease;
KW   urinary tract infection; vaginal infection; skin infection; microflora;
KW   epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KW   chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KW   incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KW   chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KW   digestion; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002081701-A1.
XX
PD   27-JUN-2002.
XX
PF   03-AUG-2001; 2001US-00922480.
XX
PR   17-MAR-1999;   99US-0124820P.
PR   17-MAR-2000; 2000US-00527345.
XX
PA   (ADLE/) ADLER D A.
PA   (SHEP/) SHEPPARD P O.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2002-635468/68.
XX
PT   Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT   useful for treating microbial infections, inflammatory conditions, dental
PT   caries and lung infections associated with cystic fibrosis.
XX
PS   Example 1; Page 29; 33pp; English.
XX
CC   The present invention relates to a new secreted salivary protein, zsig63.
CC   The invention is useful for detecting in a test sample, the presence of
CC   an antagonist or agonist of zsig63 protein activity. The invention is
CC   also useful as an immunogen for producing an antibody to zsig63
CC   polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC   protein are useful for enhancing in vivo killing of target tissues.
CC   Pharmaceutical composition comprising purified zsig63 polypeptide are
CC   useful in the treatment of conditions associated with pathological
CC   microbes, including bacterial, fungal and viral infections. High
CC   expression of zsig63 in salivary gland suggests that anti-microbial
CC   polypeptides are useful for treatment of dental caries (tooth decay),
CC   periodontal disease, thrush and gastrointestinal disease. Other
CC   applications can be used in urinary tract infections, vaginal infections,
CC   prevention of infection in skin and other epithelial wounds. The
CC   polypeptides can be used to establish normal microflora and protect
CC   against pathogenic colonisation and invasion. The invention is useful
CC   when pro-inflammatory activity is desired. Applications for such pro-
CC   inflammatory activity include the treatment of chronic tissue damage,
```

```
CC   particularly in areas having a limited or damaged vascular system e.g.,
CC   damage in extremities associated with diabetes. Antagonists to zsig63
CC   polypeptides may be useful as anti-inflammatory agents. The invention is
CC   useful for the treatment of patients having incompetent immune system,
CC   such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC   that have undergone chemotherapy, radiation treatment. The invention is
CC   also useful for the treatment of lung infections associated with cystic
CC   fibrosis and its agonists or antagonists are useful for aiding digestion.
CC   The present nucleic acid sequence represents a PCR primer that was used
CC   in the methods of the invention for identification of zsig63
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 5e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 190
AAD45054
ID   AAD45054 standard; DNA; 26 BP.
XX
AC   AAD45054;
XX
DT   27-DEC-2002  (first entry)
XX
DE   ZC7231 primer used in the identification of human zsig63 DNA.
XX
KW   Human; secreted salivary protein; zsig63 protein; host defense protein;
KW   immune modulating factor; antipathogenic; cell-cell signalling molecule;
KW   growth factor; cytokine; growth factor hormone activity; dental carries;
KW   infection; tooth decay; periodontal disease; gastrointestinal disease;
KW   thrush; urinary tract infection; vaginal infection; diabetes; obesity;
KW   anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
KW   gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KW   forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002090677-A1.
XX
PD   11-JUL-2002.
XX
PF   03-AUG-2001; 2001US-00923236.
XX
PR   17-MAR-1999;   99US-0124820P.
PR   17-MAR-2000; 2000US-00527345.
XX
PA   (ADLE/) ADLER D A.
PA   (SHEP/) SHEPPARD P O.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2002-642378/69.
XX
PT   Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
PT   agent for treating microbial infection, dental carries, periodontal
PT   disease, thrush gastrointestinal disease, and for aiding digestion.
XX
PS   Example 1; Page 29; 33pp; English.
XX
CC   The invention relates to human secreted salivary polypeptide designated
CC   as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
CC   can be used in detecting agonists and antagonists of its activity, and is
CC   also useful as a host defense polypeptide, immune modulating factor,
CC   antipathogenic polypeptide, cell-cell signalling molecule, growth factor,
CC   cytokine, or as secreted extracellular matrix associated proteins with
CC   growth factor hormone activity. It is useful for treating conditions
CC   associated with pathological microbes, including bacterial, fungal and
CC   viral infections, for treating dental carries (tooth decay), periodontal
CC   disease, thrush and gastrointestinal disease, for treating urinary tract
CC   infection, vaginal infection and for preventing infection in skin and
CC   other epithelial wounds. zsig63 is useful for establishing normal
CC   microflora and protect against pathogenic colonisation and invasion, for
CC   treating chronic tissue damage e.g. damage in extremities associated with
CC   diabetes and useful as anti-inflammatory agents. It is useful as a marker
CC   of lung dysfunction, salivary gland dysfunction, or dysfunction of
CC   prostate gland. It is also therapeutically useful for aiding digestion.
CC   Polynucleotides of the invention are used in gene therapy for increasing
CC   or inhibiting zsig63 activity, for detecting abnormalities on human
CC   chromosome 4 associated with disease or other human traits and as
CC   diagnostics in forensic DNA profiling. Sequences of the invention are
CC   useful for stimulating proliferation or differentiation of cardiac
CC   myocytes, for proliferation or differentiation of adipocytes and for
CC   inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The
CC   present sequence is a primer used in the identification of human zsig63
CC   DNA
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 5e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 191
AAD26899/c
ID   AAD26899 standard; DNA; 26 BP.
XX
AC   AAD26899;
XX
DT   09-APR-2002  (first entry)
XX
DE   Bacterial PNP DNA fragment with an out-of-frame polyA tract.
XX
KW   Hypermutable organism; dominant negative allele; mismatch repair gene;
KW   spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
KW   bacteria; ss.
XX
OS   Bacteria.
OS   Unidentified.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .5
FT                   /*tag=  a
FT                   /note= "Bacterial PNP gene"
FT   misc_feature    6. .26
FT                   /*tag=  a
FT                   /note= "Out-of-frame polyA tract"
XX
PN   WO200188192-A2.
XX
PD   22-NOV-2001.
XX
PF   14-MAY-2001; 2001WO-US015376.
XX
PR   17-MAY-2000; 2000US-0204769P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (MORP-) MORPHOTEK INC.
PA   (NICO/) NICOLAIDES N C.
PA   (SASS/) SASS P M.
PA   (GRAS/) GRASSO L.
PA   (VOGE/) VOGELSTEIN B.
PA   (KINZ/) KINZLER K W.
XX
PI   Nicolaides NC,  Sass PM,  Grasso L,  Vogelstein B,  Kinzler KW;
```

```
XX
DR   WPI; 2002-083004/11.
XX
PT   Generating mutation in gene using cells which contain defective mismatch
PT   repair gene, useful to generate genetically altered mutations with new
PT   output traits.
XX
PS   Example 5; Fig 7; 59pp; English.
XX
CC   The patent discloses a method for generating hypermutable organisms.
CC   Dominant negative alleles of human mismatch repair genes can be used to
CC   generate hypermutable cells and organisms. They increase the rate of
CC   spontaneous mutations by reducing the effectiveness of DNA repair and
CC   thereby render the cells or animals hypermutable. The method is used to
CC   produce genetically altered organisms to produce new output traits. The
CC   present sequence is a bacterial poly purine nucleotide phosphorylase
CC   (polyPNP) DNA fragment containing an out-of-frame polyA tract. This
CC   sequence is used in the exemplification of the invention
XX
SQ   Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAACTT 2191
                ||||||||||||||||||||  | |
Db         26 TTTTTTTTTTTTTTTTTTTTGCCAT 1


RESULT 192
AAD39650/c
ID   AAD39650 standard; DNA; 26 BP.
XX
AC   AAD39650;
XX
DT   22-OCT-2002  (first entry)
XX
DE   PolyPNP out-of-frame polyA tract DNA.
XX
KW   Dominant negative allele; mismatch repair gene; D-MMR; gene discovery;
KW   ITRE; inducible transcriptional regulatory element;
KW   recombinant gene mutagenesis; recombinant protein production;
KW   drug target discovery; ds.
XX
OS   Unidentified.
XX
PN   US2002055106-A1.
XX
PD   09-MAY-2002.
XX
PF   14-MAY-2001; 2001US-00853646.
XX
PR   12-MAY-2000; 2000US-0203905P.
PR   17-MAY-2000; 2000US-0204769P.
XX
PA   (NICO/) NICOLAIDES N C.
PA   (SASS/) SASS P M.
PA   (GRAS/) GRASSO L.
PA   (VOGE/) VOGELSTEIN B.
PA   (KINZ/) KINZLER K W.
XX
PI   Nicolaides NC,  Sass PM,  Grasso L,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2002-499469/53.
XX
PT   Generating a mutation in a gene using a dominant negative allele of a
PT   mismatch repair gene which results in mismatch repair deficiency in cells
PT   containing the allele is useful in gene and drug target discovery and
PT   recombinant technology.
XX
PS   Example 5; Fig 7; 25pp; English.
XX
CC   The invention relates to methods for generating a mutation in a gene of
CC   interesting using a dominant negative allele of a mismatch repair gene (D
CC   -MMR) under control of an inducible transcriptional regulatory element
CC   (ITRE). The invention is useful to provide new cell lines that can be
CC   used for gene discovery, drug target discovery, recombinant gene
CC   mutagenesis or recombinant protein production. The present sequence is a
CC   polyPNP (purine phosphorylase) out-of-frame polyA tract DNA
XX
SQ   Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTAACTT 2191
                ||||||||||||||||||||  | |
Db         26 TTTTTTTTTTTTTTTTTTTTGCCAT 1


RESULT 193
AAD43853
ID   AAD43853 standard; DNA; 26 BP.
XX
AC   AAD43853;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Primer #2 used to illustrate the method of the invention.
XX
KW   Single stranded polynucleotide tag; cleavage agent; gene expression;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   WO200259357-A2.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-DK000052.
XX
PR   24-JAN-2001; 2001DK-00000126.
PR   12-FEB-2001; 2001US-0267704P.
XX
PA   (GENO-) GENOMIC EXPRESSION APS.
XX
PI   Pedersen ML;
XX
DR   WPI; 2002-636542/68.
XX
PT   Obtaining single stranded polynucleotide tags from a biological sample,
PT   for analyzing gene expression or diagnosing clinical conditions,
PT   comprises employing nicking endonucleases that cleave complementary
PT   strands.
XX
PS   Example; Page 294; 302pp; English.
XX
CC   The invention relates to a method for obtaining a single stranded
CC   polynucleotide tag from a biological sample by cleaving one of the
CC   complementary strands of a double stranded polynucleotide with a cleavage
CC   agent capable of recognising a double stranded polynucleotide comprising
CC   complementary strands and cleaving only one of the strands of the
CC   polynucleotide in the process of generating a single stranded
CC   polynucleotide tag. The method is useful for separating, analysing,
CC   quantifying or obtaining single stranded polynucleotides comprising tags
CC   originating partly, and preferably wholly from a source of DNA and/or RNA
CC   in a sample comprising biological cells. The method is particularly for
CC   analysing gene expression (expression profiling or differential gene
CC   expression), or in diagnosing clinical conditions. The present sequence
CC   is a primer used in the exemplification of the invention
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
```

```
  Best Local Similarity   88.5%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2180
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTTT 26


RESULT 194
AAD55692
ID   AAD55692 standard; DNA; 26 BP.
XX
AC   AAD55692;
XX
DT   27-OCT-2003  (revised)
DT   07-AUG-2003  (first entry)
XX
DE   Bovine viral diarrhea virus gene 5' end amplifying PCR primer.
XX
KW   Bovine Viral Diarrhea Virus; BVDV; infection; vaccine; prophylaxis;
KW   gene therapy; PCR; primer; ss.
XX
OS   Pestivirus type 1.
XX
PN   WO2003023041-A2.
XX
PD   20-MAR-2003.
XX
PF   05-SEP-2002; 2002WO-EP009925.
XX
PR   06-SEP-2001; 2001DE-01043813.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
PI   Elbers K,  Meyer C,  Von Freyburg M,  Meyers G;
XX
DR   WPI; 2003-333043/31.
XX
PT   New DNA molecule useful for manufacturing a vaccine for the prophylaxis
PT   and treatment of Bovine Viral Diarrhea Virus (BVDV) infections, comprises
PT   a sequence complementary to a BVDV RNA.
XX
PS   Example 1; Page 20; 73pp; English.
XX
CC   The invention relates to a DNA molecule containing a sequence
CC   complementary to a Bovine Viral Diarrhea Virus (BVDV) RNA. The RNA when
CC   introduced into susceptible host cells, induces the generation of
CC   infectious BVDV particles. The attenuated BVDV clone or strain is useful
CC   in the manufacture of a vaccine for the prophylaxis and treatment of BVDV
CC   infections. The invention is useful in gene therapy. The present sequence
CC   is a PCR primer used to amplify BVDV gene. (Updated on 27-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 5e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 195
ABZ24784
ID   ABZ24784 standard; DNA; 26 BP.
XX
AC   ABZ24784;
XX
DT   07-APR-2003  (first entry)
XX
DE   Oligodeoxynucleic acid molecule ODN 24.
XX
KW   Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .26
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "thiophosphate backbone"
XX
PN   WO200295027-A2.
XX
PD   28-NOV-2002.
XX
PF   17-MAY-2002; 2002WO-EP005448.
XX
PR   21-MAY-2001; 2001AT-00000805.
XX
PA   (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI   Lingnau K,  Schellack C,  Schmidt W;
XX
DR   WPI; 2003-183880/18.
XX
PT   New oligodeoxynucleic acid molecules useful for the preparation of
PT   vaccine.
XX
PS   Example 8; Page 32; 57pp; English.
XX
CC   The present sequence is that of a thiosubstituted oligodeoxynucleic acid
CC   (ODN) molecule, ODN 24, including deoxyuridine monophosphates. The
CC   invention is based on the discovery that ODNs containing deoxyuridine
CC   residues (U-ODNs) have an immunostimulatory effect comparable to, or in
CC   many instances greater than, ODNs containing CpG motifs, producing higher
CC   numbers of specific T cells to a given antigen. The U-ODNs do not induce
CC   the systemic production of pro-inflammatory cytokines and, in contrast to
CC   CpG ODNs, are not dependent on a specific motif or a palindromic
CC   sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
CC   Combining the U-ODN with an antigen strongly increases the potential of
CC   the antigen to raise the protection/immune response of a vaccinated
CC   individual. An example of the invention demonstrated the generation of a
CC   specific immune response against a melanoma-derived peptide (see
CC   ABP58360) by injection of mice with the peptide in combination with ODN
CC   24
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 1 T; 25 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   3.8%;  Pred. No. 5e+02;
  Matches    1;  Conservative   22;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2180
              ::::::: :  :::::::::::::::|
Db          1 UUUUUUUUUUUUUUUUUUUUUUUUUU 26


RESULT 196
ABX93598
ID   ABX93598 standard; DNA; 26 BP.
XX
AC   ABX93598;
XX
DT   28-MAY-2003  (first entry)
XX
DE   Human zsig63 PCR/sequencing primer ZC7231.
XX
KW   ss; PCR; zsig63; adhesin; salivary gland; dental carries;
KW   periodontal disease; thrush; gastrointestinal disease; epithelial wound;
KW   urinary tract infection; vaginal infection; skin infection; primer;
KW   pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
```

KW lung infection; cystic fibrosis; lung dysfunction; digestive;
KW salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
KW chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
KW cell culture media; gene therapy; human chromosome 4q12-4q13;
KW dentinogenesis imperfecta; dentin dysplasia type II.
XX
OS Synthetic.
XX
PN US2002173027-A1.
XX
PD 21-NOV-2002.
XX
PF 03-AUG-2001; 2001US-00922469.
XX
PR 17-MAR-1999; 99US-0124820P.
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLE/) ADLER D A.
PA (SHEP/) SHEPPARD P O.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2003-328428/31.
XX
PT Novel isolated zsig63 polypeptide, member of the adhesin family, useful
PT for treating dental carries, periodontal disease, thrush,
PT gastrointestinal disease, urinary tract infections, vaginal infections,
PT skin infections.
XX
PS Example 1; Page 29; 32pp; English.
XX
CC The invention relates to an isolated zsig63 polypeptide comprising at
CC least 90% identity to an amino acid sequence which comprises domain 1 of
CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also
CC included are the polynucleotide encoding zsig63, a zsig63 expression
CC vector, a cultured cell comprising the vector and expressing the protein,
CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a
CC zsig63 reporter gene construct to identify zsig63 agonists, and producing
CC an anti-zsig63 antibody using zsig63 immunogenic peptides, Zsig63 is
CC useful for detecting in a test sample, the presence of antagonist of
CC zsig63 protein activity. Zsig63 has antimicrobial activity and since
CC exhibits high expression in salivary gland, can be used for treating
CC dental carries, periodontal disease, thrush, and gastrointestinal
CC disease, urinary tract infections, vaginal infections, skin infections
CC and other epithelial wounds. The polypeptides can be used to establish
CC normal microflora and protect against pathogenic colonization and
CC invasion. Zsig63 can also be used for providing pro-inflammatory activity
CC for treating chronic, tissue damage particularly in areas having limited
CC or damaged vascular system, e.g. in diabetes, and for treating
CC immunocompromised AIDS patients or in individuals that have undergone
CC chemotherapy, radiation treatment, for treating lung infections e.g. in
CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high
CC levels in the trachea may indicate that such polypeptides may serve as a
CC marker of lung dysfunction. Zsig63 is also useful in diagnosing
CC conditions associated with salivary gland or lung dysfunction including
CC salivary gland carcinoma, Pneumocystis carinii infection, emphysema,
CC chronic bronchitis, prostate dysfunctions such as prostate
CC adenocarcinoma, aiding digestion, and as components of defined cell
CC culture media and may be used to replace serum that is commonly used in
CC culture. The DNA is useful in gene therapy applications to increase or
CC inhibit zsig63 activity, and for detecting abnormalities on human
CC chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta,
CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The
CC present sequence is a primer used to isolate and sequence nucleic acdis
CC encoding human zsig63
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 0.8%; Score 21.2; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 5e+02;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||:
Db 5 TTTTTTTTTTTTTTTTTTTTV 26

RESULT 197
ACA62282
ID ACA62282 standard; DNA; 26 BP.
XX
AC ACA62282;
XX
DT 12-AUG-2003 (first entry)
XX
DE Oligo (dT) primer #1.
XX
KW ss; PCR; primer; antisense therapy; mRNA expression profile;
KW promoter containing primer.
XX
OS Synthetic.
XX
PN US2003022318-A1.
XX
PD 30-JAN-2003.
XX
PF 07-SEP-2001; 2001US-00949305.
XX
PR 25-JAN-2000; 2000US-00494212.
XX
PA (EPIC-) EPICLONE INC.
XX
PI Lin S, Ying S;
XX
DR WPI; 2003-479488/45.
XX
PT Improved polymerase thermocycling reaction for nucleic acid
PT amplification, by thermal cycling of promoter-linked nucleic acid
PT template synthesis and in vitro transcriptional amplification of nucleic
PT acid sequences.
XX
PS Example 4; Page 14; 28pp; English.
XX
CC The invention relates to an improved polymerase thermocycling reaction
CC (M1) for linear amplification of nucleic acid sequences, involves
CC denaturing a number of nucleic acid templates (I), combining the
CC denatured (I) with a promoter-containing primer (P1), a primer (P2), a
CC number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
CC a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
CC polymerase, contacting P1 with (I) to generate a number of promoter-
CC containing templates, denaturing the promoter-containing templates,
CC contacting P2 with the denatured promoter-containing templates to
CC generate a number of promoter-containing double-stranded DNA templates,
CC where the double-stranded nucleic acid templates are flanked by P1 in one
CC end and P2 in the other end of the other orientation, transcribing the
CC promoter-containing double-stranded DNA templates to form a number of
CC amplified RNA sequences, including the primer region of the promoter-
CC containing double-stranded DNA templates, contacting the amplified RNA
CC sequences with P2 to form a number of cDNAs and a number of DNA-RNA
CC hybrid templates, and denaturing the DNA-RNA hybrid templates. The method
CC is useful for improved polymerase thermocycling reaction for linear
CC amplification of nucleic acid sequences, and thus for producing mRNA
CC expression profile of a cell by M1 to generate multiple copies of the
CC mRNA. M1 is also useful for determining aberrant protein production of
CC cells in a diseased state, by generating an expression profile by the
CC above method, of cells in both normal and diseased states, comparing the
CC expression profile of the cells in the normal and diseased states,
CC determining the differences in mRNA composition of the cell(s) in the
CC diseased state, isolating the mRNA sequences of cell(s) in the diseased
CC state that differ from mRNA in cell(s) in non-diseased state, amplifying
CC the isolated mRNA by M1, and determining aberrant protein function of the
CC protein coded for by the isolated mRNA. M1 is also useful for treating a
CC cell in a diseased state caused by aberrant protein production, by
CC determining protein expression of a cell in a diseased state, determining
CC the mRNA sequence for the aberrant proteins, synthesising an antisense

```
CC   sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and
CC   delivering a pharmaceutically effective dosage of a composition
CC   comprising the anti-sense mRNA and a compatible lipid based biological
CC   carrier. M1 is also useful for predicting the efficacy of a proposed drug
CC   targeted against an aberrant protein, by determining aberrant protein
CC   production of cell in a diseased state by the above method, amplifying
CC   the aberrant protein by M1 and using recombinant techniques to determine
CC   the effect of proposed drug on the aberrant protein. M1 is also useful
CC   for differential screening of tissue-specific gene expression at a
CC   cellular level, for preparing labeled RNA/DNA probes for a gene chip
CC   technology, and for determining the efficacy of a drug regiment against a
CC   gene or its cDNAs. The present sequence is an Oligo (dT) primer used to
CC   produce second strand cDNA in the method of the invention
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   88.5%;  Pred. No. 5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTT 2180
              ||||||| |  ||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTT 26


RESULT 198
ACF36382
ID   ACF36382 standard; DNA; 26 BP.
XX
AC   ACF36382;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Nucleotide sequence of a second back primer.
XX
KW   Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW   electrophoresis; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003064691-A2.
XX
PD   07-AUG-2003.
XX
PF   28-JAN-2003; 2003WO-IB000843.
XX
PR   29-JAN-2002; 2002US-0352215P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G,  Metsis A,  Pihlak A;
PI   Montelius A;
XX
DR   WPI; 2003-618365/58.
XX
PT   Producing a population of double-stranded product DNA molecules, useful
PT   for mRNA profiling, comprises amplification by nested polymerase chain
PT   reaction.
XX
PS   Claim 6; Page 85; 105pp; English.
XX
CC   The invention relates to producing a population of double-stranded
CC   product DNA molecules comprising amplification by a nested PCR method.
CC   The method is useful in profiling mRNA transcribed in a system under
CC   investigation. The oligonucleotides are used as size standards in
CC   electrophoresis, and as internal controls allowing for calculation of
CC   relative amounts of material present. The present sequence represents a
CC   specific example of a PCR primer used in the method of the invention
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 26;
  Best Local Similarity   95.5%;  Pred. No. 5e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 199
AAV71936
ID   AAV71936 standard; DNA; 27 BP.
XX
AC   AAV71936;
XX
DT   18-FEB-1999  (first entry)
XX
DE   Anchored poly T RT-PCR primer.
XX
KW   Normalised; cDNA library; mRNA cloning; reverse transcription;
KW   immobilise; screening; hybridisation; nucleic acid amplification;
KW   expression pattern; drug development; PCR primer; RT-PCR; ss.
XX
OS   Synthetic.
XX
PN   WO9851789-A2.
XX
PD   19-NOV-1998.
XX
PF   13-MAY-1998;   98WO-DK000186.
XX
PR   13-MAY-1997;   97DK-00000547.
PR   19-MAY-1997;   97US-00871030.
PR   27-MAR-1998;   98DK-00000432.
XX
PA   (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX
PI   Warthoe PR;
XX
DR   WPI; 1999-009772/01.
XX
PT   Preparation of normalised, subdivided cDNA libraries from mRNA - by
PT   reverse transcription and amplification, used to screen for new genes and
PT   interacting proteins, potential drugs, and for diagnosis.
XX
PS   Example 1; Page 29; 71pp; English.
XX
CC   The invention relates to preparation of a normalised, subdivided library
CC   of amplified cDNA from the coding regions of mRNA in a sample. The method
CC   involves reverse transcription, with at least one cDNA primer of formula
CC   5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence
CC   of 1-100 nucleotides; dT = deoxythymidinyl; n2 is at least 1; n3 and n4
CC   are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
CC   cDNA synthesis using the first strand as template and a second cDNA
CC   primer of a similar formula, in the presence of DNA polymerase I (or its
CC   Klenow fragment) and amplification of double-stranded cDNA with a set of
CC   amplification primers. Comparison of cDNA in the prepared library with a
CC   database (a computer-generated list of molecular weights of restricted
CC   DNA fragments of known sequence) is used to determine presence of an
CC   expressed protein in a cell, also to detect changes in such expression
CC   (particularly for diagnosis of disease). Surfaces (chip) having amplified
CC   cDNA stably immobilised on it, obtained by a similar method, are used to
CC   screen for genes of a particular family, by hybridisation with nucleic
CC   acid from the family (to identify new genes) and to detect differences in
CC   expression patterns between cells. The polypeptides expressed by the
CC   libraries can be used for drug development. Sequences AAV71935 to
CC   AAV71946 represent primers used to exemplify the method of the invention
XX
SQ   Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 27;
  Best Local Similarity   88.5%;  Pred. No. 5.5e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACTTTG 2193
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                    ||||||||||||||||||    ||||
Db          1 TTTTTTTTTTTTTTTTTTTTTTTTG 26


RESULT 200
ABQ76254
ID   ABQ76254 standard; DNA; 27 BP.
XX
AC   ABQ76254;
XX
DT   08-NOV-2002  (first entry)
XX
DE   Murine SCCE 5'-RACE oligonucleotide SEQ ID 42.
XX
KW   SCCE; murine; stratum corneum chymotryptic enzyme; kallikrein 7;
KW   serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW   hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW   pruritus; atopic dermatitis; eczema; acne; itch; KLK7; ss.
XX
OS   Mus musculus.
XX
PN   WO200262135-A2.
XX
PD   15-AUG-2002.
XX
PF   08-FEB-2002; 2002WO-IB001300.
XX
PR   09-FEB-2001; 2001CA-02332655.
PR   09-FEB-2001; 2001DK-00000218.
XX
PA   (EGEL/) EGELRUD T.
PA   (HANS/) HANSSON L.
XX
PI   Egelrud T,  Hansson L;
XX
DR   WPI; 2002-643380/69.
XX
PT   Transgenic mammal or its embryo useful as model for human disease, has
PT   heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT   enzyme operably linked to promoter that drives its expression in skin.
XX
PS   Example 6; Page 36; 74pp; English.
XX
CC   This invention describes a novel non-human transgenic mammal or mammalian
CC   embryo having integrated within its genome, a heterologous nucleotide
CC   sequence comprising at least a significant part of a nucleotide sequence
CC   coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant,
CC   operably linked to a promoter that drives expression of heterologous scce
CC   or its variant in skin. The product of the invention is useful as a model
CC   for the study of disease with the aim of improving treatment, to relieve
CC   or ameliorate a pathogenic condition, for development or testing of a
CC   cosmetic or a pharmaceutical formulation, and for the development of a
CC   diagnostic method. It can also be used as a model for a skin disease or
CC   skin cancer. The invention is also useful for screening or identifying a
CC   compound or composition effective for the prevention or treatment of an
CC   abnormal or unwanted phenotype, and for screening or identifying a
CC   compound or composition effective for the prevention or treatment of
CC   inflammatory skin diseases selected from diseases consisting of epidermal
CC   hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC   pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC   with epidermal hyperkeratosis. The mammal of the invention is also useful
CC   as a model for further studies of itch mechanisms and the testing of
CC   potential compounds and compositions for relieve of various skin diseases
CC   where itch is a component. This sequence represents a 5' RACE cDNA
CC   synthesis primer used in a method of detecting homologues to human
CC   stratum corneum chymotryptic enzyme, SCCE, gene. SCCE is a serine
CC   protease synonymous with human kallikrein 7 (KLK7) and is used in the
CC   development of the transgenic mammals described in the invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 27;
  Best Local Similarity   95.5%;  Pred. No. 5.5e+02;
  Matches   21;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||||:
Db          5 TTTTTTTTTTTTTTTTTTTTV 26


RESULT 201
ABX89953
ID   ABX89953 standard; DNA; 30 BP.
XX
AC   ABX89953;
XX
DT   30-APR-2003  (first entry)
XX
DE   PolyA adapter DNA.
XX
KW   Probe; detection; genotyping; cell status; chromosomal resistance gene;
KW   array; ss.
XX
OS   Synthetic.
XX
PN   DE10117857-A1.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2001; 2001DE-01017857.
XX
PR   10-APR-2001; 2001DE-01017857.
XX
PA   (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX
PI   Ellinger T,  Ehricht R,  Wagenhaus A,  Ermantraut E;
XX
DR   WPI; 2003-068801/07.
XX
PT   Detecting specific interactions between molecular targets and probes,
PT   useful for determining genotypic and physiological status of cells, by
PT   attaching an markable adapter to the target.
XX
PS   Example 1; Page 8; 25pp; German.
XX
CC   This invention describes a novel method for detecting the specific
CC   interaction between a target sequence, especially a nucleic acid, and a
CC   probe on an array, in which adapter molecules are fixed to the target,
CC   forming a continuous sequence. Labelling of the target is independently
CC   mediated by interaction of the adapter molecule with a label. The method
CC   is used to investigate the genotypic and physiological status of cells,
CC   e.g. to detect chromosomal resistance genes in Staphylococcus aureus. The
CC   method provides a modular, specific and sensitive system for quantitative
CC   or qualitative detection of a specific target. It provides efficient,
CC   homogeneous and parallel labeling of a target, before, during or after
CC   interaction with the probe array, and both DNA and RNA can be labeled.
CC   The detection signal may be amplified and only low concentrations of
CC   label (particularly 0.1-1 micro M) are used, so non-specific signals are
CC   minimised. This sequence represents a polyA adapter used in the method
CC   described in the invention
XX
SQ   Sequence 30 BP; 5 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.8%;  Score 21.2;  DB 1;  Length 30;
  Best Local Similarity   88.5%;  Pred. No. 7.1e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTAACTTT 2192
              ||||||||||||||||||||  | |
Db          1 TTTTTTTTTTTTTTTTTTTTATATAT 26


RESULT 202
AAQ75733
ID   AAQ75733 standard; DNA; 21 BP.
XX
```

```
AC   AAQ75733;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAACT 21


RESULT 203
AAQ75757/c
ID   AAQ75757 standard; DNA; 21 BP.
XX
AC   AAQ75757;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              |||||||||||||||||||||
Db         21 ATTGAAAAAAAAAAAAAAAAA 1


RESULT 204
AAX26973
ID   AAX26973 standard; cDNA; 21 BP.
XX
AC   AAX26973;
XX
DT   25-JUN-1999  (first entry)
XX
DE   Primer used to reverse transcribe mammaglobin RNA.
XX
KW   Human; mammary-specific protein; mammaglobin; antigen; vaccine;
KW   mammaglobin-expressing cancer; breast cancer;
KW   autologous tumor lymphocyte; diagnosis; marker; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9914230-A1.
XX
PD   25-MAR-1999.
XX
PF   18-SEP-1998;   98WO-US017991.
XX
PR   18-SEP-1997;   97US-00933149.
XX
PA   (UNIW ) UNIV WASHINGTON.
XX
PI   Watson MA,  Fleming TP;
XX
DR   WPI; 1999-244021/20.
XX
PT   Mammaglobin, secreted protein overexpressed in breast cancer.
XX
PS   Example 2; Page 55; 60pp; English.
XX
CC   The present primer was used to reverse transcribe RNA encoding a human
CC   mammary-specific protein, designated mammaglobin. The specification
CC   describes a protein comprising a mammaglobin antigen that is recognized
CC   by B and/or Tc cells specific for the natural, secreted and glycosylated
CC   form of mammaglobin polypeptide. This protein, or recombinant vectors
CC   that express it, are used in vaccines for treating mammaglobin-
CC   expressing cancers, specifically of the breast. Such cancers can also be
CC   treated using autologous tumor lymphocytes activated ex vivo with an
CC   mammaglobin antigen, then returned to the patient. Expression of
CC   mammaglobin is elevated in 27% of stage I primary breast cancers, so it
CC   represents a marker useful for diagnosis of this disease
XX
```

```
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 205
AAZ44350
ID   AAZ44350 standard; DNA; 21 BP.
XX
AC   AAZ44350;
XX
DT   04-APR-2000  (first entry)
XX
DE   Protein kinase inhibiting primer #12.
XX
KW   Antimicrobial; cytostatic; immunosuppressive; protein kinase;
KW   prophylactic; therapy; treatment; cancer; autoimmune disease;
KW   pathogenic microorganism; primer; ss.
XX
OS   Unidentified.
XX
PN   US5998596-A.
XX
PD   07-DEC-1999.
XX
PF   04-APR-1995;   95US-00416214.
XX
PR   04-APR-1995;   95US-00416214.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Bergan R,  Neckers L;
XX
DR   WPI; 2000-104623/09.
XX
PT   Oligonucleotides inhibiting protein kinase, useful for treating diseases
PT   such as cancer and autoimmune disease.
XX
PS   Example 8; Col 27-28; 26pp; English.
XX
CC   This invention describes novel purified aptameric oligonucleotides which
CC   have antimicrobial, cytostatic and immunosuppressive activity. The
CC   oligonucleotides are useful for binding to and preventing or inhibiting
CC   the biological function of a protein kinase or a target molecule and for
CC   detecting the presence or absence of a target molecule in biological
CC   samples. The oligonucleotides are also useful for prophylactic and
CC   therapeutic treatment of diseases such as cancer, autoimmune diseases and
CC   diseases caused by pathogenic microorganisms. This sequence represents a
CC   primer used in the method of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 206
AAF99707
ID   AAF99707 standard; DNA; 21 BP.
XX
AC   AAF99707;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #823.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 207
AAH42480
ID   AAH42480 standard; DNA; 21 BP.
XX
AC   AAH42480;
XX
DT   01-OCT-2001  (first entry)
XX
DE   Oligonucleotide used to produce branched chain compounds.
XX
KW   Branched chain compound; nucleic acid synthesis; primer extension;
KW   reverse transcription; nucleic acid hybridization;
KW   nucleic acid amplification; ss.
XX
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "NH2-C6 attached"
FT   modified_base   4
FT                   /*tag=  b
FT                   /note= "NH2-C6 attached"
FT   misc_feature    6. .7
FT                   /*tag=  c
FT                   /note= "branch present"
XX
PN   EP1111068-A1.
XX
PD   27-JUN-2001.
XX
PF   21-DEC-1999;   99EP-00125484.
XX
PR   21-DEC-1999;   99EP-00125484.
XX
PA   (LION-) LION BIOSCIENCE AG.
PA   (VBCG-) VBC GENOMICS GMBH.
XX
PI   Schmidt W,  Hiller R,  Huber M,  Mueller M;
XX
DR   WPI; 2001-466959/51.
XX
PT   Branched compounds useful in e.g. nucleic acid synthesis reaction
PT   comprises nucleic acid moieties optionally extended by a polymerase.
XX
PS   Example 1; Page 10; 31pp; English.
XX
CC   The specification describes branched compounds containing nucleic acid
CC   moieties optionally extended by a polymerase. The branched chain
CC   compounds of the invention are used in nucleic acid synthesis reaction,
CC   primer extension reaction, reverse transcription reaction of RNA into
CC   DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC   nucleic acid), and nucleic acid amplification experiment (for analysing
CC   the expression pattern of genes). The compounds are also used in solid-
CC   phase enzymatic reactions. The present sequence was used in the course of
CC   the invention to produce branched chain compounds
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTT 21


RESULT 208
ABS78428
ID   ABS78428 standard; DNA; 21 BP.
XX
AC   ABS78428;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #912.
XX
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 35; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTT 21


RESULT 209
ABL39404
ID   ABL39404 standard; DNA; 21 BP.
XX
AC   ABL39404;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 840.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .21
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
```

```
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 309; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 210
AAD51323
ID   AAD51323 standard; DNA; 21 BP.
XX
AC   AAD51323;
XX
DT   16-APR-2003  (first entry)
XX
DE   Regular oligo dT primer used to illustrate the method of the invention.
XX
KW   Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
KW   gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
KW   musculoskeletal damage; ss.
XX
OS   Unidentified.
XX
PN   WO200290579-A1.
XX
PD   14-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-AU000553.
XX
PR   04-MAY-2001; 2001AU-00004809.
PR   29-JUN-2001; 2001US-00896941.
XX
PA   (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX
PI   Brandon RB;
XX
DR   WPI; 2003-120558/11.
XX
PT   Assessing condition e.g. athletic ability, stage of disease, presence of
PT   drugs, response to exercise, response to vaccines, therapies, nutritional
PT   states, of performance animal involves analyzing nucleic acid expression.
XX
PS   Disclosure; Page 46; 87pp; English.
XX
CC   The invention relates to a method for assessing a condition of a
CC   performance animal. The method involves determining in sample abundance
CC   of expressed target nucleic acid; transmitting digital sample signal to
CC   remote diagnostic server; processing digital sample signal at remotely
CC   located database to correlate digital signal with digital information and
CC   returning report of particular condition of animal. The method is useful
CC   for assessing a condition of a performance animal preferably human, dog
CC   or camel. The condition can be an athletic ability and a condition that
CC   enhances, hinders, impedes or does not change an expected ability of the
CC   performance animal; and also normal, pre-clinical, overt progress and/or
CC   stage of disease, undiagnosed of unclassified conditions, presence of
CC   drugs, response to exercise, response to vaccines, therapies, nutritional
CC   states and response to environmental conditions. Diseases assessed by the
CC   invention include laminitis, lameless, viral or bacterial disease,
CC   gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
CC   musculoskeletal damage or disorders and joint diseases. The present
CC   sequence is a primer used to illustrate the method of the invention
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 211
AAL62266/c
ID   AAL62266 standard; DNA; 21 BP.
XX
AC   AAL62266;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human TFAP2C DNA specific reverse PCR primer.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 14; Page 77; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
```

```
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is a PCR primer specific for
CC   human TFAP2C DNA. This sequence is used to illustrate the method of the
CC   invention
XX
SQ   Sequence 21 BP; 7 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1123 TGTCTGTGAAGCCGAATTTCC 1143
              |||||||||||||||||||||
Db         21 TGTCTGTGAAGCCGAATTTCC 1


RESULT 212
ACH03246
ID   ACH03246 standard; DNA; 21 BP.
XX
AC   ACH03246;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #881.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 33; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 213
ADB37209
ID   ADB37209 standard; DNA; 21 BP.
XX
AC   ADB37209;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #823.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 17; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 214
AAQ64724/c
ID   AAQ64724 standard; cDNA to mRNA; 22 BP.
XX
AC   AAQ64724;
XX
DT   25-MAR-2003  (revised)
DT   04-JAN-1995  (first entry)
XX
DE   2',5'-linked tetraadenylate-anti(dT)18 oligonucleotide chimeric mol.
```

```
XX
KW   antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW   RNA cleavage; antiviral therapy; chimeric molecule; PKR;
KW   protein synthesis regulation; phosphorylation; eIF-2alpha;
KW   eukaryotic translation initiation factor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .4
FT                   /*tag=  a
FT                   /label= 2',5'-linked_tetraadenylate
FT                   /note= "nucleotides linked through phosphodiester bonds
FT                   at hydroxyl groups of 2' and 5' carbons"
FT   misc_feature    4. .5
FT                   /*tag=  b
FT                   /note= "the 2-5A moiety (*tag = a) and the antisense DNA
FT                   sequence (*tag = c) are linked by two 1,4-butanediol
FT                   molecules linked through phosphodiester bonds"
FT   misc_feature    5. .22
FT                   /*tag=  c
FT                   /note= "antisense region, complementary to oligo dT"
XX
PN   WO9409129-A2.
XX
PD   28-APR-1994.
XX
PF   20-OCT-1993;   93WO-US010103.
XX
PR   21-OCT-1992;   92US-00965666.
PR   17-SEP-1993;   93US-00123449.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (CLEV-) CLEVELAND CLINIC RES INST.
XX
PI   Torrence P,  Silverman R,  Maitra R,  Lesiak K;
XX
DR   WPI; 1994-151315/18.
XX
PT   Specific cleavage of RNA, useful partic. for treating viral infection,
PT   cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
PT   of 2-5A dependent RNase.
XX
PS   Example 9; Page 66; 86pp; English.
XX
CC   This sequence was used to determine whether 2-5A-antisense chimeric
CC   molecules are inhibitory to cell growth. The molecules AAQ64709, AAQ64711
CC   and AAQ64724 all lacked cytotoxicity. In the novel 2-5A-antisense
CC   oligonucleotide chimeric molecules, the antisense region targets the
CC   chimeric molecule to a particular region of RNA to be specifically
CC   cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A
CC   RNase. Typical applications are treatment of viral infections (esp. for
CC   cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular
CC   disorders (e.g. restenosis after angioplasty), genetic disorders,
CC   osteoarthritis or rheumatoid arthritis. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db         22 TTTTTTTTTTTTTTTTTTTTT 2


RESULT 215
AAF17413/c
ID   AAF17413 standard; DNA; 22 BP.
XX
AC   AAF17413;
XX
DT   09-MAR-2001  (first entry)
XX
DE   L1 cleavage site related sequence #3.
XX
KW   Retrotransposon; genetic defect; cystic fibrosis; ds.
XX
OS   Unidentified.
XX
PN   US6150160-A.
XX
PD   21-NOV-2000.
XX
PF   28-APR-1997;   97US-00847844.
XX
PR   16-NOV-1995;   95US-0006831P.
PR   15-NOV-1996;   96US-00749805.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Moran JV,  Dombroski BA,  Kazazian HH,  Boeke JD;
XX
DR   WPI; 2001-060015/07.
XX
PT   DNAc comprising a promoter P and an L1 cassette sequence having a core
PT   retrotransposon element, useful for random insertion of a heterologous or
PT   homologous DNA sequence into a cell genome and for correcting genetic
PT   defects.
XX
PS   Disclosure; Fig 14; 87pp; English.
XX
CC   The present invention relates to DNA for a promoter and an L1 cassette
CC   sequence having a core retrotransposon element. The invention is useful
CC   for random insertion of a heterologous or homologous DNA sequence into a
CC   cell genome, and for correction of a genetic defect in the cell into
CC   which the insertion is made. Genetic defects which may be corrected
CC   includes cystic fibrosis, mutations in the dystrophin gene, genetic
CC   defects associated with blood clotting and other genetic defects
XX
SQ   Sequence 22 BP; 22 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db         22 TTTTTTTTTTTTTTTTTTTTT 2


RESULT 216
AAC62450
ID   AAC62450 standard; DNA; 23 BP.
XX
AC   AAC62450;
XX
DT   07-FEB-2001  (first entry)
XX
DE   Cleavage of nucleic acids from solid supports assay oligonucleotide #1.
XX
KW   Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW   affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW   nucleic acid purification; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        23
FT                   /*tag=  a
XX
PN   WO200058329-A1.
XX
```

PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB001190.
XX
PR 29-MAR-1999; 99GB-00007245.
XX
PA (GOLD/) GOLDSBOROUGH A.
XX
DR WPI; 2000-664908/64.
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves cleaving
PT the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS Disclosure; Page 16; 47pp; English.
XX
CC The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is
CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention
XX
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 21

RESULT 217
AAC62451
ID AAC62451 standard; RNA; 23 BP.
XX
AC AAC62451;
XX
DT 07-FEB-2001 (first entry)
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #2.
XX
KW Nucleic acid cleavage; solid support; affinity chromatography;
KW sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.
XX
OS Synthetic.
XX
PN WO200058329-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB001190.
XX
PR 29-MAR-1999; 99GB-00007245.
XX
PA (GOLD/) GOLDSBOROUGH A.
XX
DR WPI; 2000-664908/64.
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves cleaving
PT the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS Example 1; Page 32; 47pp; English.
XX
CC The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is
CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention
XX
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 0 T; 23 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 23;
Best Local Similarity 0.0%; Pred. No. 3.9e+02;
Matches 0; Conservative 21; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
::::::::::::::::::::
Db 1 UUUUUUUUUUUUUUUUUUUU 21

RESULT 218
AAF16627
ID AAF16627 standard; DNA; 23 BP.
XX
AC AAF16627;
XX
DT 13-MAR-2001 (first entry)
XX
DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.
XX
KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
KW DNA-RNA hybrid; ss.
XX
OS Homo sapiens.
XX
PN WO200071164-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-AU000498.
XX
PR 24-MAY-1999; 99AU-00000510.
XX
PA (TACH/) TACHAS G.
XX
PI Tachas G;
XX
DR WPI; 2001-025093/03.
XX
PT Treating gastric acid disturbance by administering an oligonucleotide
PT which modulates the activity of a polypeptide involved in gastric acid
PT production or secretion.
XX
PS Example 3; Page 152; 164pp; English.
XX
CC The present invention provides oligonucleotides, and methods for their
CC use, which are useful in modulating the action of proteins involved in
CC gastric acid production. The target protein is preferably the histamine
CC H2 receptor or one of the proteins which form part of the gastric proton
CC pump. The sequences and methods of the invention are useful in the
CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
CC duodenal ulcers and other gastric acid disturbances, most of which are
CC caused by Helicobacter pylori
XX
SQ Sequence 23 BP; 1 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 3 TTTTTTTTTTTTTTTTTTTT 23

```
RESULT 219
AAT99286/c
ID   AAT99286 standard; DNA; 24 BP.
XX
AC   AAT99286;
XX
DT   15-APR-1998  (first entry)
XX
DE   POLYA, a competitor oligonucleotide for binding human PUR-alpha.
XX
KW   PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW   cancer; probe; hybridisation.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5672479-A.
XX
PD   30-SEP-1997.
XX
PF   07-JUN-1995;   95US-00486421.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
PR   06-JUN-1995;   95US-00470911.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1997-488859/45.
XX
PT   Assays for PUR protein ligands or modulators - using immobilised PUR
PT   protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
PS   Example; Col 33; 64pp; English.
XX
CC   The oligonucleotides AAT99279-T99286 were used as competitor
CC   oligonucleotides for the binding of PUR prtein to DNA. The PUR sequence
CC   can be used to identify chemical or biological compounds that bind to PUR
CC   or binding fragments of PUR. Inhibitors of PUR activity may be used to
CC   treat hyperproliferative diseases such as cancer
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 220
AAV31743/c
ID   AAV31743 standard; DNA; 24 BP.
XX
AC   AAV31743;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Nucleotide sequence of the oligonucleotide POLYA.
XX
KW   PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
KW   hyperproliferative disease; ss.
XX
OS   Synthetic.
XX
PN   US5756684-A.
XX
PD   26-MAY-1998.
XX
PF   06-JUN-1995;   95US-00470911.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1998-321632/28.
XX
PT   PUR protein and its fragments - that inhibit PUR protein binding to PUR
PT   element or other proteins.
XX
PS   Example 7.1.1; Col 33; 63pp; English.
XX
CC   This is the nucleotide sequence of an oligonucleotide used as a
CC   competitor with the PUR element in the method of the invention, involving
CC   the use of the PUR protein and its fragments, which inhibit PUR protein
CC   binding to PUR element or other proteins. Inhibitors of PUR activity may
CC   be useful for treating viral infections and hyperproliferative diseases
CC   such as cancer
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 221
AAX04086/c
ID   AAX04086 standard; DNA; 24 BP.
XX
AC   AAX04086;
XX
DT   12-APR-1999  (first entry)
XX
DE   Oligonucleotide POLYA used in PUR cloning and sequencing.
XX
KW   PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW   monoclonal antibody; identification; characterisation; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5869622-A.
XX
PD   09-FEB-1999.
XX
PF   07-JUN-1995;   95US-00486809.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
PR   06-JUN-1995;   95US-00470911.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1999-152881/13.
XX
PT   Monoclonal antibody specific for PUR protein - useful for treating
PT   cancer.
XX
PS   Example; Col 33; 64pp; English.
XX
CC   The present invention describes a monoclonal antibody that specifically
```

```
CC   binds to an epitope of the PUR protein. Antibodies that bind to the PUR
CC   protein and neutralise PUR activity may be used to treat
CC   hyperproliferative diseases such as cancer. PUR antibodies may be used
CC   diagnostically to detect aberrant expression of the PUR protein and/or
CC   mutations in the PUR gene. The present sequence represents an
CC   oligonucleotide used in the cloning and sequencing of the PUR protein and
CC   its sequence element PUR repeat, in an example from the present invention
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 222
AAA40359
ID   AAA40359 standard; RNA; 24 BP.
XX
AC   AAA40359;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 9.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
XX
DR   WPI; 2000-442381/38.
XX
PT   Inserting a nucleic acid into a circular vector comprising joining their
PT   ends, melting, and reannealing ends at two different concentrations,
PT   useful for cloning small amounts of nucleic acids and forming genomic
PT   libraries.
XX
PS   Example 3; Page 67; 71pp; English.
XX
CC   This invention describes a novel method (M1) for inserting a nucleic acid
CC   (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC   under a first nucleic acid concentration, melting hybridized cohesive
CC   circularization ends, and reannealing the ends at a second concentration.
CC   The methods are useful for the cloning small amounts of nucleic acids and
CC   forming genomic libraries of complex populations of DNA or cDNA. The
CC   methods allow the cloning of minute amounts of nucleic acids efficiently
CC   and avoids the size selection problems of prior art systems. Larger
CC   nucleic acid fragments are just as easily cloned, allowing highly
CC   representative libraries to be made. Vector to vector ligation is avoided
CC   using the methods. AAA40351-A40366 represents primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 16 T; 8 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   66.7%;  Pred. No. 4.4e+02;
  Matches   14;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||:||:||:||:||:||:||:
Db          1 TTUTTUTTUTTUTTUTTUTU 21


RESULT 223
AAA40353
ID   AAA40353 standard; DNA; 24 BP.
XX
AC   AAA40353;
XX
DT   10-NOV-2000  (first entry)
XX
DE   pBluescriptSK+ phagemid primer SEQ ID NO: 3.
XX
KW   Primer; cloning; ligation; ss.
XX
OS   Synthetic.
XX
PN   WO200036088-A1.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US030277.
XX
PR   17-DEC-1998;   98US-00213834.
XX
PA   (ROMA/) ROMANTCHIKOV Y.
XX
PI   Romantchikov Y;
XX
DR   WPI; 2000-442381/38.
XX
PT   Inserting a nucleic acid into a circular vector comprising joining their
PT   ends, melting, and reannealing ends at two different concentrations,
PT   useful for cloning small amounts of nucleic acids and forming genomic
PT   libraries.
XX
PS   Example 1; Page 66; 71pp; English.
XX
CC   This invention describes a novel method (M1) for inserting a nucleic acid
CC   (N1) into a circular vector (V1) comprising joining ends of N1 and V1
CC   under a first nucleic acid concentration, melting hybridized cohesive
CC   circularization ends, and reannealing the ends at a second concentration.
CC   The methods are useful for the cloning small amounts of nucleic acids and
CC   forming genomic libraries of complex populations of DNA or cDNA. The
CC   methods allow the cloning of minute amounts of nucleic acids efficiently
CC   and avoids the size selection problems of prior art systems. Larger
CC   nucleic acid fragments are just as easily cloned, allowing highly
CC   representative libraries to be made. Vector to vector ligation is avoided
CC   using the methods. AAA40351-A40366 represents primers used to illustrate
CC   the method of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 224
AAF99756
ID   AAF99756 standard; DNA; 24 BP.
XX
AC   AAF99756;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #872.
```

```
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 57; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 225
AAF99304
ID   AAF99304 standard; DNA; 24 BP.
XX
AC   AAF99304;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #420.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 46; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 226
AAF99757/c
ID   AAF99757 standard; DNA; 24 BP.
XX
AC   AAF99757;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #873.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
```

PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 57; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 24 TTTTTTTTTTTTTTTTTTTT 4

RESULT 227
ABV14842
ID ABV14842 standard; cDNA; 24 BP.
XX
AC ABV14842;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 14833.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 2483; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 21

RESULT 228
ABS78477
ID ABS78477 standard; DNA; 24 BP.
XX
AC ABS78477;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #961.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also

CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 21

RESULT 229
ABS77949
ID ABS77949 standard; DNA; 24 BP.
XX
AC ABS77949;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #433.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 27; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 21

RESULT 230
ABS78478/c
ID ABS78478 standard; DNA; 24 BP.
XX
AC ABS78478;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #962.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 36; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 231
ABL39405
ID   ABL39405 standard; DNA; 24 BP.
XX
AC   ABL39405;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 841.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .24
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 309; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 232
ABA98840/c
ID   ABA98840 standard; DNA; 24 BP.
XX
AC   ABA98840;
XX
DT   01-JUL-2002  (first entry)
XX
DE   A24 oligonucleotide for the creation of Pc-A24.
XX
KW   Component detection; clinical diagnosis; cell detection; drug detection;
KW   metabolite detection; pesticide detection; ligand detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    24
FT                    /*tag=  a
FT                    /label= OTHER
FT                    /note= "modified by PO2OCH2CH2CH2SSCH2CH2CH2OH"
XX
PN   WO200184157-A2.
XX
PD   08-NOV-2001.
XX
PF   03-MAY-2001; 2001WO-US014528.
XX
PR   04-MAY-2000; 2000US-00564230.
XX
PA   (DADE-) DADE BEHRING INC.
XX
PI   Pease JS,  Cromer R,  Patel R,  Kurn N,  De Keczer S;
XX
DR   WPI; 2002-164078/21.
XX
PT   Detection of multiple analytes, e.g. ligands, receptors, polynucleotides
PT   and pollutants, involves adding a combination of sensitizer reagents and
PT   reactive reagent Actuatable by a product of the sensitizer reagents.
XX
PS   Example; Page 58; 87pp; English.
XX
CC   The invention relates to the detection of multiple components in a
CC   medium, comprising combining the medium with at least two sensitiser
CC   reagents, and at least one reactive reagent activated by a product
CC   generated by the sensitiser reagents when activated; and differentially
CC   activating the sensitiser reagents. The combination of sensitiser
CC   reagents and reactive reagent(s) allows differential detection of the
CC   components. Methods of the invention may be used for the detection of
CC   ligands, receptors and polynucleotides, and also for the detection of
CC   e.g. cells, various drugs, metabolites, pesticides (e.g. polyhalogenated
CC   biphenyls, phosphate esters, thiophosphates, carbamates and
CC   polyhalogenated sulfenamides) and pollutants. Methods of the invention
CC   allow the detection of multiple analytes in a single test medium. An
CC   application of the methods of the present invention would be in the field
CC   of clinical diagnostics. The current sequence represents A24
CC   oligonucleotide for the creation of oligonucleotide coated phthalocyanine
CC   sensitiser particles (Pc-A24)
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4
```

```
RESULT 233
AAS17869/c
ID   AAS17869 standard; DNA; 24 BP.
XX
AC   AAS17869;
XX
DT   08-MAY-2002  (first entry)
XX
DE   A24 oligonucleotide used to create dopTAR chemiluminescer particles.
XX
KW   Polymorphism detection; sequence detection; mutation detection; A24;
KW   probe; non-dissociative termolecular complex; dopTAR sensitiser particle;
KW   single nucleotide polymorphism; SNP; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   24
FT                   /*tag=  a
FT                   /note= "A is covalently linked to a
FT                   PO2OCH2CH2CH2SSCH2CH2CH2OH moiety"
XX
PN   WO200190399-A2.
XX
PD   29-NOV-2001.
XX
PF   17-MAY-2001; 2001WO-US016089.
XX
PR   19-MAY-2000; 2000US-00574596.
XX
PA   (DADE-) DADE BEHRING INC.
XX
PI   Patel RD;
XX
DR   WPI; 2002-097664/13.
XX
PT   Detecting presence of polynucleotide, differences between polynucleotide
PT   sequences, useful for detecting single nucleotide polymorphism and
PT   alleles of polynucleotide sequence involves use of three competitive
PT   probes.
XX
PS   Example; Page 47; 75pp; English.
XX
CC   This invention represents a method for detecting the presence of a
CC   polynucleotide sequence, differences in polynucleotide sequences or
CC   mutations in genomic DNA. The method involves contacting 3
CC   oligonucleotide probes with a sample containing a polynucleotide. The
CC   first probe hybridises to a region of the polynucleotide sequence and the
CC   second and third probes can bind a second region of the polynucleotide
CC   sequence. The second and third probes are identical except for the
CC   presence or difference of one or more nucleotides. The reaction medium is
CC   then subjected to conditions for forming substantially non-dissociative
CC   termolecular complexes, which can be at least one of, the polynucleotide
CC   sequence with the first and second probes or the polynucleotide sequence
CC   with the first and third probes. The oligonucleotide probes have labels
CC   non-covalently bound to allow for their detection upon binding. The
CC   method of the invention is useful for detecting the presence of a single
CC   nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method
CC   can be used for the direct detection of nucleic acid in very small
CC   quantities without amplification. In addition, the method may be carried
CC   out with amplification of the target and reference sequences. This
CC   sequence represents an oligonucleotide probe A24 used to create dopTAR
CC   chimiluminescer sensitiser particles in the method of the invention.
CC   Binding the nucleic acid to a suspendable particle acts as a support and
CC   provides a means of segregating the bound polynucleotide target from the
CC   bulk solution
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
             ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 234
ABK15639
ID   ABK15639 standard; DNA; 24 BP.
XX
AC   ABK15639;
XX
DT   08-MAY-2002  (first entry)
XX
DE   RNA-PCR procedure primer poly(dT)24.
XX
KW   RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy;
KW   mRNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense;
KW   high throughput screening; D-RNAi; DNA-RNA interference; RdRp;
KW   RNA dependent RNA polymerase; posttranscriptional gene silencing.
XX
OS   Synthetic.
XX
PN   WO200210374-A2.
XX
PD   07-FEB-2002.
XX
PF   02-AUG-2001; 2001WO-US024412.
XX
PR   02-AUG-2000; 2000US-0222479P.
XX
PA   (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI   Lin S,  Chuong C,  Widelitz RB;
XX
DR   WPI; 2002-188740/24.
XX
PT   Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or
PT   treating or preventing microbe related genes, comprises thermocycling
PT   steps of promoter-linked double-stranded cDNA or RNA synthesis.
XX
PS   Example 5; Page 26; 53pp; English.
XX
CC   The invention relates to generating mRNA-cDNA hybrids, comprising (a)
CC   providing a solution containing a nucleic acid template, one or more
CC   primers complementary to the sense conformation of the nucleic acid
CC   template, and one or more promoter-linked primers complementary to the
CC   antisense conformation of the nucleic acid template, and with an RNA
CC   promoter, (b) treating the nucleic acid template with the one of more
CC   primers to synthesise a first cDNA strand, (c) treating the first cDNA
CC   strand with one or more promoter-linked primers to synthesise a promoter-
CC   linked double-stranded nucleic acid, (d) treating the promoter-linked
CC   double-stranded nucleic acid to synthesise amplified mRNA fragments and
CC   (e) treating the mRNA fragments with one or more primers to synthesise
CC   mRNA-cDNA hybrids by reverse transcription of the amplified mRNA
CC   fragments. The method is useful for preparing high amounts of pure and
CC   specific mRNA-cDNA hybrids for transducing biological effects of interest
CC   in vitro as well as in vivo, for inhibiting gene function in prokaryotes
CC   and eukaryotes in vivo and in vitro, for suppressing cancer-related
CC   genes, in treating or preventing microbe related genes, in studying
CC   candidate molecular pathways with systematic knock out of involved
CC   molecules, in high throughput screening of gene functions based on
CC   microarray analysis, and as a tool in studying gene function in
CC   physiological conditions. The mRNA-cDNA hybrids may be used to screen for
CC   special gene functions, for manipulating gene expression in vitro, and
CC   for designing therapy for genetic diseases in vivo. The cDNA part of a D-
CC   RNAi (DNA-RNA interference) can be modified by nucleotide analogue
CC   incorporation to increase the stability and effectiveness of transfected
CC   probe activities. The RdRp (RNA dependent RNA polymerase) enzyme may
CC   provide higher affinity of the mRNA template of a D-RNAi compared to ds-
CC   RNA due to lower binding interaction between DNA-RNA duplexes than RNA-
CC   RNA duplexes. The cDNA part of a D-RNAi provides further antisense gene
CC   knockout activity in addition to the posttranscriptional gene silencing
```

```
CC   (PTGS) mechanisms of the sense-RNA template, resulting in multiple
CC   specific gene interference effects with one probe. The present sequence
CC   is a poly(dT) PCR primer used in conjunction with oligo(dC)10N primers to
CC   reverse transcribe mRNA into first strand cDNA in the method of the
CC   invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 235
ACA58802
ID   ACA58802 standard; DNA; 24 BP.
XX
AC   ACA58802;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Gastric ulcer treatment immunostimulatory nucleic acid #148.
XX
KW   Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;
KW   Heliobacter pylori.
XX
OS   Synthetic.
XX
PN   US2002198165-A1.
XX
PD   26-DEC-2002.
XX
PF   01-AUG-2001; 2001US-00920313.
XX
PR   01-AUG-2000; 2000US-0222248P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
XX
PI   Bratzler RL,  Petersen DM;
XX
DR   WPI; 2003-370798/35.
XX
PT   Prevention or treatment of gastric ulcer involves administering nucleic
PT   acid.
XX
PS   Disclosure; Page 14; 45pp; English.
XX
CC   The invention relates to a method of prevention or treatment of gastric
CC   ulcer comprising administering a nucleic acid to a subject in need for
CC   treatment of gastric ulcer. A nucleic acid sample comprising
CC   oligonucleotide 2006 was administered to a mouse model by an oral route
CC   or a vehicle control. Colonisation of mice by Heliobacter pylori was
CC   assessed at time points from 1 day to 1 month after treatment. The
CC   ability of the nucleic acid to reduce H. pylori colonisation was
CC   assessed. The method is useful for preventing or treating a gastric ulcer
CC   on a subject e.g. human or non-human vertebrate animal including dog,
CC   cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,
CC   rabbit, turkey, chicken, primate, rat and mouse. The method effectively
CC   treats or prevents gastric ulcers. The present sequence represents an
CC   immunostimulatory nucleic acid for the treatment of gastric ulcers
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 236
ABX79809
ID   ABX79809 standard; cDNA; 24 BP.
XX
AC   ABX79809;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #134.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 579; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 237
ABZ80181
```

```
ID   ABZ80181 standard; DNA; 24 BP.
XX
AC   ABZ80181;
XX
DT   23-MAY-2003  (first entry)
XX
DE   Immunostimulatory oligonucleotide SEQ ID NO:53.
XX
KW   Immunostimulation; immune response; natural killer cell; interferon;
KW   type 1 interferon; IFN; cancer; infectious disease; allergic disorder;
KW   immune related disorder; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .24
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optionally phosphorothioate backbone"
XX
PN   WO2003015711-A2.
XX
PD   27-FEB-2003.
XX
PF   19-AUG-2002; 2002WO-US026468.
XX
PR   17-AUG-2001; 2001US-0313273P.
PR   03-JUL-2002; 2002US-0393952P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
PA   (COLE-) COLEY PHARM GMBH.
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Krieg AM,  Vollmer J,  Ulhman E;
XX
DR   WPI; 2003-268241/26.
XX
PT   New immunostimulatory nucleic acid, useful for preparing a composition
PT   for treating an allergic condition.
XX
PS   Example 1; Page 44; 115pp; English.
XX
CC   The present invention describes immunostimulatory nucleic acids of 14-100
CC   nucleotides in length comprising the formula 5' X1DCGHX2 3' (I), where X1
CC   or X2 = independently any sequence 0-10 nucleotides; D = nucleotide other
CC   than C; C = cytosine; G = guanine; H = nucleotide other than G. The
CC   immunostimulatory nucleic acid further comprises a sequence consisting of
CC   P and N positioned immediately 5' to X1 or 3' to X2 and N is a B cell
CC   neutralising sequence, where N begins with a CGG trinucleotide and is at
CC   least 10 nucleotides long and P is GC-rich palindrome containing sequence
CC   at least 10 nucleotides long. Also described: (1) a pharmaceutical
CC   composition comprising the immunostimulatory nucleic acid and a carrier;
CC   and (2) treating an allergic condition. (I) has antiallergic activity and
CC   can be used in gene therapy. (I) can be used for preparing a composition
CC   for treating a variety of immune related disorders such as cancer,
CC   infectious diseases and allergic disorders. (I) also stimulates the
CC   activation of natural killer cells and the production of type 1
CC   interferon (IFN). The present sequence represents an immunostimulatory
CC   oligonucleotide, which is used in an example from the present invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTT 21


RESULT 238
ACA62284
ID   ACA62284 standard; DNA; 24 BP.
XX
AC   ACA62284;
XX
DT   12-AUG-2003  (first entry)
XX
DE   Oligo (dT)24 RT-PCR primer.
XX
KW   ss; PCR; RT-PCR; primer; reverse transcriptase PCR; antisense therapy;
KW   mRNA expression profile; promoter containing primer.
XX
OS   Synthetic.
XX
PN   US2003022318-A1.
XX
PD   30-JAN-2003.
XX
PF   07-SEP-2001; 2001US-00949305.
XX
PR   25-JAN-2000; 2000US-00494212.
XX
PA   (EPIC-) EPICLONE INC.
XX
PI   Lin S,  Ying S;
XX
DR   WPI; 2003-479488/45.
XX
PT   Improved polymerase thermocycling reaction for nucleic acid
PT   amplification, by thermal cycling of promoter-linked nucleic acid
PT   template synthesis and in vitro transcriptional amplification of nucleic
PT   acid sequences.
XX
PS   Example 7; Page 14; 28pp; English.
XX
CC   The invention relates to an improved polymerase thermocycling reaction
CC   (M1) for linear amplification of nucleic acid sequences, involves
CC   denaturing a number of nucleic acid templates (I), combining the
CC   denatured (I) with a promoter-containing primer (P1), a primer (P2), a
CC   number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
CC   a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
CC   polymerase, contacting P1 with (I) to generate a number of promoter-
CC   containing templates, denaturing the promoter-containing templates,
CC   contacting P2 with the denatured promoter-containing templates to
CC   generate a number of promoter-containing double-stranded DNA templates,
CC   where the double-stranded nucleic acid templates are flanked by P1 in one
CC   end and P2 in the other end of the other orientation, transcribing the
CC   promoter-containing double-stranded DNA templates to form a number of
CC   amplified RNA sequences, including the primer region of the promoter-
CC   containing double-stranded DNA templates, contacting the amplified RNA
CC   sequences with P2 to form a number of cDNAs and a number of DNA-RNA
CC   hybrid templates, and denaturing the DNA-RNA hybrid templates. The method
CC   is useful for improved polymerase thermocycling reaction for linear
CC   amplification of nucleic acid sequences, and thus for producing mRNA
CC   expression profile of a cell by M1 to generate multiple copies of the
CC   mRNA. M1 is also useful for determining aberrant protein production of
CC   cells in a diseased state, by generating an expression profile by the
CC   above method, of cells in both normal and diseased states, comparing the
CC   expression profile of the cells in the normal and diseased states,
CC   determining the differences in mRNA composition of the cell(s) in the
CC   diseased state, isolating the mRNA sequences of cell(s) in the diseased
CC   state that differ from mRNA in cell(s) in non-diseased state, amplifying
CC   the isolated mRNA by M1, and determining aberrant protein function of the
CC   protein coded for by the isolated mRNA. M1 is also useful for treating a
CC   cell in a diseased state caused by aberrant protein production, by
CC   determining protein expression of a cell in a diseased state, determining
CC   the mRNA sequence for the aberrant proteins, synthesising an antisense
CC   sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and
CC   delivering a pharmaceutically effective dosage of a composition
CC   comprising the anti-sense mRNA and a compatible lipid based biological
CC   carrier. M1 is also useful for predicting the efficacy of a proposed drug
CC   targeted against an aberrant protein, by determining aberrant protein
CC   production of cell in a diseased state by the above method, amplifying
CC   the aberrant protein by M1 and using recombinant techniques to determine
```

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CC   the effect of proposed drug on the aberrant protein. M1 is also useful
CC   for differential screening of tissue-specific gene expression at a
CC   cellular level, for preparing labeled RNA/DNA probes for a gene chip
CC   technology, and for determining the efficacy of a drug regiment against a
CC   gene or its cDNAs. The present sequence is an Oligo (dT)24 RT-(reverse
CC   transcriptase) PCR primer used to produce first strand cDNA in the method
CC   of the invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 239
ACD99729
ID   ACD99729 standard; DNA; 24 BP.
XX
AC   ACD99729;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #415.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 20; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 240
ACH03285/c
ID   ACH03285 standard; DNA; 24 BP.
XX
AC   ACH03285;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #920.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 34; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 241
ACH03284
ID   ACH03284 standard; DNA; 24 BP.
XX
AC   ACH03284;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #919.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
```

```
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 34; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 242
ADA66379/c
ID   ADA66379 standard; mRNA; 24 BP.
XX
AC   ADA66379;
XX
DT   20-NOV-2003  (first entry)
XX
DE   mRNA poly A.
XX
KW   ss; nucleic acid amplification; multiple step elimination;
KW   varying reaction condition elimination; poly A tract.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     1. .24
FT                   /*tag=  a
FT                   /note= "Binds to nucleotides 42-19 of the 1st strand cDNA
FT                   synthesis primer"
XX
PN   US6582938-B1.
XX
PD   24-JUN-2003.
XX
PF   11-MAY-2001; 2001US-00854317.
XX
PR   11-MAY-2001; 2001US-00854317.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Su X,  Dong H,  Ryder TB;
XX
DR   WPI; 2003-656427/62.
XX
PT   Amplification of nucleic acids, where the promoter is blocked from
PT   extension at the 3' end, useful for eliminating multiple step reactions.
XX
PS   Disclosure; Fig 2; 9pp; English.
XX
CC   The invention relates to a method of amplification of nucleic acid which
CC   comprises primer extension by reverse transcriptase and hybridising an
CC   oligonucleotide to the single stranded DNA, where the oligonucleotide is
CC   blocked from extension at the 3' end. The method is useful for
CC   amplification of nucleic acids. In the new method, a promoter is
CC   protected from degradation throughout the method. The promoter is
CC   constructed so that it does not serve as a primer for extension of a
CC   sequence that is complementary to the target sequence, i.e. it is
CC   blocked. The method can be combined with other processes to eliminate the
CC   need for multiple steps and varying reaction conditions and their
CC   associated problems. At least three otherwise separate enzymatic
CC   reactions can occur consecutively in one phase (i.e., without organic
CC   extraction and precipitation), more preferably in the same reaction
CC   vessel. Preferably, cDNA synthesis according to the new method may occur
CC   in a modified low salt buffer. The present sequence represents the poly A
CC   tract of a mRNA used to illustrate the method of the invention.
XX
SQ   Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          24 TTTTTTTTTTTTTTTTTTTT 4


RESULT 243
ADB37258
ID   ADB37258 standard; DNA; 24 BP.
XX
AC   ADB37258;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #872.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
```

PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 18; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 21

RESULT 244
ADB36806
ID ADB36806 standard; DNA; 24 BP.
XX
AC ADB36806;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #420.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 11; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 21

RESULT 245
ADB37259/c
ID ADB37259 standard; DNA; 24 BP.
XX
AC ADB37259;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #873.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 18; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 24 TTTTTTTTTTTTTTTTTTTT 4

RESULT 246
ADD31867
ID ADD31867 standard; DNA; 24 BP.
XX
AC ADD31867;
XX
DT 15-JAN-2004 (first entry)
XX
DE Butterfly biliverdin binding protein BBP-B1X oligonucleotide SEQ ID:106.
XX
KW recombination product; synthetic gene technology; butterfly;
KW biliverdin binding protein; ss.
XX
OS synthetic.
XX

```
PN   WO2003064611-A2.
XX
PD   07-AUG-2003.
XX
PF   29-JAN-2003; 2003WO-US002612.
XX
PR   30-JAN-2002; 2002US-00062188.
XX
PA   (EGEA-) EGEA BIOSCIENCES INC.
XX
PI   Evans GA;
XX
DR   WPI; 2003-663477/62.
XX
PT   Creating recombination products between two distinct nucleotide
PT   sequences, useful in the field of synthetic gene technology, and in
PT   assembling a library, or a population or a collection of polypeptide
PT   variants.
XX
PS   Example 3; SEQ ID NO 106; 132pp; English.
XX
CC   The present invention describes a method for creating a collection of
CC   recombination products between two nucleotide sequences. The method
CC   comprises combining an initial set of oligonucleotides corresponding to a
CC   first nucleotide sequence with a subsequent set of oligonucleotides
CC   corresponding to a distinct nucleotide sequence and further combining the
CC   initial and subsequent sets of combination oligonucleotides having a
CC   sequence region corresponding to the initial nucleotide sequence and a
CC   sequence region corresponding to the second oligonucleotide sequence.
CC   Also described is a method of creating a collection of recombination
CC   products between two genes. The methods and compositions of the present
CC   invention are useful in the field of synthetic gene technology, and more
CC   specifically, to generating a collection of recombination products
CC   between distinct nucleotide sequences. They can also be used in
CC   assembling a library, or a population or a collection of polypeptide
CC   variants that correspond to single or multiple polynucleotide
CC   recombination products. The present sequence is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTT 21


RESULT 247
ADE25524
ID   ADE25524 standard; DNA; 24 BP.
XX
AC   ADE25524;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Rolling circle amplification related probe control oigo POS1/2.
XX
KW   RCA; rolling circle amplification; genotyping;
KW   single-nucleotide polymorphism; single base extension; SBE;
KW   immuno-hybridisation; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   24
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "optional biotin label"
XX
PN   WO2003066817-A2.
XX
PD   14-AUG-2003.
XX
PF   06-FEB-2003; 2003WO-US003533.
XX
PR   06-FEB-2002; 2002US-0355374P.
XX
PA   (AMSH ) AMERSHAM BIOSCIENCES AB.
XX
PI   Xia J;
XX
DR   WPI; 2003-697450/66.
XX
PT   Detecting nucleic acid targets, useful e.g. for diagnosing single
PT   nucleotide polymorphisms, by extension of capture probe complementary to
PT   open circle probe.
XX
PS   Example 1; Fig 5; 66pp; English.
XX
CC   The invention is directed to novel methods of amplifying and detecting
CC   DNA using rolling circle amplification (RCA). The invention relates to
CC   detecting a target sequence (I), which involves using a capture probe
CC   (CP) that is complementary to an open circle probe and includes a
CC   cleavage site. The method comprises: attaching a capture probe (CP) to a
CC   substrate, at both ends, where the CP includes one domain complementary
CC   to an OCP (open circle probe) and a second domain that contains a
CC   cleavage site (CS), to form a device; treating CP with (I) and OCP for
CC   form a hybridisation complex (HC); treating HC with a ligase so that OCP
CC   is circularised, forming a second complex (HC2); treating CP with a
CC   cleavage agent, to cut at CS, and adding an extension enzyme (EE) and
CC   nucleotide triphosphates (NTPs) to form an extended CP, which is
CC   detected. The method is used for detecting (I) that comprises two target
CC   domains (TD1, TD2) and (I) that comprises two adjacent target domains.
CC   The method is used for detection, genotyping and/or quantification of
CC   target sequences, for research, clinical use, quality control or field
CC   testing, particularly detection of single-nucleotide polymorphisms. The
CC   method permits a high level of multiplexing, and since it provides
CC   localized product detection, with linear kinetics, is sensitive enough
CC   for direct detection and quantitation of unmodified targets. The present
CC   sequence is that of a single base extension (SBE) probe used in SNP
CC   genotyping with RCA signal amplification to demonstrate the method of the
CC   invention.
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTT 21


RESULT 248
AAQ95960
ID   AAQ95960 standard; DNA; 25 BP.
XX
AC   AAQ95960;
XX
DT   06-FEB-1996  (first entry)
XX
DE   Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method.
XX
KW   Immobilisation; solid support; salt; cationic detergent; capture probe;
KW   hybridisation; primer; template-dependent extension; target organism;
KW   sequencing; genetic polymorphism; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
```

```
FT                   /note= "biotinylated"
XX
PN   WO9515970-A1.
XX
PD   15-JUN-1995.
XX
PF   06-DEC-1994;   94WO-US014096.
XX
PR   06-DEC-1993;   93US-00162397.
PR   16-NOV-1994;   94US-00341148.
XX
PA   (MOLE-) MOLECULAR TOOL INC.
XX
PI   Nikiforov T,  Knapp MR;
XX
DR   WPI; 1995-224282/29.
XX
PT   Immobilising synthetic nucleic acid on solid support - by incubation in
PT   presence of salt or cationic detergent, for use in hybridisation assays,
PT   sequencing and analysis of polymorphism.
XX
PS   Example 1; Page 18; 61pp; English.
XX
CC   Oligonucleotides AAQ95959-82 are examples of oligonucleotides used in a
CC   novel method of immobilising oligonucleotides to a solid support by
CC   incubating in the presence of a salt or cationic detergent e.g. NaCl (50-
CC   250 mM, pH 6.0-8.0) or 1-ethyl-3-(3'-dimethyl amino propyl)-1,3
CC   carbodiimide hydrochloride (ECD). The oligonucleotides can be capture
CC   probes for detection of specific nucleic acids by hybridisation or can be
CC   primers for template-dependent extension from the immobilised primers on
CC   nucleic acid from a target organism. The method can be used in
CC   hybridisation assays, sequencing and analysis of genetic polymorphism
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 249
AAX84258
ID   AAX84258 standard; DNA; 25 BP.
XX
AC   AAX84258;
XX
DT   08-SEP-1999  (first entry)
XX
DE   PCR primer for human Nck associated protein 1 coding sequence.
XX
KW   Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW   therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931239-A1.
XX
PD   24-JUN-1999.
XX
PF   14-DEC-1998;   98WO-JP005646.
XX
PR   15-DEC-1997;   97JP-00363183.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SAKA/) SAKAKI Y.
XX
PI   Sakaki Y;
XX
DR   WPI; 1999-395181/33.
XX
PT   Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT   Alzheimer's disease.
XX
PS   Example 1; Page 76; 90pp; Japanese.
XX
CC   This sequence represents a PCR primer used to isolate DNA encoding the
CC   human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC   apoptosis. The protein can be used in the investigation, diagnosis and
CC   treatment (e.g. by gene therapy) of Alzheimer's disease
XX
SQ   Sequence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 250
AAX84260
ID   AAX84260 standard; DNA; 25 BP.
XX
AC   AAX84260;
XX
DT   08-SEP-1999  (first entry)
XX
DE   PCR primer for human Nck associated protein 1 coding sequence.
XX
KW   Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW   therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931239-A1.
XX
PD   24-JUN-1999.
XX
PF   14-DEC-1998;   98WO-JP005646.
XX
PR   15-DEC-1997;   97JP-00363183.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SAKA/) SAKAKI Y.
XX
PI   Sakaki Y;
XX
DR   WPI; 1999-395181/33.
XX
PT   Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT   Alzheimer's disease.
XX
PS   Disclosure; Page 77; 90pp; Japanese.
XX
CC   This sequence represents a PCR primer used to isolate DNA encoding the
CC   human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC   apoptosis. The protein can be used in the investigation, diagnosis and
CC   treatment (e.g. by gene therapy) of Alzheimer's disease
XX
SQ   Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21
```

```
RESULT 251
AAA39306
ID   AAA39306 standard; RNA; 25 BP.
XX
AC   AAA39306;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Rapid capture probe designated Neu-probe SEQ ID NO:1.
XX
KW   Rapid detection; probe; target nucleic acid; enzymatic amplification;
KW   isolation; detection; ss.
XX
OS   Synthetic.
XX
PN   US6060246-A.
XX
PD   09-MAY-2000.
XX
PF   13-NOV-1997;   97US-00969813.
XX
PR   15-NOV-1996;   96US-0030963P.
XX
PA   (AVIB-) AVI BIOPHARMA INC.
XX
PI   Wages JM,  Summerton JE,  Weller DD;
XX
DR   WPI; 2000-364413/31.
XX
PT   Reagent for rapidly detecting or isolating target nucleic acid sequences
PT   in polynucleotide-containing sample, comprises capture component and
PT   target-specific probe linked to solid substrate.
XX
PS   Example 3; Col 17; 24pp; English.
XX
CC   The present invention describes a rapid pairing reagent (I) for the
CC   isolation or detection of a polynucleotide (PN) analyte molecule having a
CC   selected target base sequence, in a sample containing the analyte
CC   molecule and non-target polynucleotide, comprising a capture component
CC   (A) and a target-specific probe (B) linked to a solid substrate. The
CC   isolated sequences are useful for enzymatic amplification. (I) is capable
CC   of rapidly binding nucleic acids in the sample and placing them in close
CC   proximity to target probes on the reagent, thus enabling binding under
CC   low stringency. Combination of rapid capture and concentration of
CC   polynucleotides with selective targeting of analyte molecules, greatly
CC   enhances the isolation process. Non-ionic morpholino oligomers used as
CC   probes are not extended by polymerases and therefore do not interfere
CC   with amplification of target molecule. AAA39306 to AAA39316 represent
CC   oligonucleotides used in the exemplification of the present invention
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 0 T; 25 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   0.0%;  Pred. No. 4.9e+02;
  Matches    0;  Conservative   21;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              :::::::::::::::::::::
Db          1 UUUUUUUUUUUUUUUUUUUUU 21


RESULT 252
AAZ30267
ID   AAZ30267 standard; DNA; 25 BP.
XX
AC   AAZ30267;
XX
DT   11-FEB-2000  (first entry)
XX
DE   Capture probe CP125 specific for c-myc fusion targets.
XX
KW   c-myc fusion; non-nucleoside spacer; capture probe;
KW   nucleic acid-protein fusion; ribosome display particle; ss.
XX
OS   Synthetic.
XX
PN   WO9951773-A1.
XX
PD   14-OCT-1999.
XX
PF   31-MAR-1999;   99WO-US007203.
XX
PR   03-APR-1998;   98US-0080686P.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Kuimelis RG,  Wagner R;
XX
DR   WPI; 2000-013048/01.
XX
PT   Attaching capture probes to solid phases through non-nucleic spacers,
PT   producing arrays for detecting interactions of proteins with other
PT   compounds, e.g. for drug screening.
XX
PS   Example 8; Page 29; 57pp; English.
XX
CC   The present sequence represents a capture probe specific for a c-myc
CC   fusion target. It is used in the method of the invention. The
CC   specification describes the use of non-nucleoside spacers to immobilise
CC   an array of capture probes on a solid support. The solid support carries
CC   an array of capture probes, each consisting of non-nucleoside spacers
CC   plus an oligonucleotide to which a nucleic acid-protein fusion or a
CC   ribosome display particle is bound. Non-nucleoside spacers prevent
CC   interaction of proteins with the support surface, ensuring efficient
CC   hybridisation between capture probes and bound nucleic acid/protein
CC   fusions, while minimising denaturation of the protein which may then
CC   adopt its native folded structure. The arrays of capture probes are used
CC   to screen for interactions between proteins and compounds (e.g. other
CC   proteins, ligands or nucleic acids), particularly to identify potential
CC   therapeutic agents, enzyme substrates or unknown proteins that interact
CC   with drugs, but also for diagnosis (detecting disease-associated
CC   proteins) and for quantifying target molecules in a sample
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTT 21


RESULT 253
ABK49986
ID   ABK49986 standard; DNA; 25 BP.
XX
AC   ABK49986;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Example oligonucleotide #2 prepared on glass-synthetic resin membrane.
XX
KW   Glass-synthetic resin membrane; pore glass-polytetrafluoroethylene resin;
KW   chromatography membrane; PTFE; ss.
XX
OS   Synthetic.
XX
PN   US6261497-B1.
XX
PD   17-JUL-2001.
XX
PF   04-MAY-1999;   99US-00305219.
```

```
XX
PR   21-FEB-1996;   96US-00604440.
XX
PA   (CPGC-) CPG INC.
XX
PI   Wong YN,  Chen R;
XX
DR   WPI; 2001-534961/59.
XX
PT   Preparation of controlled pore glass-polytetrafluoroethylene resin
PT   chromatography membrane by heating, calendering and sintering mixture of
PT   controlled pore glass and aqueous dispersion of polytetrafluoroethylene.
XX
PS   Example 12; Col 8; 6pp; English.
XX
CC   The invention relates to a method of preparing a controlled pore glass-
CC   polytetrafluoroethylene (PTFE) resin chromatography membrane, comprising
CC   combining controlled pore glass and an aqueous dispersion of PTFE to form
CC   a paste-like mass, heating the paste-like mass at 50-70 plus oC,
CC   calendering to form a foldable sheet, and sintering the sheet to produce
CC   a rigid, porous sheet. The method prepares a controlled pore glass-PTFE
CC   resin chromatography membrane for use in various biotechnical procedures.
CC   The membrane is useful in place of controlled pore glass as a support for
CC   the synthesis, isolation, and purification of nucleic acids and for the
CC   isolation and purification of proteins. The method produces a membrane
CC   that may be used in lieu of controlled pore glass. The present sequence
CC   represents an oligonucleotide prepared on the membrane in an example
CC   which demonstrates the method of the invention
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 254
ADC54009
ID   ADC54009 standard; DNA; 25 BP.
XX
AC   ADC54009;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Oligonucleotide of the invention SEQ ID NO:4.
XX
KW   ss; probe carrier; discharge.
XX
OS   Synthetic.
XX
PN   JP2003035711-A.
XX
PD   07-FEB-2003.
XX
PF   28-MAR-2002; 2002JP-00093023.
XX
PR   28-MAR-2001; 2001JP-00094400.
XX
PA   (CANO ) CANON KK.
XX
DR   WPI; 2003-535999/51.
XX
PT   Probe carrier manufacturing method for inkjet system, involves scanning
PT   liquid discharge head in direction orthogonal to scanning direction, at
PT   angle satisfying predetermined relation.
XX
PS   Example 2; SEQ ID NO 4; 17pp; Japanese.
XX
CC   The invention relates to a novel probe carrier and the method for
CC   manufacturing the carrier. The invention enables stable discharge of
CC   solution, and removes liquid droplets adhering to discharge nozzle. The
CC   present sequence is used in the exemplification of the invention.
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 255
ADC54008/c
ID   ADC54008 standard; DNA; 25 BP.
XX
AC   ADC54008;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Oligonucleotide of the invention SEQ ID NO:3.
XX
KW   ss; probe carrier; discharge.
XX
OS   Synthetic.
XX
PN   JP2003035711-A.
XX
PD   07-FEB-2003.
XX
PF   28-MAR-2002; 2002JP-00093023.
XX
PR   28-MAR-2001; 2001JP-00094400.
XX
PA   (CANO ) CANON KK.
XX
DR   WPI; 2003-535999/51.
XX
PT   Probe carrier manufacturing method for inkjet system, involves scanning
PT   liquid discharge head in direction orthogonal to scanning direction, at
PT   angle satisfying predetermined relation.
XX
PS   Example 2; SEQ ID NO 3; 17pp; Japanese.
XX
CC   The invention relates to a novel probe carrier and the method for
CC   manufacturing the carrier. The invention enables stable discharge of
CC   solution, and removes liquid droplets adhering to discharge nozzle. The
CC   present sequence is used in the exemplification of the invention.
XX
SQ   Sequence 25 BP; 25 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 4.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db         25 TTTTTTTTTTTTTTTTTTTT 5


RESULT 256
AAI73048
ID   AAI73048 standard; DNA; 26 BP.
XX
AC   AAI73048;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Scaffold oligonucleotide.
XX
```

KW Molecular scaffold; fluorophore; fluorescence; energy transfer;
KW emission wavelength; excitation wavelength; multiple; single nucleotide;
KW polymorphism; ss.
XX
OS Synthetic.
XX
PN WO200222883-A1.
XX
PD 21-MAR-2002.
XX
PF 11-SEP-2001; 2001WO-US028967.
XX
PR 11-SEP-2000; 2000US-00658077.
PR 31-JUL-2001; 2001US-0309156P.
XX
PA (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Ju J, Li Z, Tong A, Russo JJ;
XX
DR WPI; 2002-575158/61.
XX
PT Composition of matter useful for multi-component analyses, comprises
PT multiple fluorophores bound to molecular scaffold at preset positions to
PT permit fluorescence energy transfer between two fluorophores.
XX
PS Disclosure; Page 43; 113pp; English.
XX
CC This sequence represents a molecular scaffold which may be used in a
CC composition of matter comprising multiple fluorophores. The fluorophores
CC are bound to the molecular scaffold at separate predetermined positions,
CC to permit fluorescence energy transfer between two fluorophores. The
CC fluorophores are characterized by maximum emission wavelength of one
CC being greater than the minimum excitation wavelength of the other. The
CC composition is useful for determining whether a preselected nucleotide
CC residue is present at a predetermined position within a nucleic acid. It
CC is also useful in multicomponent analysis including multiplex biological
CC analysis, and identifying multiple single nucleotide polymorphisms. The
CC presence of a number of given nucleotide residues is determined
CC simultaneously by the composition of the invention
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTTT 21

RESULT 257
AAS20672
ID AAS20672 standard; DNA; 26 BP.
XX
AC AAS20672;
XX
DT 09-APR-2002 (first entry)
XX
DE Human zalpha11 Ligand sequencing primer ZC7764b.
XX
KW Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW natural killer cell proliferation; T-cell proliferation;
KW B-cell proliferation; anti-tumour response; immune system;
KW immunostimulant; cytostatic; human; sequencing primer; ss.
XX
OS Homo sapiens.
XX
PN US6307024-B1.
XX
PD 23-OCT-2001.
XX
PF 09-MAR-2000; 2000US-00522217.
XX
PR 09-MAR-1999; 99US-0123547P.
PR 11-MAR-1999; 99US-0123904P.
PR 01-JUL-1999; 99US-0142013P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX
DR WPI; 2002-040208/05.
XX
PT New zalpha11 ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
PT antigenic response.
XX
PS Example 7; Col 139; 105pp; English.
XX
CC The present invention relates to the isolation of a novel cytokine,
CC zalpha11 Ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalpha11 receptor and the polynucleotide
CC encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC zalpha11 Ligand polypeptide is also useful in preparing antibodies that
CC bind to zalpha11 Ligand epitopes. The zalpha11 Ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalpha11 Ligand gene,
CC and in gene therapy. Zalpha11 Ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC a sequencing primer used to sequence cDNA clones in the isolation of
CC human zalpha11 Ligand
XX
SQ Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTTT 2186
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTTT 21

RESULT 258
ABX93461
ID ABX93461 standard; DNA; 26 BP.
XX
AC ABX93461;
XX
DT 27-MAY-2003 (first entry)
XX
DE LS147-specific polynucleotide sequencing related universal primer #1.
XX
KW LS147; cancer; lung cancer; gene therapy; cytostatic; ss; sequencing;
KW primer; EST clone; expressed sequence tag clone.
XX
OS Synthetic.
XX
PN US2002188114-A1.
XX
PD 12-DEC-2002.
XX
PF 05-JUN-1998; 98US-00092296.
XX
PR 05-JUN-1997; 97US-0048810P.
XX
PA (BILL/) BILLINGEL P.
PA (COHE/) COHEN M.

```
PA   (COLP/) COLPITTS T L.
PA   (FRIE/) FRIEDMAN P N.
PA   (KLAS/) KLASS M R.
PA   (RUSS/) RUSSELL J C.
PA   (STRO/) STROUPE S.
XX
PI   Billingel P,  Cohen M,  Colpitts TL,  Friedman PN,  Klass MR;
PI   Russell JC,  Stroupe S;
XX
DR   WPI; 2003-341045/32.
XX
PT   New LS147 polypeptide, useful for preparing a composition for treating
PT   e.g., lung cancer.
XX
PS   Example 2; Page 39; 47pp; English.
XX
CC   The invention describes a purified polypeptide or its fragment derived
CC   from the LS147 gene capable of selectively hybridising to the nucleic
CC   acid of the gene and has at least 50% identity with the polynucleotide.
CC   The LS147 polypeptide is useful for preparing a composition for treating
CC   cancer, e.g. lung cancer using gene therapy. This sequence represents a
CC   universal primer used to sequence LS147 expressed sequence tag (EST)-
CC   clones
XX
SQ   Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 5.4e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 21


RESULT 259
AAX15434
ID   AAX15434 standard; DNA; 27 BP.
XX
AC   AAX15434;
XX
DT   07-MAY-1999  (first entry)
XX
DE   PCR primer used to amplify DNA encoding trehalose phosphorylase.
XX
KW   Trehalose phosphorylase; trehalose; D-glucose;
KW   alpha-D-glucose-1-phosphate; PCR primer; ss.
XX
OS   Synthetic.
OS   Grifola frondosa.
XX
PN   WO9844116-A1.
XX
PD   08-OCT-1998.
XX
PF   30-MAR-1998;   98WO-JP001423.
XX
PR   31-MAR-1997;   97JP-00098173.
XX
PA   (KURE ) KUREHA CHEM IND CO LTD.
XX
PI   Horinouchi S,  Saitoh K,  Takahashi E;
XX
DR   WPI; 1998-557113/47.
XX
PT   Trehalose phosphorylase from Grifola frondosa and gene encoding it - for
PT   producing enzyme for industrial scale production of trehalose.
XX
PS   Example 5; Page 25; 52pp; Japanese.
XX
CC   The present PCR primer was used to amplify DNA encoding a trehalose
CC   phosphorylase enzyme, and is derived from Grifola frondosa. Vectors and
CC   cells containing the nucleic acid sequence can be used in the large scale
CC   production of trehalose phosphorylase for industrial-scale manufacture of
CC   trehalose from D-glucose and alpha-D-glucose-1-phosphate. Trehalose is
CC   used in the foodstuff and drug industries
XX
SQ   Sequence 27 BP; 1 A; 3 C; 4 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||
Db          7 TCCTTTTTTTTTTTTTTTTT 27


RESULT 260
ABS53863
ID   ABS53863 standard; DNA; 27 BP.
XX
AC   ABS53863;
XX
DT   25-NOV-2002  (first entry)
XX
DE   Human androgen receptor complex-associated protein 5'RACE PCR primer #1.
XX
KW   Human; androgen receptor complex-associated protein; ARCAP; primer; ss;
KW   androgen receptor; AR; cancer; liver tumour; cytostatic; PCR; 5'RACE.
XX
OS   Homo sapiens.
XX
PN   EP1227150-A2.
XX
PD   31-JUL-2002.
XX
PF   16-JAN-2002; 2002EP-00250305.
XX
PR   17-JAN-2001; 2001US-0262312P.
PR   12-FEB-2001; 2001US-00781693.
XX
PA   (VETE-) VETERANS GEN HOSPITAL.
XX
PI   Tai-Jay C;
XX
DR   WPI; 2002-676576/73.
XX
PT   Novel substantially pure androgen receptor (AR) complex-associated
PT   protein which binds to AR and increases ability of AR to transactivate
PT   androgen-responsive gene, useful as drug target for treating liver
PT   cancer.
XX
PS   Example; Page 11; 26pp; English.
XX
CC   The invention relates to an androgen receptor complex-associated protein
CC   (ARCAP) sequence and the cDNA encoding it. The protein is useful for
CC   screening a compound that decreases AR-mediated (androgen receptor
CC   mediated) transactivation which involves contacting the ARCAP protein
CC   with a protein complex comprising an AR in the presence of a candidate
CC   compound, measuring the extent of binding between the polypeptide, and
CC   determining if the extent of binding is less than the extent of binding
CC   between the polypeptide and the protein complex in the absence of the
CC   candidate compound. The ARCAP DNA is useful for determining if a sample
CC   contains cancerous cells which involves providing a sample from a human
CC   patient and detecting ARCAP expression in the sample. The sequences are
CC   useful for determining whether a sample contains liver tumour cells. This
CC   sequence represents a 5'RACE PCR primer used to amplify human ARCAP DNA
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
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                    ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTT 21


RESULT 261
ABS54324
ID   ABS54324 standard; DNA; 27 BP.
XX
AC   ABS54324;
XX
DT   10-DEC-2002  (first entry)
XX
DE   Human ARCAP associated 5'RACE PCR primer.
XX
KW   Human; androgen receptor complex-coupled protein; ARCAP; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   JP2002262871-A.
XX
PD   17-SEP-2002.
XX
PF   28-FEB-2001; 2001JP-00055192.
XX
PR   12-FEB-2001; 2001US-00781693.
XX
PA   (VETE-) VETERANS GEN HOSPITAL.
XX
PI   Tai-Jay C;
XX
DR   WPI; 2002-676576/73.
XX
PT   Novel substantially pure androgen receptor (AR) complex-associated
PT   protein which binds to AR and increases ability of AR to transactivate
PT   androgen-responsive gene, useful as drug target for treating liver
PT   cancer.
XX
PS   Example; Page 15; 18pp; Japanese.
XX
CC   The present invention relates to the isolation of human androgen receptor
CC   complex-coupled protein (ARCAP), and the polynucleotide sequence encoding
CC   it. The ARCAP polypeptide complexes with an androgen receptor to increase
CC   the activity of the androgen receptor, transactivating the androgen
CC   responsing gene. The invention also describes a a vector containing the
CC   ARCAP polynucleotide sequence, and a host cell containing the ARCAP
CC   polynucleotide sequence. The ARCAP polypeptide can be used as a treating
CC   agent. The present sequence represents a PCR primer used in the example
CC   of the present invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
                ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTTT 21


RESULT 262
AAS11744/c
ID   AAS11744 standard; DNA; 28 BP.
XX
AC   AAS11744;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Human haemoglobin alpha 2 transcript (extreme 3' end).
XX
KW   Peptide-based cDNA characterisation; haemoglobin alpha 2; human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200161051-A1.
XX
PD   23-AUG-2001.
XX
PF   16-FEB-2001; 2001WO-US005305.
XX
PR   16-FEB-2000; 2000US-0182983P.
XX
PA   (SEQU-) SEQUEL GENETICS INC.
XX
PI   Jarvik JW;
XX
DR   WPI; 2001-514778/56.
XX
PT   Transcript, genetic, and especially nucleic acid sequence analysis
PT   comprises analysis of hybrid peptide products.
XX
PS   Example 11; Page 30; 48pp; English.
XX
CC   The invention relates to a method of peptide-based transcript or genetic
CC   analysis comprising: (a) providing multiple polynucleotides (I) derived
CC   from mRNAs from a biological sample, where (I) has homology to a known
CC   reference sequence (II); (b) expressing (I); and (c) assessing a physical
CC   property of the expression products to determine the sequences of (I) by
CC   comparison with the predicted properties of polypeptides encoded by (II).
CC   The method is useful for transcript or genetic analysis, especially
CC   nucleic acid analysis where the method comprises expressing polypeptides
CC   from two or more reading frames and determining the masses to create a
CC   peptide mass signature characteristic of the nucleic acid molecule. The
CC   peptide is considerably smaller than the DNA molecule that encodes it
CC   (individual amino acids averages about 110 Daltons each whereas the
CC   trinucleotides (triplets) that encode them average N Daltons each). Also,
CC   the peptides are much more diverse in composition than nucleic acids, as
CC   they are composed of combinations of 20 different amino acids instead of
CC   combinations of 4 different nucleotides, e.g., two random DNA fragments
CC   of identical composition (e.g., with 10 adenines, 10 thymines, 15
CC   guanines, and 15 cytosines) are extremely unlikely to encode peptides of
CC   identical composition. This means that whereas the two nucleic acids have
CC   identical masses and cannot be distinguished on the basis of mass, the
CC   peptides that they encode will, except in statistically very rare cases,
CC   have different masses and can be readily distinguished in the basis of
CC   mass. The present sequence represents the coding sequence of human
CC   haemoglobin alpha 2 transcript (extreme 3' end) used in an example to
CC   demonstrate the method of the invention
XX
SQ   Sequence 28 BP; 23 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 6.5e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
                ||||||||||||||||||||
Db          28 TTTTTTTTTTTTTTTTTTTTT 8


RESULT 263
AAQ97396
ID   AAQ97396 standard; DNA; 29 BP.
XX
AC   AAQ97396;
XX
DT   25-MAR-2003  (revised)
DT   01-APR-1996  (first entry)
XX
DE   Rat type I steroid 5-alpha reductase cDNA PCR primer.
XX
KW   Steroid 5-alpha reductase; sexual development; differentiation; probe;
KW   recombinant; inhibit; prostatic hyperplasia; acne; hirsutism;
KW   male pattern baldness; endometriosis; prostate cancer; testosterone;
KW   dihydroxytestosterone; ss.
XX
```

OS Rattus sp.
XX
PN US5422262-A.
XX
PD 06-JUN-1995.
XX
PF 18-NOV-1991; 91US-00795859.
XX
PR 30-APR-1990; 90US-00517661.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Andersson S, Russell DW;
XX
DR WPI; 1995-214658/28.
XX
PT Steroid 5 alpha-reductase nucleic acid segments and recombinant vectors -
PT where the sequences are useful in e.g. analysis of normal and abnormal
PT sexual differentiation.
XX
PS Example 1; Col 21; 72pp; English.
XX
CC 5-alpha reductase enzymes catalyse the conversion of testosterone to
CC dihydroxytestosterone. The rat steroid 5-alpha reductase I (SRD5A-I) cDNA
CC sequence has been isolated and purified using the PCR primer AAQ97396.
CC The rat enzyme cDNA can be used in the prepn. of genetic constructs for
CC the large scale production of SRD5A or as probes for enzyme-encoding
CC sequences from alternative sources. The sequences are also useful in the
CC analysis of normal and abnormal sexual differentiation, benign prostatic
CC hyperplasia, male pattern baldness; acne; hirsutism and endometriosis.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 29 BP; 1 A; 4 C; 4 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 9 CTTTTTTTTTTTTTTTTTTT 29

RESULT 264
AAT99803
ID AAT99803 standard; DNA; 29 BP.
XX
AC AAT99803;
XX
DT 20-MAR-1998 (first entry)
XX
DE Primer for rat steroid 5alpha-reductase coding sequence.
XX
KW Steroid 5alpha-reductase; enzyme; testosterone conversion; inhibitor;
KW rat; PCR primer; amplify; ss.
XX
OS Synthetic.
OS Rattus sp.
XX
PN US5679521-A.
XX
PD 21-OCT-1997.
XX
PF 01-JUN-1995; 95US-00457616.
XX
PR 30-APR-1990; 90US-00517661.
PR 18-NOV-1991; 91US-00795859.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Russell DW, Andersson S;
XX
DR WPI; 1997-525718/48.
XX
PT Production of recombinant steroid 5alpha-reductase enzyme - by culturing
PT cell containing DNA encoding the enzyme.
XX
PS Example 1; Col 20; 70pp; English.
XX
CC This sequence is a primer for the DNA encoding rat steroid 5alpha-
CC reductase. The encoded enzyme can be produced by the method of the
CC invention. The method is for producing a steroid 5alpha-reductase, and
CC comprises preparing a recombinant host cell containing a DNA segment
CC encoding a steroid 5alpha-reductase and culturing the cell under
CC conditions such that the steroid 5alpha-reductase is produced by the
CC cell. The steroid 5alpha-reductase produced by the method is used for
CC identifying substances that affect the enzymatic activity of steroid
CC 5alpha-reductase. Substances identified as inhibiting steroid 5alpha-
CC reductase activity can be used for inhibiting the conversion of
CC testosterone
XX
SQ Sequence 29 BP; 1 A; 4 C; 4 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 9 CTTTTTTTTTTTTTTTTTTT 29

RESULT 265
AAT69677/c
ID AAT69677 standard; DNA; 30 BP.
XX
AC AAT69677;
XX
DT 25-MAR-2003 (revised)
DT 19-FEB-1998 (first entry)
XX
DE Downstream primer for synthetic full length CAT sense RNA.
XX
KW PCR primer; CAT RNA; detection; quantification; determination; ss.
XX
OS Synthetic.
XX
PN EP780479-A2.
XX
PD 25-JUN-1997.
XX
PF 19-DEC-1996; 96EP-00120480.
XX
PR 23-DEC-1995; 95DE-01048680.
XX
PA (BOEF) BOEHRINGER MANNHEIM GMBH.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Leying H, Hinzpeter M, Wittor H, Fritton H;
XX
DR WPI; 1997-322152/30.
XX
PT Detection and quantitation of nucleic acid using probe with label and
PT binding group - and after hybridisation treatment with RNase and capture
PT on solid phase, particularly for RNA.
XX
PS Example 2; Page 7; 13pp; German.
XX
CC The present sequence is a PCR primer for synthetic full length CAT sense
CC RNA, which was used in a novel method for the detection and quantitative
CC determination of specific oligonucleotides (ON) or polynucleotides (PN).
CC The method comprises combining a sample containing RNA or single stranded
CC DNA with a lysis/hybridisation buffer, treating the homogenised solution
CC with 1 or more probes, which are essentially complementary to the ON or
CC PN and contain at least 2 different labels, one a specific binding group
CC and the other a detectable chemical group, hybridising under stringent

```
CC   conditions, diluting the mixture and adding an agent that cleaves single
CC   stranded nucleic acid into mononucleotides or ON, transferring the
CC   mixture to a vessel or well, coated with a substance that binds at least
CC   1 label, immobilising ON and PN hybrids (modified with 2 different labels
CC   or 1 label) to the solid phase and detecting immobilised ON or PN, or the
CC   non-immobilised labelled product, directly or via an enzyme labelled
CC   antibody. The method can be used to detect specific mRNA in human, animal
CC   or plant samples. The method is easy to perform and suitable for
CC   automation, does not require preliminary RNA isolation, can be made
CC   quantitative and has a low background. (Updated on 25-MAR-2003 to correct
CC   PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 30 BP; 2 A; 3 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||||
Db         22 TGAAAAAAAAAAAAAAAAAAA 2


RESULT 266
ABL35095/c
ID   ABL35095 standard; DNA; 30 BP.
XX
AC   ABL35095;
XX
DT   04-APR-2002  (first entry)
XX
DE   RNA/DNA hybrid control oligonucleotide SEQ ID NO: 1.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .30
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 29; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 7.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTT 2179
              ||  |||||||  | ||||||||||||||
Db         29 TTTTTTTTTTAACGTTTTTTTTTTTTT 1


RESULT 267
ABL35096/c
ID   ABL35096 standard; DNA; 30 BP.
XX
AC   ABL35096;
XX
DT   04-APR-2002  (first entry)
XX
DE   Phosphorothioate substituted RNA/DNA hybrid oligonucleotide SEQ ID NO: 2.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .30
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
FT   misc_RNA         1. .12
FT                    /*tag=  b
FT   misc_RNA         19. .30
FT                    /*tag=  c
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 29; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
```

```
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 7.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
                ||  |||||||  | ||||||||||||||
Db         29 TTTTTTTTTTTAACGTTTTTTTTTTTTT 1


RESULT 268
ABL35097/c
ID   ABL35097 standard; DNA; 30 BP.
XX
AC   ABL35097;
XX
DT   04-APR-2002  (first entry)
XX
DE   Phosphorothioate substituted RNA/DNA hybrid oligonucleotide SEQ ID NO: 3.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .30
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
FT   misc_RNA         13. .18
FT                    /*tag=  b
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 29; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 7.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
                ||  |||||||  | ||||||||||||||
Db         29 TTTTTTTTTTTAACGTTTTTTTTTTTTT 1


RESULT 269
ABL35105/c
ID   ABL35105 standard; DNA; 30 BP.
XX
AC   ABL35105;
XX
DT   04-APR-2002  (first entry)
XX
DE   RNA/DNA hybrid assay control oligonucleotide SEQ ID NO: 11.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .30
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 30; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
```

```
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 2 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 7.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTT 2179
              ||  |||||||   ||||||||||||||
Db         29 TTTTTTTTTTAAGCTTTTTTTTTTTTT 1


RESULT 270
ABL35098/c
ID   ABL35098 standard; RNA; 30 BP.
XX
AC   ABL35098;
XX
DT   04-APR-2002  (first entry)
XX
DE   Phosphorothioate substituted RNA SEQ ID NO: 4.
XX
KW   DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW   infection; allergy; cancer; hypersensitivity; bio-warfare;
KW   immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW   immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW   antiinflammatory; antibacterial; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .30
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
XX
PN   WO200193902-A2.
XX
PD   13-DEC-2001.
XX
PF   07-JUN-2001; 2001WO-US018276.
XX
PR   07-JUN-2000; 2000US-0209797P.
XX
PA   (BIOS-) BIOSYNEXUS INC.
XX
PI   Mond JJ,  Flora M,  Klinman DM;
XX
DR   WPI; 2002-130570/17.
XX
PT   New immunostimulatory compositions comprising RNA/DNA hybrid
PT   oligonucleotides, useful for enhancing an immune response or inducing
PT   cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT   HIV infection.
XX
PS   Example 1; Page 29; 68pp; English.
XX
CC   The present invention relates to an immunostimulatory composition, which
CC   comprises at least one oligonucleotide comprising both an RNA region and
CC   a DNA region. The composition is useful for enhancing an immune response
CC   or inducing cytokines. It can be used as a vaccine adjuvant and in
CC   treating diseases, including pathogenic infection, (non-)malignant
CC   tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC   colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC   (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC   hepatitis, HIV or malaria. The composition is also useful for treating,
CC   preventing or ameliorating the symptoms resulting from exposure to a bio-
CC   warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC   an immunostimulatory oligonucleotide described in the exemplification of
CC   the invention
XX
SQ   Sequence 30 BP; 26 A; 1 C; 1 G; 0 T; 2 U; 0 Other;

  Query Match              0.7%;  Score 21;  DB 1;  Length 30;
  Best Local Similarity   82.8%;  Pred. No. 7.7e+02;
  Matches   24;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTT 2179
              ||  |||||||  | ||||||||||||||
Db         29 TTTTTTTTTTAACGTTTTTTTTTTTTT 1


RESULT 271
ABN83375
ID   ABN83375 standard; DNA; 32 BP.
XX
AC   ABN83375;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Mononucleotide repeat locus BAT26 probe #2.
XX
KW   Mononucleotide repeat locus; human; BAT26; probe; microsatellite; tumour;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Labelled with LightCycler fluorescent dye LC-Red-
FT                   640"
XX
PN   EP1207210-A1.
XX
PD   22-MAY-2002.
XX
PF   13-NOV-2001; 2001EP-00126930.
XX
PR   15-NOV-2000; 2000EP-00124897.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
PA   (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
PI   Dietmaier W;
XX
DR   WPI; 2002-437469/47.
XX
PT   Analyzing repeat sequences in DNA using a probe which hybridizes to
PT   adjacent repetitive and non-repetitive regions and determining hybrid
PT   melting point is useful to detect microsatellite instability such as in
PT   hereditary cancer.
XX
PS   Claim 16; Page 7; 19pp; English.
XX
CC   The present invention relates to a method for analysing a target nucleic
CC   acid consisting of repetitive and non-repetitive sequences. The method
CC   comprises hybridising a polynucleotide probe comprising a segment
CC   complementary to a non-repetitive region and a segment complementary to
CC   an adjacent repetitive region, where the second segment consists of a
CC   defined number of repeats, and determining the melting point temperature
CC   of the hybrid. The method is used to analyse microsatellites, especially
CC   microsatellite instability, particularly as a means for detecting
CC   hereditary tumours. Alternatively, the method is used to identify an
CC   individual in a population. The present sequence is a probe for
CC   Mononucleotide repeat locus BAT26, and was used to illustrate the
CC   invention
XX
SQ   Sequence 32 BP; 27 A; 1 C; 2 G; 2 T; 0 U; 0 Other;
```

Query Match 0.7%; Score 21; DB 1; Length 32;
Best Local Similarity 82.8%; Pred. No. 9e+02;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       2776 GTTAGAATTGAAAAAAAAAAAAAAAAAA 2804
              | || ||   ||||||||||||||||||
Db          4 GGTAAAAAAAAAAAAAAAAAAAAAAAAAA 32
```

RESULT 272
AAV03988
ID AAV03988 standard; DNA; 32 BP.
XX
AC AAV03988;
XX
DT 13-MAY-1998 (first entry)
XX
DE Primer B for Non-A non-B hepatitis viral peptide coding sequence.
XX
KW Non-A non-B hepatitis virus; antibody production; infection diagnosis;
KW PCR primer; amplify; ss.
XX
OS Synthetic.
OS Hepatitis virus.
XX
PN JP04084887-A.
XX
PD 18-MAR-1992.
XX
PF 25-JUL-1990; 90JP-00198588.
XX
PR 25-JUL-1990; 90JP-00198588.
XX
PA (KAGA) KAGAKU OYOBI KESSEI RYOHO.
XX
DR WPI; 1992-145501/18.
XX
PT Nucleic acid fragment coding peptide of non-A non-B hepatitis virus - for
PT the early diagnosis of non-A non-B hepatitis by ELISA or agglutination
PT methods.
XX
PS Example 2; Page 7; 12pp; Japanese.
XX
CC This sequence represents a primer for the coding sequence for a non-A non
CC -B hepatitis virus peptide. The protein encoded by the amplified sequence
CC can be used to prepare an antibody specific for non-A non-B hepatitis
CC virus. The peptide and antibody can be used in both ELISA and
CC agglutination methods and is useful in the early diagnosis of non-A non-B
CC hepatitis
XX
SQ Sequence 32 BP; 1 A; 5 C; 5 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2165 CTTTTTTTTTTTTTTTTTTTT 2185
              |||||||||||||||||||||
Db         12 CTTTTTTTTTTTTTTTTTTTT 32
```

RESULT 273
AAQ43973
ID AAQ43973 standard; DNA; 32 BP.
XX
AC AAQ43973;
XX
DT 25-MAR-2003 (revised)
DT 28-OCT-1993 (first entry)
XX
DE Triple helix forming oligonucleotide I.
XX
KW Purine; pyrimidine; tracts; intramolecular triplex; therapeutic;
KW diagnostic; control; gene expresssion; mRNA synthesis suppression; ss.
XX
OS Synthetic.
XX
PN WO9312230-A1.
XX
PD 24-JUN-1993.
XX
PF 11-DEC-1992; 92WO-US010792.
XX
PR 13-DEC-1991; 91US-00808452.
PR 21-JAN-1992; 92US-00826934.
XX
PA (STRI) SRI INT.
XX
PI Jayasena SD, Johnston BH;
XX
DR WPI; 1993-214172/26.
XX
PT New oligo:nucleotide(s) forming triple helix with target nucleic acid -
PT contain purine and pyrimidine tracts in specific orientations, useful
PT therapeutically or diagnostically e.g. for inactivating HIV RNA, etc.
XX
PS Disclosure; Page 47; 101pp; English.
XX
CC The sequence is that of an oligonucleotide, I, which is able to form a
CC triple helix with a duplex nucleic acid (dsNA) contg. a target sequence
CC which comprises at least one pyrimidine tract, and at least one adjacent
CC purine tract. It is useful for therapeutic or diagnostic control of gene
CC expression, e.g. suppression of mRNA synthesis from a target gene. A
CC specified application is targetting of RNA in the HIV-1 genome. When
CC appropriately labelled it may also be used as a probe. Attachment of
CC cleavage agents caused permanent inactivation of the target by site-
CC specific cleavage. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 32 BP; 8 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 0.7%; Score 21; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||||
Db          9 TTTTTTTTTTTTTTTTTTTT 29
```

RESULT 274
AAT77235
ID AAT77235 standard; DNA; 32 BP.
XX
AC AAT77235;
XX
DT 12-FEB-1998 (first entry)
XX
DE Rat fibroblast growth factor FGF-10 RACE primer X.
XX
KW Fibroblast growth factor; rat; human; recombinant DNA; bone disease;
KW wound healing; cartilage; RACE primer; ss.
XX
OS Synthetic.
OS Rattus rattus.
XX
PN WO9720929-A1.
XX
PD 12-JUN-1997.
XX
PF 06-DEC-1996; 96WO-JP003579.
XX
PR 07-DEC-1995; 95JP-00345689.
PR 28-MAR-1996; 96JP-00103240.
PR 24-JUL-1996; 96JP-00214378.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.

```
XX
PI   Itoh N,  Negoro T,  Katsumata T,  Tagashira S;
XX
DR   WPI; 1997-319776/29.
XX
PT   Recombinant fibroblast growth factor FGF-10 and related DNA - useful for
PT   the treatment of bone disease and for wound healing.
XX
PS   Example 1; Page 36; 51pp; Japanese.
XX
CC   The present sequence represents a RACE primer involved in the
CC   amplification of rat fibroblast growth factor FGF-10. Recombinant FGF-10,
CC   vectors, containing the DNA, and host cells, containing the vectors, are
CC   useful for the recombinant production of FGF-10. The recombinant FGF-10
CC   is useful for the treatment of diseases and injury of bone or cartilage,
CC   and as a wound healing promoter
XX
SQ   Sequence 32 BP; 3 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         12 CTTTTTTTTTTTTTTTTTTT 32


RESULT 275
AAT94579
ID   AAT94579 standard; DNA; 32 BP.
XX
AC   AAT94579;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Antifungal polypeptide 3' antisense PCR primer.
XX
KW   Antifungal polypeptide; AlyAFP; inhibition; transgenic plants; primer;
KW   phytopathogenic fungus; resistance; rapid amplification of cDNA ends;
KW   PCR; RACE; antisense; ss.
XX
OS   Synthetic.
OS   Alyssum sp.
XX
PN   WO9737024-A2.
XX
PD   09-OCT-1997.
XX
PF   27-MAR-1997;   97WO-US005709.
XX
PR   29-MAR-1996;   96US-00627706.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Liang J,  Shah D,  Wu Y,  Rosenberger CA;
XX
DR   WPI; 1997-503109/46.
XX
PT   Alyssum antifungal polypeptide and corresponding DNA - used in the
PT   production of transgenic plants resistant to phytopathogenic fungi.
XX
PS   Example 4; Page 66; 92pp; English.
XX
CC   Primers AAT94578-9 were used to PCR amplify the 3' end of the sequence
CC   encoding the antifungal polypeptide AlyAFP (AAW35558), by a 3' RACE
CC   (Rapid Amplification of cDNA Ends) method. This 32-mer primer anneals to
CC   the polyA tail of the sequence. The primers amplify the sequence shown in
CC   AAT94580. The polypeptide can be used to control phytopathogenic fungi,
CC   whilst the coding DNA can be used to produce transgenic plants that
CC   express the polypeptide, making them resistant to the phytopathogenic
CC   fungi
XX
SQ   Sequence 32 BP; 3 A; 3 C; 5 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||
Db         12 TCCTTTTTTTTTTTTTTTTT 32


RESULT 276
ADC87763
ID   ADC87763 standard; DNA; 32 BP.
XX
AC   ADC87763;
XX
DT   01-JAN-2004  (first entry)
XX
DE   F. culmorum  FCWP1 isolation PCR primer #4.
XX
KW   Antifungal protein; ribosomal protein; FCWP1; AlyAFP;
KW   plant fungal infection; Alternaria; Ascochyta; Botrytis; Cercospora;
KW   Colletotrichum; Diplodia; Fusarium; Gaeumanomyces; Helminthosporium;
KW   Macrophomina; Mycosphaerella; Nectria; Peronospora; Phoma;
KW   Phymatotrichum; Phytophthora; Plasmopara; Podosphaera; Puccinia; Puthium;
KW   Pyrenophora; Pyricularia; Pythium; Rhizoctonia; Scerotium; Sclerotinia;
KW   Septoria; Thielaviopsis; Venturia; Verticillium; ss; PCR; primer.
XX
OS   Synthetic.
OS   Fusarium culmorum.
XX
PN   US6573361-B1.
XX
PD   03-JUN-2003.
XX
PF   07-DEC-2000; 2000US-00732210.
XX
PR   07-DEC-1999;   99US-0169340P.
PR   07-DEC-1999;   99US-0169513P.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Bunkers GJ,  Liang J,  Mittanck CA,  Seale JW,  Wu YS;
XX
DR   WPI; 2003-754558/71.
XX
PT   Novel antifungal protein FCWP1, isolated from Fusarium culmorum, useful
PT   for controlling fungal infections in plants.
XX
PS   Example 11; SEQ ID NO 16; 27pp; English.
XX
CC   The invention relates to an isolated antifungal ribosomal protein from
CC   fusarium culmorum, FCWP1. Also included is a fusion protein between the
CC   signal peptide of the antifungal protein AlyAFP from Alyssum and FCWP1,
CC   encoded by the nucleic acid appearing as ADC87758. The FCWP1 proteins are
CC   useful for controlling fungal infections in plants, such as those caused
CC   by Alternaria (e.g. Alternaria brassicola , Alternaria solani ),
CC   Ascochyta (e.g. Ascochyta pisi ); Botrytis (e.g. Botrytis cinerea ),
CC   Cercospora (e.g. Cercospora kikuchii , Cercospora zaea-maydis ),
CC   Colletotrichum (e.g. Colletotrichum lindemuthianum ), Diplodia (e.g.
CC   Diplodia maydis ), Fusarium (e.g. Fusarium nivale , Fusarium oxysporum ,
CC   Fusarium graminearum , Fusarium culmorum , Fusarium solani , Fusarium
CC   moniliforme , Fusarium roseum ), Gaeumanomyces (e.g. Gaeumanomyces
CC   graminis f.sp. tritici), Helminthosporium (e.g. Helminthosporium turcicum
CC   , Helminthosporium carbonum , Helminthosporium maydis ), Macrophomina
CC   (e.g. Macrophomina phaseolina , Maganaporthe grisea ), Mycosphaerella
CC   (e.g. Mycosphaerella figiensis ), Nectria ( Nectria heamatococca ),
CC   Peronospora (e.g. Peronospora manshurica , Peronospora tabacina ), Phoma
CC   (e.g. Phoma betae ), Phymatotrichum (e.g. Phymatotrichum omnivorum ),
CC   Phytophthora (e.g. Phytophthora cinnamomi , Phytophthora cactorum ,
CC   Phytophthora phaseoli , Phytophthora parasitica , Phytophthora
CC   citrophthora , Phytophthora megasperma f.sp. sojae, Phytophthora
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CC   infestans ), Plasmopara (e.g. Plasmopara viticola ), Podosphaera (e.g.
CC   Podosphaera leucotricha ), Puccinia (e.g. Puccinia sorghi , Puccinia
CC   striiformis , Puccinia graminis f.sp. tritici, Puccinia asparagi ,
CC   Puccinia recondita , Puccinia arachidis ), Puthium (e.g. Puthium
CC   aphanidermatum ), Pyrenophora (e.g. Pyrenophora tritici-repentens ),
CC   Pyricularia (e.g. Pyricularia oryzae ), Pythium (e.g. Pythium ultimum ),
CC   Rhizoctonia (e.g. Rhizoctonia solani , Rhizoctonia cerealis ), Scerotium
CC   (e.g. Scerotium rolfsii ), Sclerotinia (e.g. Sclerotinia sclerotiorum ),
CC   Septoria (e.g. Septoria lycopersici , Septoria glycines , Stagonospora
CC   nodorum / Phaeosphaeria nodorum , Septoria tritici ), Thielaviopsis (e.g.
CC   Thielaviopsis basicola ), Uncinula (e.g. Uncinula necator ), Venturia
CC   (e.g. Venturia inaequalis ) or Verticillium (e.g. Verticillium dahliae ,
CC   Verticillium albo-atrum ). Mutations in the proteolytic consensus
CC   sequences contained within FCWP1 provides improved stability of its
CC   antifungal activity. Also disclosed are ribosomal proteins with similar
CC   PI (>7|) and molecular weight (<20kDa) to FCWP1, which may act as
CC   antifungal proteins. The present sequence is a PCR primer used to isolate
CC   cDNA for FCWP1. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6573361B1.
XX
SQ   Sequence 32 BP; 3 A; 3 C; 5 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 9e+02;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTT 2183
              |||||||||||||||||||||
Db         12 TCCTTTTTTTTTTTTTTTTTT 32


RESULT 277
AAS95728/c
ID   AAS95728 standard; DNA; 45 BP.
XX
AC   AAS95728;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Allele discrimination P1 primer #12.
XX
KW   Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW   exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW   Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW   Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW   diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW   lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW   melanoma; PCR primer; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200177390-A2.
XX
PD   18-OCT-2001.
XX
PF   05-APR-2001; 2001WO-US011151.
XX
PR   05-APR-2000; 2000US-0194843P.
XX
PA   (MOLE-) MOLECULAR STAGING INC.
XX
PI   Abarzua P;
XX
DR   WPI; 2002-049157/06.
XX
PT   Detecting single nucleotide polymorphism involves amplifying target
PT   sequences using small primer probe that matches or mismatches to target
PT   sequence and extending primer probe which is then detected.
XX
PS   Claim 15; Page 41; 67pp; English.
XX
CC   The invention relates to detecting single nucleotide polymorphisms by
CC   contacting an allele-specific oligonucleotide primer (P1) with a target
CC   polynucleotide to form a hybridisation complex, where the target sequence
CC   is complementary to P1 at one end but the terminal nucleotide and the
CC   third nucleotide from the terminal at the other end of P1 may not be
CC   complementary. The complex is then contacted with an exonuclease
CC   deficient DNA polymerase enzyme under conditions that promote extension
CC   of P1 with the target DNA as the template, thereby forming an extended
CC   segment of P1. Oligonucleotide probes hybridising to one or more target
CC   polynucleotides distinguish between matched and mismatched 3' ends, hence
CC   the absence of sequence amplification indicates the presence of a single
CC   nucleotide mismatch. Primer sequences complementary to a sequence on an
CC   amplification target circle can be used in rolling circle amplification
CC   (RCA). The method is useful for diagnosing a disease caused by, induced
CC   by or related to a mutation in at least one gene, such as Parkinson's
CC   disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC   disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC   obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC   lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC   melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC   fluorescence decorators used in the detection of RCA products
XX
SQ   Sequence 45 BP; 2 A; 5 C; 0 G; 38 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||||
Db         37 TGAAAAAAAAAAAAAAAAAAA 17


RESULT 278
AAS95724/c
ID   AAS95724 standard; DNA; 45 BP.
XX
AC   AAS95724;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Allele discrimination P1 primer #8.
XX
KW   Rolling circle amplification; single nucleotide polymorphism; anaemia;
KW   exonuclease deficient DNA polymerase; amplification target circle; RCA;
KW   Parkinson's disease; polycystic kidney disease; Tay-Sachs disease; ss;
KW   Huntington disease; sickle cell anaemia; haemophilia; cystic fibrosis;
KW   diabetes; obesity; cancer; head; neck; skin; brain; oesophagus; stomach;
KW   lung; breast; colon; ovary; testis; prostate; leukaemia; lymphoma;
KW   melanoma; PCR primer; sequencing primer; probe.
XX
OS   Homo sapiens.
XX
PN   WO200177390-A2.
XX
PD   18-OCT-2001.
XX
PF   05-APR-2001; 2001WO-US011151.
XX
PR   05-APR-2000; 2000US-0194843P.
XX
PA   (MOLE-) MOLECULAR STAGING INC.
XX
PI   Abarzua P;
XX
DR   WPI; 2002-049157/06.
XX
PT   Detecting single nucleotide polymorphism involves amplifying target
PT   sequences using small primer probe that matches or mismatches to target
PT   sequence and extending primer probe which is then detected.
XX
PS   Claim 15; Page 41; 67pp; English.
XX
CC   The invention relates to detecting single nucleotide polymorphisms by
```

```
CC   contacting an allele-specific oligonucleotide primer (P1) with a target
CC   polynucleotide to form a hybridisation complex, where the target sequence
CC   is complementary to P1 at one end but the terminal nucleotide and the
CC   third nucleotide from the terminal at the other end of P1 may not be
CC   complementary. The complex is then contacted with an exonuclease
CC   deficient DNA polymerase enzyme under conditions that promote extension
CC   of P1 with the target DNA as the template, thereby forming an extended
CC   segment of P1. Oligonucleotide probes hybridising to one or more target
CC   polynucleotides distinguish between matched and mismatched 3' ends, hence
CC   the absence of sequence amplification indicates the presence of a single
CC   nucleotide mismatch. Primer sequences complementary to a sequence on an
CC   amplification target circle can be used in rolling circle amplification
CC   (RCA). The method is useful for diagnosing a disease caused by, induced
CC   by or related to a mutation in at least one gene, such as Parkinson's
CC   disease, polycystic kidney disease, Tay-Sachs disease, Huntington
CC   disease, sickle cell anaemia, haemophilia, cystic fibrosis, diabetes,
CC   obesity, cancers of the head, neck, skin, brain, oesophagus, stomach,
CC   lung, breast, colon, ovary, testis or prostate, leukaemia, lymphoma and
CC   melanoma. Sequences AAS95711-AAS95745 represent primers, targets and
CC   fluorescence decorators used in the detection of RCA products
XX
SQ   Sequence 45 BP; 1 A; 6 C; 0 G; 38 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 21;  DB 1;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+03;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              |||||||||||||||||||||
Db         37 TGAAAAAAAAAAAAAAAAAAA 17


RESULT 279
AAZ00877
ID   AAZ00877 standard; DNA; 24 BP.
XX
AC   AAZ00877;
XX
DT   27-SEP-1999  (first entry)
XX
DE   PCR primer PGRT32 for PG1 coding sequence.
XX
KW   PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker;
KW   cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW   PSA; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9932644-A2.
XX
PD   01-JUL-1999.
XX
PF   22-DEC-1998;   98WO-IB002133.
XX
PR   22-DEC-1997;   97US-00996306.
PR   09-SEP-1998;   98US-0099658P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I,  Bougueleret L;
XX
DR   WPI; 1999-405178/34.
XX
PT   Use of a prostate cancer associated gene and biallelic markers derived
PT   from it.
XX
PS   Example 6; Page 42; 385pp; English.
XX
CC   The invention relates to a mammalian PG1 gene and protein, and a set of
CC   PG1 biallelic markers. The PG1 polynucleotide and biallelic markers are
CC   used in a hybridisation assay, a sequencing assay, or in an allele-
CC   specific amplification assay for determining the identity of a nucleotide
CC   at a PG1-related biallelic marker. The methods can be used to detect and
CC   to assess the risk of developing cancer or prostate cancer. Early-stage
CC   diagnosis of prostate cancer relies on prostate specific antigen (PSA)
CC   dosage. However, the effectiveness of this is limited due to its
CC   inability to discriminate between malignant and non-malignant affections
CC   of the organ. A need exists for both a reliable diagnostic procedure
CC   which would enable early-stage diagnosis, and for preventative and
CC   curative treatments of the disease. The PG1 gene can be used for
CC   detection of prostate cancer, and the risk of developing it in the
CC   future, and can also be used to determine therapies for the disease
XX
SQ   Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 24;
  Best Local Similarity   91.7%;  Pred. No. 4.8e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||||| || |
Db          1 TTTTTTTTTTTTTTTTTTGAAAT 24


RESULT 280
AAZ00877/c
ID   AAZ00877 standard; DNA; 24 BP.
XX
AC   AAZ00877;
XX
DT   27-SEP-1999  (first entry)
XX
DE   PCR primer PGRT32 for PG1 coding sequence.
XX
KW   PG1 gene; biallelic marker; PCR primer; PG1-related biallelic marker;
KW   cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
KW   PSA; human; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9932644-A2.
XX
PD   01-JUL-1999.
XX
PF   22-DEC-1998;   98WO-IB002133.
XX
PR   22-DEC-1997;   97US-00996306.
PR   09-SEP-1998;   98US-0099658P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I,  Bougueleret L;
XX
DR   WPI; 1999-405178/34.
XX
PT   Use of a prostate cancer associated gene and biallelic markers derived
PT   from it.
XX
PS   Example 6; Page 42; 385pp; English.
XX
CC   The invention relates to a mammalian PG1 gene and protein, and a set of
CC   PG1 biallelic markers. The PG1 polynucleotide and biallelic markers are
CC   used in a hybridisation assay, a sequencing assay, or in an allele-
CC   specific amplification assay for determining the identity of a nucleotide
CC   at a PG1-related biallelic marker. The methods can be used to detect and
CC   to assess the risk of developing cancer or prostate cancer. Early-stage
CC   diagnosis of prostate cancer relies on prostate specific antigen (PSA)
CC   dosage. However, the effectiveness of this is limited due to its
CC   inability to discriminate between malignant and non-malignant affections
CC   of the organ. A need exists for both a reliable diagnostic procedure
CC   which would enable early-stage diagnosis, and for preventative and
CC   curative treatments of the disease. The PG1 gene can be used for
CC   detection of prostate cancer, and the risk of developing it in the
CC   future, and can also be used to determine therapies for the disease
```

```
XX
SQ   Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 24;
  Best Local Similarity   91.7%;  Pred. No. 4.8e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAA 2804
              | || ||||||||||||||||||||
Db         24 ATTTCAAAAAAAAAAAAAAAAAAA 1


RESULT 281
ABX79828/c
ID   ABX79828 standard; cDNA; 27 BP.
XX
AC   ABX79828;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #153.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 717; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 27;
  Best Local Similarity   91.7%;  Pred. No. 6.4e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
              || | ||||||||||||||||||||
Db         27 AAATAAAAAAAAAAAAAAAAAAAA 4


RESULT 282
AAZ43904/c
ID   AAZ43904 standard; DNA; 27 BP.
XX
AC   AAZ43904;
XX
DT   10-MAR-2000  (first entry)
XX
DE   M. tuberculosis rpo-beta primer 17.
XX
KW   RNA polymerase; rpo-beta; detection; diagnostic; trap probe; primer; ss.
XX
OS   Mycobacterium tuberculosis.
XX
PN   EP962536-A1.
XX
PD   08-DEC-1999.
XX
PF   29-MAY-1999;   99EP-00110458.
XX
PR   04-JUN-1998;   98DE-01024900.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Weindel K,  Brand J;
XX
DR   WPI; 2000-055287/05.
XX
PT   Selective detection of nucleic acids by amplification with labeled
PT   primers and detection with a trap probe.
XX
PS   Example 1c; Page 19; 27pp; German.
XX
CC   This invention describes a novel method for the selective detection of
CC   nucleic acids which comprises amplification of the nucleic acid with the
CC   help of labeled primers and detection with a trap probe. The methods and
CC   reagents are used for the detection of a marker primer and at least 2
CC   immobilized (or immobilizable) trap probes with the corresponding nucleic
CC   acid sequence of interest for mutation analysis. The method can be used
CC   to detect a specific sequence in a sample of one or more nucleic acids by
CC   using several sets of primers and trap probes (i.e. in an array). The
CC   methods are useful in molecular biology and diagnostic applications,
CC   especially for simultaneous detection of multi-pathogens, typing of
CC   organisms, analyzing genetic diversity and sequencing of genes or
CC   genomes. This sequence represents a primer used in the method of the
CC   invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 6.4e+02;
  Matches   22;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              |:||  ||||||||||||||||||||
Db         27 ARAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 283
AAS63424/c
ID   AAS63424 standard; DNA; 32 BP.
XX
AC   AAS63424;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Oligonucleotide-nanoparticle probe #48.
```

```
XX
KW   Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW   nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200173123-A2.
XX
PD   04-OCT-2001.
XX
PF   28-MAR-2001; 2001WO-US010071.
XX
PR   28-MAR-2000; 2000US-0192699P.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
PR   26-JUN-2000; 2000US-0213906P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Park S,  Li Z;
XX
DR   WPI; 2001-656926/75.
XX
PT   Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT   comprises reaction with nanoparticles that carry oligonucleotides
PT   complementary to parts of the target.
XX
PS   Example 18; Page 148; 404pp; English.
XX
CC   The invention relates to a method for detection of nucleic acid (I)
CC   having at least 2 portions, comprising treatment with nanoparticles that
CC   carry oligonucleotides complementary to at least 2 parts of (I), where
CC   detectable change caused by hybridisation of the oligonucleotide to (I)
CC   is observed. The method is used to detect (or to separate) specific (I),
CC   e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC   analysis etc., and generally to detect analytes other than (I). The
CC   oligonucleotide-derivatised nanoparticles are also useful for preparing
CC   nanostructures useful, for example, as biochips, biofilters, mechanical
CC   devices, separation membranes, chemical sensors, in computers, and for
CC   drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
CC   produced, allowing their direct use (as probes) in polymerase chain
CC   reaction, i.e. they survive multiple heating/cooling cycles so do not
CC   need to be added after amplification. (I) are detected by simple colour
CC   change, without the need for special equipment, making possible rapid
CC   field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC   oligonucleotide-nanoparticle probes, and related sequences, used in the
CC   method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTTT 1


RESULT 284
AAS10367/c
ID   AAS10367 standard; DNA; 32 BP.
XX
AC   AAS10367;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Alkanethiol-modified oligonucleotide, SA2012F.
XX
KW   Nanoparticle; alkanethiol-modified oligonucleotide; DNA detection;
KW   DNA isolation; genetic disease; bacterial disease; viral disease;
KW   forensic science; paternity testing; gene therapy; ss; SA2012F.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "A is covalently linked to a hexythiol moiety"
FT   misc_feature    12
FT                   /*tag=  b
FT                   /note= "T is covalently linked to a fluorescein moiety"
XX
PN   WO200151665-A2.
XX
PD   19-JUL-2001.
XX
PF   12-JAN-2001; 2001WO-US001190.
XX
PR   13-JAN-2000; 2000US-0176409P.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
PR   12-JAN-2001; 2001US-00760500.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Li Z;
XX
DR   WPI; 2001-451868/48.
XX
PT   Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
PT   viral diseases, by contacting the nucleic acid with oligonucleotides
PT   attached to nanoparticles and having sequences complementary a portion of
PT   the nucleic acid.
XX
PS   Example 18; Page 320; 323pp; English.
XX
CC   The sequence represents an alkanethiol-modified oligonucleotide which may
CC   be coupled with colloidal gold particles (nanoparticles) and used to
CC   demonstrate the method of the invention. The invention relates to
CC   isolating or detecting a nucleic acid of interest, in a mixture of
CC   nucleic acids, by binding it to 2 or more complimentary nucleotides which
CC   have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
CC   colloidal gold) are used to both isolate and detect (e.g. by linking the
CC   particle to a fluorescent probe) the resultant complex. The methods are
CC   useful for detecting nucleic acids, natural or synthetic, and modified or
CC   unmodified. The methods may also be applied in the diagnosis of genetic,
CC   bacterial and viral diseases, in forensics, in DNA sequencing, for
CC   paternity testing, for cell line authentication, and for monitoring gene
CC   therapy. The methods are further useful in research and analytical
CC   laboratories in DNA sequencing, in the field to detect the presence of
CC   specific pathogens, for quick identification of an infection to assist in
CC   drug prescription, and in homes and health centres for inexpensive first-
CC   line screening. The methods, which are based on observing colour change
CC   with the naked eye, are cheap, fast, simple, robust (reagents are
CC   stable), do not require specialised or expensive equipment, and little or
CC   no instrumentation is required
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTTT 1
```

```
RESULT 285
AAH28290
ID   AAH28290 standard; RNA; 32 BP.
XX
AC   AAH28290;
XX
DT   05-SEP-2001  (first entry)
XX
DE   3' untranslated region sequence from GADD45 gene.
XX
KW   mRNA protein complex; tumour development; cell aging; death;
KW   ribonomic profile; RNA-binding protein; ss.
XX
OS   Unidentified.
XX
PN   WO200148480-A1.
XX
PD   05-JUL-2001.
XX
PF   28-DEC-2000; 2000WO-US035583.
XX
PR   28-DEC-1999;   99US-0173338P.
XX
PA   (KEEN/) KEENE J D.
XX
PI   Keene JD,  Tenenbaum SA,  Carson C;
XX
DR   WPI; 2001-425706/45.
XX
PT   Partitioning endogenous mRNA-protein complexes in vivo, by contacting
PT   sample comprising the complex with ligand that binds to a component of
PT   the complex and separating complex by binding ligand with a binding
PT   molecule.
XX
PS   Example 6; Page 30; 49pp; English.
XX
CC   The specification describes a method for partitioning endogenous cellular
CC   mRNA-protein (mRNP) complexes. The method comprises contacting a
CC   biological sample comprising mRNP complex with ligand that specifically
CC   binds a component of mRNP complex, separating mRNP complex by binding the
CC   ligand with a molecule specific for ligand, which is attached to the
CC   solid support and then collecting the mRNP complex by removing the
CC   complex from the support. The method is useful for in vivo partitioning
CC   of cellular mRNA protein complexes in a biological sample. The method is
CC   useful for determining the ribonomic profile of a cell which has numerous
CC   uses including monitoring of tumour development, state of growth or state
CC   of development, perturbations of a biological system such as disease,
CC   drug or toxin treatment and the state of cell aging or death,
CC   distinguishing ribonomic profiles among organisms, to discriminate
CC   between transcriptional and post-transcriptional contributions to gene
CC   expression and to track the movement of RNAs through RNP complexes,
CC   including the interactions of combinations of proteins with RNAs in RNP
CC   complexes. AAH28281-AAH28316 represent sequences derived from the 3'
CC   untranslated region (UTR) of mRNA of various genes. The sequences contain
CC   target sequences for RNA-binding proteins
XX
SQ   Sequence 32 BP; 2 A; 2 C; 2 G; 0 T; 26 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   3.1%;  Pred. No. 9.7e+02;
  Matches    1;  Conservative   24;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              : ::::: : |:::::::::::::  : ::: :
Db          1 UAUUUUUUUUCUUUUUUUUUUUGGUCUUUAU 32


RESULT 286
ABK65031/c
ID   ABK65031 standard; DNA; 32 BP.
XX
AC   ABK65031;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Nanoparticle-oligonucleotide #51.
XX
KW   Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200218643-A2.
XX
PD   07-MAR-2002.
XX
PF   10-AUG-2001; 2001WO-US025237.
XX
PR   11-AUG-2000; 2000US-0224631P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-258024/30.
XX
PT   Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT   bacterial disease, comprises hybridizing nanoparticles with attached
PT   oligonucleotides to nucleic acid and detecting change brought about by
PT   hybridization.
XX
PS   Example 18; Page 162; 412pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid (NA) having
CC   at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC   attached oligonucleotides (OGN), where OGN has a sequence complementary
CC   to the sequence of NA; (b) contacting NA and NP under conditions
CC   effective to allow hybridisation of OGN with NA; and (c) observing a
CC   detectable change brought about by hybridisation of OGN with NA. The
CC   method is useful for detecting a nucleic acid, separating a selected
CC   nucleic acid from others and methods of nanofabrication. Detecting
CC   analytes such as nucleic acids and proteins are useful for the diagnosis
CC   of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC   cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC   In particular assays using OGN-NP conjugates prepared using linkers
CC   comprising a steroid residue attached to a cyclic disulphide have been
CC   found to be approximately 10 times more sensitive than assays employing
CC   conjugates prepared using alkanethiols or acyclic disulphides as the
CC   linker. The OGN-NP conjugates are stable allowing them to be used
CC   directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC   target to be PCR amplified can be carried through the 30 or 40 heating
CC   cooling cycles of the PCR and are still able to detect the amplicons
CC   without opening the tubes and causing contamination. ABK64981-ABK65055
CC   represent nanoparticle-oligonucleotides of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTTT 1


RESULT 287
ABS64669/c
ID   ABS64669 standard; DNA; 32 BP.
XX
AC   ABS64669;
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XX
DT   15-NOV-2002  (first entry)
XX
DE   Nucleic acid detection method associated polynucleotide #51.
XX
KW   Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW   nanoparticle; viral RNA detection; bacterial DNA detection;
KW   fungal DNA detection; nanoprobe conjugate; ss.
XX
OS   Synthetic.
XX
PN   WO200246472-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US046418.
XX
PR   08-DEC-2000; 2000US-0254392P.
PR   08-DEC-2000; 2000US-0254418P.
PR   11-DEC-2000; 2000US-0255235P.
PR   11-DEC-2000; 2000US-0255236P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
PR   09-APR-2001; 2001US-0282640P.
PR   10-AUG-2001; 2001US-00927777.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-608256/65.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 18; Page 436; 442pp; English.
XX
CC   The invention describes a method of detecting (M1) a nucleic acid having
CC   two portions, involving providing nanoparticles having oligonucleotides
CC   attached to it, which has a sequence complementary to sequence of two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC   allow hybridisation of oligonucleotides with two or more portions of
CC   nucleic acid, and observing a detectable change brought about by
CC   hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC   conjugates (II) and the aggregate probe are useful for detecting two or
CC   more nucleic acids (from a biological source) having at least two
CC   portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC   with a disease, synthetic, or structurally-modified natural or synthetic
CC   RNA or DNA, or a product of a polymerase chain reaction amplification.
CC   (II) is useful for preparing a nanoprobe conjugate for detecting an
CC   analyte, and for detecting a nucleic acid bound to an electrode surface.
CC   (I) and (II) are useful for fabrication, and for separating a selected
CC   nucleic acid having two portions from other nucleic acids. (I), (II) and
CC   the aggregate probe are useful for detecting an analyte (especially
CC   polyvalent analyte) in a sample. This sequence represents a
CC   polynucleotide used to demonstrate the method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTTT 1


RESULT 288
ACD27316/c
ID   ACD27316 standard; DNA; 32 BP.
XX
AC   ACD27316;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #50.
XX
KW   Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW   virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW   cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW   sexually transmitted disease; inherited disorder; forensic;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
PN   US2002155461-A1.
XX
PD   24-OCT-2002.
XX
PF   12-OCT-2001; 2001US-00976378.
XX
PR   29-JUL-1996;    96US-0031809P.
PR   21-JUL-1997;    97WO-US012783.
PR   29-JAN-1999;    99US-00240755.
PR   25-JUN-1999;    99US-00344667.
PR   26-APR-2000;  2000US-0200161P.
PR   26-JUN-2000;  2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-228115/22.
XX
PT   Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT   comprises use of nanoparticles which have oligonucleotides attached to
PT   them that are complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 40; 130pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid
CC   having 2 portions. The method comprises providing nanoparticles having
CC   oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC   has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC   The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC   the oligonucleotide on the nanoparticle with two or more portions of
CC   nucleic acid and observing a detectable change brought about by the
CC   hybridisation. The method of the invention is useful for separating a
CC   selected nucleic acid having 2 portions, from other nucleic acids, and
CC   for detecting nucleic acids having 2 portions. The method of the
CC   invention is useful for detecting any type of nucleic acids which may be
CC   used for diagnosis of disease and in sequencing of nucleic acids.
CC   Preferably, the method is useful for detecting nucleic acids for
CC   diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC   virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC   virus), bacterial diseases, sexually transmitted diseases, inherited
CC   disorders, in forensics, in DNA sequencing, for paternity testing, for
CC   cell line authentication, for monitoring gene therapy, etc. This method
CC   involves detecting nucleic acids based on observing a colour change with
CC   the naked eye so is cheap, fast, simple and robust, and does not require
CC   specialised expensive equipment. The present sequence represents an
CC   oligonucleotide used to demonstrate the method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTTT 1
```

```
RESULT 289
AAL61641/c
ID   AAL61641 standard; DNA; 32 BP.
XX
AC   AAL61641;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Thiol-modified oligo #2 used in the nucleic acid detection method.
XX
KW   Nucleic acid detection; fabrication; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "Linked to HS(CH2)6 group"
FT   misc_feature    32
FT                   /*tag=  b
FT                   /note= "Linked to (CH2)6-F (fluorescein)"
XX
PN   WO2003035829-A2.
XX
PD   01-MAY-2003.
XX
PF   08-OCT-2002; 2002WO-US032088.
XX
PR   09-OCT-2001; 2001US-0327864P.
PR   07-DEC-2001; 2001US-00008978.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Park S,  Taton TA,  Mirkin CA;
XX
DR   WPI; 2003-430409/40.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 18; Page 167; 467pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid having two
CC   portions. The method involves providing nanoparticles having
CC   oligonucleotides attached to it which has a sequence complementary to
CC   sequence of two portions of nucleic acid, contacting nucleic acid and
CC   nanoparticles to allow hybridisation of oligonucleotides with two or more
CC   portions of nucleic acid and observing a detectable change brought about
CC   by hybridisation. The method and aggregate probes are useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic or structurally modified natural or
CC   synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. The invention is useful for preparing a nanoprobe
CC   conjugate for detecting an analyte and for detecting a nucleic acid bound
CC   to an electrode surface. It is also useful for fabrication and for
CC   separating a selected nucleic acid having two portions from other nucleic
CC   acids. The present sequence is an oligo used to illustrate the method of
CC   the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
                | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTTT 1
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RESULT 290
ABX79177/c
ID   ABX79177 standard; DNA; 32 BP.
XX
AC   ABX79177;
XX
DT   15-APR-2003  (first entry)
XX
DE   Fluorescein-labelled alkanethiol-modified oligonucleotide #2.
XX
KW   Nanoparticle; ss; nucleic acid detection; viral disease;
KW   human immunodeficiency virus infection; hepatitis virus infection;
KW   herpes virus infection; cytomegalovirus infection; forensic science;
KW   Epstein-Barr virus infection; bacterial disease; gene therapy;
KW   sexually transmitted disease; inherited disorder; DNA sequencing;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
PN   US2002155462-A1.
XX
PD   24-OCT-2002.
XX
PF   12-OCT-2001; 2001US-00976577.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-198491/19.
XX
PT   Detecting nucleic acids having at least 2 portions comprises use of
PT   nanoparticles which have oligonucleotides attached to them that are
PT   complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 40; 130pp; English.
XX
CC   The invention relates to detecting a nucleic acid (NA) having at least 2
CC   portions, comprises providing a type of nanoparticles (NP) having
CC   attached to oligonucleotides (O) ((O) on each NP has a sequence
CC   complementary to sequence of at least 2 portions of NA), contacting NA
CC   and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
CC   and observing a detectable change brought about by hybridisation of (O)
CC   on NP with NA. The nanoparticle is useful for separating a selected
CC   nucleic acid having at least 2 portions, from other nucleic acids, and
CC   for detecting nucleic acids having at least 2 portions. The method of
CC   using NP is useful for detecting any type of nucleic acids which may be
CC   used for diagnosis of disease and in sequencing of nucleic acids.
CC   Preferably, the method is useful for detecting nucleic acids for
CC   diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC   virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC   virus), bacterial diseases, sexually transmitted diseases, inherited
CC   disorders, in forensics, in DNA sequencing, for paternity testing, for
CC   cell line authentication and for monitoring gene therapy. The method is
CC   useful in research and analytical laboratories in DNA sequencing and in
CC   the field to detect the presence of specific pathogens. Detecting nucleic
CC   acids based on observing a colour change with the naked eye is cheap,
CC   fast, simple and robust, and do not require specialised expensive
CC   equipment. The present sequence is a fluorescein labelled oligonucleotide
CC   used to demonstrate the method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
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  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1


RESULT 291
ABX92173/c
ID   ABX92173 standard; DNA; 32 BP.
XX
AC   ABX92173;
XX
DT   12-MAY-2003  (first entry)
XX
DE   Nanoparticle-associated oligonucleotide SEQ ID 51.
XX
KW   Nonoparticle; nucleic acid detection; hybridisation; diagnosis;
KW   sequencing; viral infection; human immunodeficiency virus; HIV;
KW   hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;
KW   bacterial infection; sexually transmitted disease; inherited disorder;
KW   forensic; paternity testing; cell line authentication; gene therapy; ss.
XX
OS   Synthetic.
XX
PN   US2002155458-A1.
XX
PD   24-OCT-2002.
XX
PF   28-SEP-2001; 2001US-00967409.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-182627/18.
XX
PT   Detecting nucleic acids having at least two portions involves use of
PT   nanoparticles which have oligonucleotides attached to them that are
PT   complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 59; 130pp; English.
XX
CC   This invention describes a novel method of detecting nucleic acid having
CC   at least two portions. The method involves providing nanoparticles
CC   attached to oligonucleotides, where the oligonucleotide on each
CC   nanoparticle have a sequence complementary to a sequence of at least two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticle to
CC   allow hybridisation of the oligonucleotide on the nanoparticle with two
CC   or more portions of nucleic acid and observing a detectable change
CC   brought about by hybridisation of the oligonucleotide nanoparticle with
CC   nucleic acid. The method is useful for separating a selected nucleic acid
CC   having at least two portions, from other nucleic acids and for detecting
CC   nucleic acids having at least two portions. The method is useful for
CC   detecting any type of nucleic acids which may be used for diagnosis of
CC   disease and in sequencing of nucleic acids. Preferably, the method is
CC   useful for detecting nucleic acids for diagnosis and/or monitoring of
CC   viral infections (human immunodeficiency virus (HIV), hepatitis virus,
CC   herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial
CC   diseases, sexually transmitted diseases, inherited disorders, in
CC   forensics, in DNA sequencing, for paternity testing, for cell line
CC   authentication, and for monitoring gene therapy. The method is useful in
CC   research and analytical laboratories in DNA sequencing, in the field to
CC   detect the presence of specific pathogens. Detecting nucleic acids based
CC   on observing a colour change with the naked eye is cheap, fast, simple
CC   and robust and does not require specialised expensive equipment. ABX92123
CC   -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the
CC   method of the invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTT 1


RESULT 292
ACD27251/c
ID   ACD27251 standard; DNA; 32 BP.
XX
AC   ACD27251;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #50.
XX
KW   Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW   virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW   cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW   sexually transmitted disease; inherited disorder; forensic;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
PN   US2002155459-A1.
XX
PD   24-OCT-2002.
XX
PF   11-OCT-2001; 2001US-00975062.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-228114/22.
XX
PT   Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT   comprises use of nanoparticles which have oligonucleotides attached to
PT   them that are complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 40; 129pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid
CC   having 2 portions. The method comprises providing nanoparticles having
CC   oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC   has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC   The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC   the oligonucleotide on the nanoparticle with two or more portions of
CC   nucleic acid and observing a detectable change brought about by the
CC   hybridisation. The method of the invention is useful for separating a
CC   selected nucleic acid having 2 portions, from other nucleic acids, and
CC   for detecting nucleic acids having 2 portions. The method of the
CC   invention is useful for detecting any type of nucleic acids which may be
CC   used for diagnosis of disease and in sequencing of nucleic acids.
CC   Preferably, the method is useful for detecting nucleic acids for
```

CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication, for monitoring gene therapy, etc. This method
CC involves detecting nucleic acids based on observing a colour change with
CC the naked eye so is cheap, fast, simple and robust, and does not require
CC specialised expensive equipment. The present sequence represents an
CC oligonucleotide used to demonstrate the method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
| | ||||||||||||||||||||||
Db 24 TGCGTTTTTTTTTTTTTTTTTTTT 1

RESULT 293
ACD27121/c
ID ACD27121 standard; DNA; 32 BP.
XX
AC ACD27121;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
KW DNA sequencing; paternity testing; cell line authentication.
XX
OS Synthetic.
XX
PN US2002164605-A1.
XX
PD 07-NOV-2002.
XX
PF 28-SEP-2001; 2001US-00966312.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-247253/24.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change,
PT useful in forensics.
XX
PS Example 18; Page 40; 130pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acid
CC sequences having two portions. The method involves providing
CC nanoparticles having oligonucleotides attached to them, which has a
CC sequence complementary to sequence of two portions of nucleic acid,
CC contacting nucleic acid and nanoparticles, to allow hybridisation of
CC oligonucleotides with two or more portions of nucleic acid, and observing
CC a detectable change brought about by hybridisation. The method of the
CC invention and the aggregate probes are useful for detecting two or more
CC nucleic acids (from a biological source) having at least two portions,
CC such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with
CC a disease, synthetic, or structurally- modified natural or synthetic RNA
CC or DNA, or a product of a polymerase chain reaction amplification.
CC Nanoparticles and nanoparticle- oligonucleotide conjugates of the
CC invention are useful for nanofabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. The method of
CC the invention is useful in forensics, DNA sequencing, for paternity
CC testing, cell line authentication, and monitoring gene therapy.
CC Diagnostic assays employing the nanoparticle-oligonucleotide conjugates
CC of the invention improve the sensitivity of the nucleic acid detection
CC assay. The present sequence represents an oligonucleotide used to
CC demonstrate the method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
| | ||||||||||||||||||||||
Db 24 TGCGTTTTTTTTTTTTTTTTTTTT 1

RESULT 294
ACD27381/c
ID ACD27381 standard; DNA; 32 BP.
XX
AC ACD27381;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #50.
XX
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KW pathogen detection.
XX
OS Synthetic.
XX
PN US2002182611-A1.
XX
PD 05-DEC-2002.
XX
PF 28-SEP-2001; 2001US-00966491.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-596264/56.
XX
PT Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.
XX
PS Example 18; Page 40; 109pp; English.
XX
CC This invention relates to a novel method for detecting a nucleic acid by
CC contacting a nucleic acid with at least two types of nanoparticles having
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides
CC on the nanoparticles, and observing a detectable change. The
CC oligonucleotides on each nanoparticle have a sequence complementary to
CC its respective portion of the sequence of the nucleic acid to be
CC detected. The method of the invention may be used for the detection of a
CC nucleic acid used in, e.g. research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens, in

CC the doctor's office for quick identification of an infection to assist in
CC prescribing a drug for treatment, and in homes and health centres for
CC inexpensive first-line screening. The method of the invention detects
CC nucleic acids based on observing a colour change with the naked eye. This
CC method is cheap, fast, simple, robust and does not require specialised or
CC expensive equipment. The present sequence represents an oligonucleotide
CC used to demonstrate the method of the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
| | ||||||||||||||||||||||
Db 24 TGCGTTTTTTTTTTTTTTTTTTT 1

RESULT 295
ACD27186/c
ID ACD27186 standard; DNA; 32 BP.
XX
AC ACD27186;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #50.
XX
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing.
XX
OS Synthetic.
XX
PN US2002182613-A1.
XX
PD 05-DEC-2002.
XX
PF 12-OCT-2001; 2001US-00976971.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-596265/56.
XX
PT Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.
XX
PS Example 18; Page 40; 107pp; English.
XX
CC This invention relates to a novel method for detecting a nucleic acid by
CC contacting nucleic acid with at least two types of nanoparticles having
CC oligonucleotides, allowing hybridisation of the oligonucleotides on the
CC nanoparticles, and observing a detectable change. The oligonucleotides on
CC each nanoparticle have a sequence complementary to its respective portion
CC of the sequence of the nucleic acid. The method of the invention may be
CC used for the detection of a nucleic acid used in, e.g. research and
CC analytical laboratories in DNA sequencing, in the field to detect the
CC presence of specific pathogens, in the doctor's office for quick
CC identification of an infection to assist in prescribing a drug for
CC treatment, and in homes and health centres for inexpensive first-line
CC screening. The inventive method of detecting nucleic acids based on
CC observing a colour change with the naked eye are cheap, fast, simple,
CC robust (the reagents are stable), do not require specialised or expensive
CC equipment, and little or no instrumentation is required. The present
CC sequence represents an oligonucleotide used to demonstrate the method of
CC the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
| | ||||||||||||||||||||||
Db 24 TGCGTTTTTTTTTTTTTTTTTTT 1

RESULT 296
ACD27056/c
ID ACD27056 standard; DNA; 32 BP.
XX
AC ACD27056;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS Synthetic.
XX
PN US2003044805-A1.
XX
PD 06-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00981344.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-521746/49.
XX
PT Detection of nucleic acid having -2 portions used to prepare biomaterials
PT and in nanofabrication methods, comprises providing nanoparticles,
PT contacting nucleic acid and nanoparticles, and observing change.
XX
PS Example 18; Page 40; 130pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acids. The
CC method comprises providing nanoparticles with oligonucleotides attached
CC to them, which have a sequence complementary to a sequence of two
CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC to allow hybridisation of the oligonucleotides with two or more portions
CC of the nucleic acid, and observing a detectable change brought about by
CC the hybridisation. The nucleic acid to be detected must have at least two
CC portions and the distances between these are chosen so that when the
CC nanoparticle-oligonucleotide conjugate binds the target sequence a
CC detectable change occurs. The method of the invention is useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic, or structurally- modified natural
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC and for detecting a nucleic acid bound to an electrode surface.
CC Nanoparticles and nanoparticle conjugates of the invention are useful for

CC nanofabrication and for separating a selected nucleic acid having two
CC portions from other nucleic acids. Diagnostic assays employing
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC nucleic acid detection methods and can be used to detect nucleic acids
CC that are present in only small amounts in a sample. The invention also
CC provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC conjugates are stable with tailored hybridisation abilities. The present
CC sequence represents an oligonucleotide used to demonstrate the method of
CC the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
| | ||||||||||||||||||||||
Db 24 TGCGTTTTTTTTTTTTTTTTTTTT 1

RESULT 297
ACH00060/c
ID ACH00060 standard; DNA; 32 BP.
XX
AC ACH00060;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS Synthetic.
XX
PN US2003049631-A1.
XX
PD 13-MAR-2003.
XX
PF 10-OCT-2001; 2001US-00974500.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-634854/60.
XX
PT Detection of nucleic acid having at least two portions, by contacting
PT nucleic acid and nanoparticles under conditions, which allows
PT hybridization of oligonucleotides on nanoparticles with at least two
PT portions of nucleic acid.
XX
PS Example 18; Page 40; 108pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acids. The
CC method comprises providing nanoparticles with oligonucleotides attached
CC to them, which have a sequence complementary to a sequence of two
CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC to allow hybridisation of the oligonucleotides with two or more portions
CC of the nucleic acid, and observing a detectable change brought about by
CC the hybridisation. The nucleic acid to be detected must have at least two
CC portions and the distances between these are chosen so that when the
CC nanoparticle-oligonucleotide conjugate binds the target sequence a
CC detectable change occurs. The method of the invention is useful for
CC detecting two or more nucleic acids (from a biological source) having at
CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC associated with a disease, synthetic, or structurally- modified natural
CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC and for detecting a nucleic acid bound to an electrode surface.
CC Nanoparticles and nanoparticle conjugates of the invention are useful for
CC nanofabrication and for separating a selected nucleic acid having two
CC portions from other nucleic acids. Diagnostic assays employing
CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC nucleic acid detection methods and can be used to detect nucleic acids
CC that are present in only small amounts in a sample. The invention also
CC provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC conjugates are stable with tailored hybridisation abilities. The present
CC sequence represents an oligonucleotide used to demonstrate the method of
CC the invention
XX
SQ Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 91.7%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2163 TCCTTTTTTTTTTTTTTTTTTTT 2186
| | ||||||||||||||||||||||
Db 24 TGCGTTTTTTTTTTTTTTTTTTTT 1

RESULT 298
ADA06155/c
ID ADA06155 standard; DNA; 32 BP.
XX
AC ADA06155;
XX
DT 06-NOV-2003 (first entry)
XX
DE Nanoparticle labelled oligonucleotides, spacer DNA #1.
XX
KW ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;
KW nanostructure; viral disease; human immunodeficiency virus infection;
KW hepatitis virus infection; herpes virus infection;
KW cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;
KW sexually transmitted disease; inherited disorders; paternity testing;
KW cell line authentication; gene therapy.
XX
OS Synthetic.
XX
PN US2003068622-A1.
XX
PD 10-APR-2003.
XX
PF 12-OCT-2001; 2001US-00976863.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-576420/54.
XX
PT Detecting nucleic acids having at least 2 portions comprises use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the target nucleic acid sequence.
XX
PS Example 18; Page 40; 130pp; English.
XX

```
CC   The invention relates to detecting a nucleic acid (NA) having at least 2
CC   portions comprises providing a type of nanoparticles (NP. e.g. colloidal
CC   gold) having oligonucleotides (O) attached (where (O) on each NP has a
CC   sequence complementary to sequence of at least two portions of NA),
CC   contacting NA and NP to allow hybridisation of (O) on NP with 2 or more
CC   portions of NA, and observing a detectable change brought about by
CC   hybridization of (O) on NP with NA. Also included are aggregate probes,
CC   core probes, substrate having NP attached to it, a metallic or
CC   semiconductor NP having (O) attached to it, nanomaterials/nanostructures
CC   comprising nanoparticles and methods of nanofabrication utilising
CC   nanoparticles and satellite probes. The methods, probes nucleic acids,
CC   nanoparticles and oligonucleotides are useful for separating a selected
CC   nucleic acid having at least two portions, from other nucleic acids, and
CC   for detecting nucleic acids having at least two portions, for detecting
CC   NA having at least two portions. The method is useful for detecting any
CC   type of nucleic acids which may be used for diagnosis of disease and in
CC   sequencing of nucleic acids. Preferably, the method is useful for
CC   detecting nucleic acids for diagnosis and/or monitoring of viral diseases
CC   (human immunodeficiency virus, hepatitis virus, herpes virus,
CC   cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually
CC   transmitted diseases, inherited disorders, in forensics, in DNA
CC   sequencing, for paternity testing, for cell line authentication, for
CC   monitoring gene therapy, etc. The method is useful in research and
CC   analytical laboratories in DNA sequencing, in the field to detect the
CC   presence of specific pathogens, etc. Detecting nucleic acids based on
CC   observing a colour change with the naked eye is cheap, fast, simple and
CC   robust, and do not require specialised expensive equipment. The present
CC   sequence is a spacer oligonucleotide used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTTT 1


RESULT 299
ACD26991/c
ID   ACD26991 standard; DNA; 32 BP.
XX
AC   ACD26991;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #50.
XX
KW   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS   Synthetic.
XX
PN   US2003049630-A1.
XX
PD   13-MAR-2003.
XX
PF   20-SEP-2001; 2001US-00957318.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-615795/58.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 18; Page 40 ; 129pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The present sequence
CC   represents an oligonucleotide used to demonstrate the method of the
CC   invention
XX
SQ   Sequence 32 BP; 23 A; 3 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.8;  DB 1;  Length 32;
  Best Local Similarity   91.7%;  Pred. No. 9.7e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTT 2186
              | | ||||||||||||||||||||||
Db         24 TGCGTTTTTTTTTTTTTTTTTTTT 1


RESULT 300
ADE71592/c
ID   ADE71592 standard; DNA; 32 BP.
XX
AC   ADE71592;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Magneto-gold nanoparticle probe #2.
XX
KW   Magneto-gold nanoparticle; probe; ss; core nanoparticle;
KW   non-alloying gold shell; shell nanoparticle; gold salt.
XX
OS   Synthetic.
XX
PN   US2003129608-A1.
XX
PD   10-JUL-2003.
XX
PF   22-MAY-2002; 2002US-00153483.
XX
PR   25-MAY-2001; 2001US-0293861P.
PR   28-DEC-2001; 2001US-00034451.
PR   28-DEC-2001; 2001WO-US050825.
XX
PA   (MIRK/) MIRKIN C A.
PA   (CAOY/) CAO Y.
PA   (JINR/) JIN R.
```

XX
PI Mirkin CA, Cao Y, Jin R;
XX
DR WPI; 2004-031299/03.
XX
PT Core/shell nanoparticle for detecting target molecules, e.g. nucleic
PT acids, comprises inner metal-containing nanoparticle core, outer non-
PT alloying gold shell, and oligonucleotides attached to gold shell.
XX
PS Example 5; Page 8; 21pp; English.
XX
CC The invention relates to a core/shell nanoparticle comprising an inner
CC metal-containing nanoparticle core and an outer non-alloying gold shell
CC surrounding the nanoparticle core. Oligonucleotides may be attached to
CC the gold shell. The invention also relates to preparation of core/shell
CC nanoparticles by treating inner metal-containing nanoparticle cores
CC simultaneously with a solution containing gold salt and a solution
CC containing a reducing agent to produce a non-alloying gold shell
CC surrounding the nanoparticle cores, and isolating the core/shell
CC nanoparticles. Detection of target analytes, e.g. a nucleic acid, bound
CC to a surface comprises contacting the surface with a solution comprising
CC a core/shell nanoparticle receptor conjugate under conditions effective
CC to allow binding of nanoparticle conjugates with the bound nucleic acid,
CC subjecting the nanoparticle conjugate to an external magnetic field to
CC accelerate movement of the nanoparticle conjugate to the surface, to
CC promote binding interaction between the nanoparticle conjugate and target
CC analyte, removing any nanoparticle conjugates that have not bound with
CC the target analyte and observing a detectable change brought about by a
CC binding interaction of the target analyte with the nanoparticle
CC conjugates. The invention is used for detecting target molecules such as
CC nucleic acids, peptides and proteins. The optical properties of
CC core/shell nanoparticles form a new calorimetric channel for nanoparticle
CC -based DNA detection. This sequence represents a magneto-gold
CC nanoparticle probe used in the scope of the invention.
XX
SQ Sequence 32 BP; 24 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 32;
Best Local Similarity 78.1%; Pred. No. 9.7e+02;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy       2154 ATTTTTTTCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||| ||      |||||||||||||||||||
Db         32 ATTATTAGGGAGTTTTTTTTTTTTTTTTTTT 1
```

RESULT 301
AAL07489
ID AAL07489 standard; DNA; 47 BP.
XX
AC AAL07489;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human reproductive system related antigen DNA SEQ ID NO: 10177.
XX
KW Human; reproductive system related antigen; reproductive system disorder;
KW cancer; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200155320-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001339.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465570/50.
XX
PT Isolated nucleic acid molecule encoding a reproductive system antigen is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; SEQ ID NO 10177; 1297pp + Sequence Listing; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of human reproductive system related antigens. These can be used
CC in the prevention and treatment of reproductive system disorders,
CC including cancer. The present sequence is a genomic sequence encoding a
CC protein of the invention
XX
SQ Sequence 47 BP; 36 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.8; DB 1; Length 47;
Best Local Similarity 78.1%; Pred. No. 2e+03;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2773 CTTGTTAGAATTGAAAAAAAAAAAAAAAAAAA 2804
|| || || ||||||||||||||||||
Db 1 CTGCCTAAAAAAAAAAAAAAAAAAAAAAAAAA 32

RESULT 302
AAV71935/c
ID AAV71935 standard; DNA; 27 BP.
XX
AC AAV71935;
XX
DT 18-FEB-1999 (first entry)
XX
DE Anchored poly T RT-PCR primer.
XX
KW Normalised; cDNA library; mRNA cloning; reverse transcription;
KW immobilise; screening; hybridisation; nucleic acid amplification;
KW expression pattern; drug development; PCR primer; RT-PCR; ss.
XX
OS Synthetic.
XX
PN WO9851789-A2.
XX
PD 19-NOV-1998.
XX
PF 13-MAY-1998; 98WO-DK000186.
XX
PR 13-MAY-1997; 97DK-00000547.
PR 19-MAY-1997; 97US-00871030.
PR 27-MAR-1998; 98DK-00000432.
XX
PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
XX
PI Warthoe PR;
XX
DR WPI; 1999-009772/01.
XX
PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
PT reverse transcription and amplification, used to screen for new genes and
PT interacting proteins, potential drugs, and for diagnosis.
XX
PS Example 1; Page 29; 71pp; English.
XX
CC The invention relates to preparation of a normalised, subdivided library
CC of amplified cDNA from the coding regions of mRNA in a sample. The method
CC involves reverse transcription, with at least one cDNA primer of formula
CC 5'-Con1-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence
CC of 1-100 nucleotides; dT = deoxythymidinyl; n2 is at least 1; n3 and n4
CC are both 0. or n3 is 1 and n4 is at least 1; followed by second strand
CC cDNA synthesis using the first strand as template and a second cDNA
CC primer of a similar formula, in the presence of DNA polymerase I (or its
CC Klenow fragment) and amplification of double-stranded cDNA with a set of
CC amplification primers. Comparison of cDNA in the prepared library with a
CC database (a computer-generated list of molecular weights of restricted
CC DNA fragments of known sequence) is used to determine presence of an
CC expressed protein in a cell, also to detect changes in such expression
CC (particularly for diagnosis of disease). Surfaces (chip) having amplified
CC cDNA stably immobilised on it, obtained by a similar method, are used to
CC screen for genes of a particular family, by hybridisation with nucleic
CC acid from the family (to identify new genes) and to detect differences in
CC expression patterns between cells. The polypeptides expressed by the
CC libraries can be used for drug development. Sequences AAV71935 to
CC AAV71946 represent primers used to exemplify the method of the invention
XX
SQ Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 20.6;  DB 1;  Length 27;
  Best Local Similarity   85.2%;  Pred. No. 7e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAAAAAAA 2803
              ||| ||   ||||||||||||||||||
Db         27 TTAAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 303
ABX89953/c
ID   ABX89953 standard; DNA; 30 BP.
XX
AC   ABX89953;
XX
DT   30-APR-2003  (first entry)
XX
DE   PolyA adapter DNA.
XX
KW   Probe; detection; genotyping; cell status; chromosomal resistance gene;
KW   array; ss.
XX
OS   Synthetic.
XX
PN   DE10117857-A1.
XX
PD   24-OCT-2002.
XX
PF   10-APR-2001; 2001DE-01017857.
XX
PR   10-APR-2001; 2001DE-01017857.
XX
PA   (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX
PI   Ellinger T,  Ehricht R,  Wagenhaus A,  Ermantraut E;
XX
DR   WPI; 2003-068801/07.
XX
PT   Detecting specific interactions between molecular targets and probes,
PT   useful for determining genotypic and physiological status of cells, by
PT   attaching an markable adapter to the target.
XX
PS   Example 1; Page 8; 25pp; German.
XX
CC   This invention describes a novel method for detecting the specific
CC   interaction between a target sequence, especially a nucleic acid, and a
CC   probe on an array, in which adapter molecules are fixed to the target,
CC   forming a continuous sequence. Labelling of the target is independently
CC   mediated by interaction of the adapter molecule with a label. The method
CC   is used to investigate the genotypic and physiological status of cells,
CC   e.g. to detect chromosomal resistance genes in Staphylococcus aureus. The
CC   method provides a modular, specific and sensitive system for quantitative
CC   or qualitative detection of a specific target. It provides efficient,
CC   homogeneous and parallel labeling of a target, before, during or after
CC   interaction with the probe array, and both DNA and RNA can be labeled.
CC   The detection signal may be amplified and only low concentrations of
CC   label (particularly 0.1-1 micro M) are used, so non-specific signals are
CC   minimised. This sequence represents a polyA adapter used in the method
CC   described in the invention
XX
SQ   Sequence 30 BP; 5 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.6;  DB 1;  Length 30;
  Best Local Similarity   85.2%;  Pred. No. 9e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2804
              || |  | ||||||||||||||||||
Db         27 TATATATAAAAAAAAAAAAAAAAAAA 1


RESULT 304
ABS55182/c
ID   ABS55182 standard; DNA; 31 BP.
XX
AC   ABS55182;
XX
DT   12-DEC-2002  (first entry)
XX
DE   Tumour-suppressor gene associated oligonucleotide.
XX
KW   Tumour-suppressor; cancer; ss.
XX
OS   Unidentified.
XX
PN   KR2001061173-A.
XX
PD   07-JUL-2001.
XX
PF   28-DEC-1999;  99KR-00063661.
XX
PR   28-DEC-1999;  99KR-00063661.
XX
PA   (CHAE/) CHAE J H.
PA   (CHOI/) CHOI W H.
PA   (CHUN/) CHUNG T J.
PA   (JUNG/) JUNG H J.
PA   (KIMC/) KIM C G.
PA   (KIMH/) KIM H G.
PA   (PARK/) PARK C I.
PA   (PARK/) PARK J H.
XX
PI   Chae JH,  Choi WH,  Chung TJ,  Jung HJ,  Kim CG,  Kim HG,  Park CI;
PI   Park JH;
XX
DR   WPI; 2002-016333/02.
XX
PT   Vector containing polymerase chain reaction primers of tumor-suppressor
PT   gene, useful for diagnosis of cancer.
XX
PS   Disclosure; Page 11; 19pp; Korean.
XX
CC   The present invention relates to a new vector comprising polymerase chain
CC   reaction (PCR) primers of tumour-suppressor gene. The invention can be
CC   useful for the diagnosis of cancer. The present nucleic acid sequence
CC   represents an oligonucleotide as described in the invention
XX
SQ   Sequence 31 BP; 22 A; 0 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.6;  DB 1;  Length 31;
  Best Local Similarity   85.2%;  Pred. No. 9.7e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTGAA 2195
              |||||||||||||||||| |  || ||
Db         31 TTTTTTTTTTTTTTTTTTCATATTCAA 5


RESULT 305
ABQ95487
ID   ABQ95487 standard; DNA; 36 BP.
XX
AC   ABQ95487;
XX
DT   28-OCT-2002  (first entry)
XX
DE   Tumour suppression-related oligonucleotide #1138.
XX
KW   Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
KW   tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW   viral infection; cell degeneration disease; neurodegeneration; ds;
KW   Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS   Homo sapiens.
XX
```

```
PN   FR2819824-A1.
XX
PD   26-JUL-2002.
XX
PF   23-JAN-2001; 2001FR-00000899.
XX
PR   23-JAN-2001; 2001FR-00000899.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI   Telerman A,  Amson R,  Tuijnder M,  Susini L;
XX
DR   WPI; 2002-610803/66.
XX
PT   New nucleic acid implicated e.g. in tumor suppression, useful for
PT   diagnosis of tumors, viral infection and cellular degeneration and for
PT   drug screening.
XX
PS   Claim 1; Page 323; 623pp; French.
XX
CC   The present invention relates to novel human nucleic acid sequences (I).
CC   The present sequence is one such nucleic acid sequence. Expression of (I)
CC   are implicated in tumour suppression or reversion and apoptosis and viral
CC   resistance. (I) are useful as probes or primers for detecting,
CC   identifying, measuring and/or amplifying nucleic acid sequences, as
CC   antisense reagents and for recombinant production of polypeptides. (I),
CC   polypeptides (II) encoded by (I), vector containing (I), cells containing
CC   these vectors and antibodies (Ab) against (II) are all useful for
CC   treatment/prevention of viral, tumour and cell degeneration diseases
CC   (especially neurodegeneration, such as Alzheimer's disease and
CC   schizophrenia). Analysing the expression of (I) is also useful for
CC   diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC   (I) are used for studying the aetiology of these diseases (also immune
CC   and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC   to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC   in the specification
XX
SQ   Sequence 36 BP; 27 A; 2 C; 2 G; 4 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 20.6;  DB 1;  Length 36;
  Best Local Similarity   85.2%;  Pred. No. 1.4e+03;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2804
             || |  | ||||||||||||||||||||
Db          2 TACAGGTAAAAAAAAAAAAAAAAAAAA 28


RESULT 306
ABK86169
ID   ABK86169 standard; DNA; 24 BP.
XX
AC   ABK86169;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Oligo dT primer #2 used in method to study gene expression.
XX
KW   Oligo dT primer; gene expression analysis; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200236828-A2.
XX
PD   10-MAY-2002.
XX
PF   01-NOV-2001; 2001WO-US045401.
XX
PR   01-NOV-2000; 2000US-0244933P.
XX
PA   (GENO-) GENOMIC SOLUTIONS INC.
XX
PI   Kane MD,  Dombkowski AA,  Nagel AC;
XX
DR   WPI; 2002-508123/54.
XX
PT   Identifying and characterizing gene expression in samples, for
PT   identifying mRNAs expressed at different levels, comprises employing an
PT   identimer having a oligo-dT primer of a specific sequence and a
PT   detectable marker at its 5' end.
XX
PS   Disclosure; Page 11; 45pp; English.
XX
CC   The invention relates to systems for identification and characterisation
CC   of gene expression in one or more samples, comprising an identimer having
CC   a specific oligo-dT primer sequence, where the identimer comprises a
CC   detectable marker at its 5' end. The system is useful for identifying any
CC   or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC   as the relative differences in mRNA between 2 or more samples, where
CC   desired, for supporting discovery of new genes, and for identifying mRNAs
CC   that are expressed at different levels between 2 or more samples. The new
CC   system or method addresses limitations of prior methods by comprising
CC   compositions and systems that incorporate new strategies where molecular
CC   or biochemical assay compositions and systems are linked to DNA or RNA
CC   sequence databases for optimal resource efficiency in assaying gene
CC   expression. The system has the following advantages over existing
CC   methods: (a) prior sequence information or clone library construction is
CC   not needed to enable the assay; (b) provides immediate sequence
CC   information in addition to information concerning changes or differences
CC   in mRNA level, to determine mRNA expression level and mRNA identification
CC   in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC   sample for subsequent investigation by common molecular biology
CC   techniques; and (d) does not require prior knowledge of the sequence of
CC   the genome of the organism under investigation and can be employed in
CC   organisms lacking significant genomic sequence in formation. The present
CC   sequence represents an oligo dT primer used in the method of the
CC   invention
XX
SQ   Sequence 24 BP; 20 A; 0 C; 1 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 24;
  Best Local Similarity   95.5%;  Pred. No. 5.6e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAAA 2804
              || ||||||||||||||||||||
Db          2 TTTAAAAAAAAAAAAAAAAAAA 23


RESULT 307
ABK86168/c
ID   ABK86168 standard; DNA; 24 BP.
XX
AC   ABK86168;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Oligo dT primer #1 used in method to study gene expression.
XX
KW   Oligo dT primer; gene expression analysis; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200236828-A2.
XX
PD   10-MAY-2002.
XX
PF   01-NOV-2001; 2001WO-US045401.
XX
PR   01-NOV-2000; 2000US-0244933P.
XX
PA   (GENO-) GENOMIC SOLUTIONS INC.
XX
PI   Kane MD,  Dombkowski AA,  Nagel AC;
XX
DR   WPI; 2002-508123/54.
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XX
PT   Identifying and characterizing gene expression in samples, for
PT   identifying mRNAs expressed at different levels, comprises employing an
PT   identimer having a oligo-dT primer of a specific sequence and a
PT   detectable marker at its 5' end.
XX
PS   Disclosure; Page 11; 45pp; English.
XX
CC   The invention relates to systems for identification and characterisation
CC   of gene expression in one or more samples, comprising an identimer having
CC   a specific oligo-dT primer sequence, where the identimer comprises a
CC   detectable marker at its 5' end. The system is useful for identifying any
CC   or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC   as the relative differences in mRNA between 2 or more samples, where
CC   desired, for supporting discovery of new genes, and for identifying mRNAs
CC   that are expressed at different levels between 2 or more samples. The new
CC   system or method addresses limitations of prior methods by comprising
CC   compositions and systems that incorporate new strategies where molecular
CC   or biochemical assay compositions and systems are linked to DNA or RNA
CC   sequence databases for optimal resource efficiency in assaying gene
CC   expression. The system has the following advantages over existing
CC   methods: (a) prior sequence information or clone library construction is
CC   not needed to enable the assay; (b) provides immediate sequence
CC   information in addition to information concerning changes or differences
CC   in mRNA level, to determine mRNA expression level and mRNA identification
CC   in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC   sample for subsequent investigation by common molecular biology
CC   techniques; and (d) does not require prior knowledge of the sequence of
CC   the genome of the organism under investigation and can be employed in
CC   organisms lacking significant genomic sequence in formation. The present
CC   sequence represents an oligo dT primer used in the method of the
CC   invention
XX
SQ   Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 24;
  Best Local Similarity   95.5%;  Pred. No. 5.6e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||||
Db         23 TTTAAAAAAAAAAAAAAAAAAA 2


RESULT 308
AAI66361/c
ID   AAI66361 standard; DNA; 24 BP.
XX
AC   AAI66361;
XX
DT   23-JAN-2002  (first entry)
XX
DE   Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX
KW   Human; phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer;
KW   haemopathy; development disorder; HIV infection; immunological disease;
KW   inflammation; gene therapy; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175014-A2.
XX
PD   11-OCT-2001.
XX
PF   16-MAR-2001; 2001WO-CN000328.
XX
PR   17-MAR-2000; 2000CN-00114973.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-025836/03.
XX
PT   New human phosphatidylinositol-3 (PTDINS3) kinase 35 for diagnosing and
PT   treating malignant tumor, hemopathy, human immunodeficiency virus
PT   infection, immunological diseases and various inflammations.
XX
PS   Example 2; Page 12; 34pp; Chinese.
XX
CC   The present invention provides the protein and coding sequences of human
CC   phosphatidylinositol-3 (PTDINS-3) kinase 35. The sequences can be used in
CC   the treatment of cancer, haemopathy, HIV infection, development
CC   disorders, immunological diseases and inflammation. The present sequence
CC   is a PCR primer for the coding sequence of the invention
XX
SQ   Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 24;
  Best Local Similarity   95.5%;  Pred. No. 5.6e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2804
              || |||||||||||||||||||
Db         22 TTAAAAAAAAAAAAAAAAAAA 1


RESULT 309
AAD25661/c
ID   AAD25661 standard; DNA; 30 BP.
XX
AC   AAD25661;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Oligonucleotide #7 related to method for production of RNA viruses.
XX
KW   Cytostatic; replication defective gene transfer; encapsidated RNA virus;
KW   gene therapy; cancer therapy; ss.
XX
OS   Unidentified.
XX
PN   WO200190302-A2.
XX
PD   29-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-US015449.
XX
PR   24-MAY-2000; 2000US-0206997P.
XX
PA   (FENG/) FENG Y.
PA   (TANG/) TANG H.
XX
PI   Feng Y,  Tang H;
XX
DR   WPI; 2002-066766/09.
XX
PT   Producing encapsidated RNA virus by coexpressing RNA virus genomic
PT   sequence linked to bacteriophage promoter, and coding sequence for
PT   bacteriophage polymerase linked to poxvirus promoter in eukaryotic cell
PT   cytoplasm.
XX
PS   Disclosure; Page 38; 49pp; English.
XX
CC   The patent discloses methods to produce RNA viral sequences, recombinant
CC   RNA viruses, mutants of RNA viruses and RNA virus-derived vectors in cell
CC   culture and in vitro using non-viable, replication defective helper
CC   vaccinia recombinants. These methods generate RNA viral genomes and viral
CC   particles in cell culture and in vitro independent of their natural
CC   replication pathways, bypassing the limitation of any cellular barriers.
CC   The invention also relates to a method for producing encapsidated RNA
CC   virus comprising coexpressing polypeptide coding sequences capable of
CC   forming capsid and packaging RNA viral genomic sequence in eukaryotic
CC   cell, a construct comprising RNA viral genomic sequence linked to
CC   bacteriophage promoter and transcription terminator and bacteriophage
CC   polymerase coding sequence, which is operably compatible with the
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CC   promoter and is linked to poxvirus promoter. The methods are useful for
CC   producing infectious or non-infectious, replication-defective,
CC   encapsidated RNA viruses such as hepatitis virus comprising an RNA genome
CC   e.g. hepatitis C virus (HCV), immature hepatitis B virus or hepatitis A
CC   virus, lentivirus, rhinovirus, influenza virus, LCMV, arenavirus,
CC   parainfluenza virus, reovirus, rotavirus, astrovirus, filovirus, or
CC   coronavirus. They are preferably useful for producing encapsidated human
CC   immunodeficiency virus (HIV)-1, where the HIV-1 lacks a Rev-response
CC   element (RRE) or an envelope sequence. Methods of the invention are also
CC   useful for producing replication defective gene transfer and gene therapy
CC   vectors, particularly to transfer nucleic acids to human cells in vivo
CC   and in vitro. The methods can be used for packaging therapeutic sequences
CC   as gene therapy vector preparations that are substantially free of helper
CC   virus and used as pharmaceuticals in e.g. gene replacement therapy, or
CC   cancer therapy. The present sequence is an oligonucleotide which is
CC   related to a method for production of RNA viruses
XX
SQ   Sequence 30 BP; 6 A; 0 C; 2 G; 22 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 9.7e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2775 TGTTAGAATTGAAAAAAAAAAAAAAAAAA 2804
              | ||  |||   ||||||||||||||||||
Db         30 TATTTAAATCCTAAAAAAAAAAAAAAAAAA 1


RESULT 310
AAT69677
ID   AAT69677 standard; DNA; 30 BP.
XX
AC   AAT69677;
XX
DT   25-MAR-2003  (revised)
DT   19-FEB-1998  (first entry)
XX
DE   Downstream primer for synthetic full length CAT sense RNA.
XX
KW   PCR primer; CAT RNA; detection; quantification; determination; ss.
XX
OS   Synthetic.
XX
PN   EP780479-A2.
XX
PD   25-JUN-1997.
XX
PF   19-DEC-1996;   96EP-00120480.
XX
PR   23-DEC-1995;   95DE-01048680.
XX
PA   (BOEF ) BOEHRINGER MANNHEIM GMBH.
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Leying H,  Hinzpeter M,  Wittor H,  Fritton H;
XX
DR   WPI; 1997-322152/30.
XX
PT   Detection and quantitation of nucleic acid using probe with label and
PT   binding group - and after hybridisation treatment with RNase and capture
PT   on solid phase, particularly for RNA.
XX
PS   Example 2; Page 7; 13pp; German.
XX
CC   The present sequence is a PCR primer for synthetic full length CAT sense
CC   RNA, which was used in a novel method for the detection and quantitative
CC   determination of specific oligonucleotides (ON) or polynucleotides (PN).
CC   The method comprises combining a sample containing RNA or single stranded
CC   DNA with a lysis/hybridisation buffer, treating the homogenised solution
CC   with 1 or more probes, which are essentially complementary to the ON or
CC   PN and contain at least 2 different labels, one a specific binding group
CC   and the other a detectable chemical group, hybridising under stringent
CC   conditions, diluting the mixture and adding an agent that cleaves single
CC   stranded nucleic acid into mononucleotides or ON, transferring the
CC   mixture to a vessel or well, coated with a substance that binds at least
CC   1 label, immobilising ON and PN hybrids (modified with 2 different labels
CC   or 1 label) to the solid phase and detecting immobilised ON or PN, or the
CC   non-immobilised labelled product, directly or via an enzyme labelled
CC   antibody. The method can be used to detect specific mRNA in human, animal
CC   or plant samples. The method is easy to perform and suitable for
CC   automation, does not require preliminary RNA isolation, can be made
CC   quantitative and has a low background. (Updated on 25-MAR-2003 to correct
CC   PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 30 BP; 2 A; 3 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   95.5%;  Pred. No. 9.7e+02;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTTTTCA 22


RESULT 311
ABL56888
ID   ABL56888 standard; DNA; 30 BP.
XX
AC   ABL56888;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly a.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
```

CC high (amplification of primer dimers is delayed), and the limit of
CC quantitation is reduced. Complex probes are not needed, and amplification
CC can be monitored in real time. The working graph for data analysis
CC (automatically generated by a computer) has a higher correlation
CC coefficient than conventional graphs so more accurate quantitation is
CC possible. The current sequence represents a synthetic
CC deoxyribooligonucleotide that was used for investigating the base
CC selectivity of a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 9.7e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
|| || ||||| | ||||||||||||||
Db 1 ATATATATTTTTTTGTTTTTTTTTTTTT 30

RESULT 312
ABA97612
ID ABA97612 standard; DNA; 30 BP.
XX
AC ABA97612;
XX
DT 11-APR-2002 (first entry)
XX
DE Poly a nucleotide sequence.
XX
KW ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS Unidentified.
XX
PN JP2001286300-A.
XX
PD 16-OCT-2001.
XX
PF 20-APR-2000; 2000JP-00120097.
XX
PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 9.7e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
|| || ||||| | ||||||||||||||
Db 1 ATATATATTTTTTTGTTTTTTTTTTTTT 30

RESULT 313
AAD33517/c
ID AAD33517 standard; DNA; 30 BP.
XX
AC AAD33517;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS5-30-0001 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.
XX
OS Unidentified.
XX
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001EP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX
CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibration probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX
SQ Sequence 30 BP; 24 A; 4 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 9.7e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2155 TTTTTTTCTCCTTTTTTTTTTTTTTTTT 2184
|||||| ||||||||||||||||||
Db 30 TTTTTTGGGAGATTTTTTTTTTTTTTTT 1

RESULT 314
ABL95885
ID ABL95885 standard; DNA; 30 BP.
XX
AC ABL95885;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly a for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.

```
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 30;
  Best Local Similarity   80.0%;  Pred. No. 9.7e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTTTTTT 2179
              ||  || ||||| |  ||||||||||||||
Db          1 ATATATATTTTTTTTGTTTTTTTTTTTTTT 30


RESULT 315
AAQ99582
ID   AAQ99582 standard; cDNA; 31 BP.
XX
AC   AAQ99582;
XX
DT   25-MAR-2003  (revised)
DT   30-APR-1996  (first entry)
XX
DE   Human TPO anti-sense primer hTPO-3mix #3.
XX
KW   Thrombopoietin; TPO; humoral factor; platelet; antibody; therapy; AIDS;
KW   thrombocytopenia; hypoplastic anaemia; thrombotic thombocytopenia;
KW   disseminated intravascular coagulation syndrome; PCR; primer; amplify;
KW   polymerase chain reaction; rat; human; ss.
XX
OS   Synthetic.
XX
PN   WO9521919-A2.
XX
PD   17-AUG-1995.
XX
PF   14-FEB-1995;   95WO-JP000208.
XX
PR   14-FEB-1994;   94JP-00039090.
PR   14-MAR-1994;   94US-00212164.
PR   25-MAR-1994;   94JP-00079842.
PR   01-APR-1994;   94US-00221020.
PR   01-JUN-1994;   94JP-00155126.
PR   15-JUN-1994;   94JP-00167328.
PR   20-JUL-1994;   94US-00278083.
PR   17-AUG-1994;   94JP-00193169.
PR   17-AUG-1994;   94JP-00227159.
PR   18-AUG-1994;   94JP-00193916.
PR   11-OCT-1994;   94US-00320300.
PR   01-NOV-1994;   94JP-00304167.
PR   01-DEC-1994;   94JP-00298669.
PR   22-DEC-1994;   94US-00361811.
PR   28-DEC-1994;   94JP-00341200.
PR   31-JAN-1995;   95US-00318478.
XX
PA   (KIRI ) KIRIN BREWERY KK.
XX
PI   Miyazaki H, Kato T, Ohgami K, Iwamatsu A, Akahori H, Kuroki R;
PI   Shimizu T, Muto T;
XX
DR   WPI; 1995-293120/38.
XX
PT   Thrombopoietin polypeptide which specifically stimulates or increases
PT   platelet production - useful in treatment of thrombocytopenia, also
PT   related DNA and vectors.
XX
PS   Example 19; Page 127; 383pp; English.
XX
CC   AAQ99576-Q99584 represent amplification primers based on regions of the
CC   human thrombopoietin (TPO) cDNA (see AAQ99552). These sequences were used
CC   to obtain a full length TPO sequence, as AAQ99552 did not have a complete
CC   3' terminus. TPO is a humoral factor capable of promoting platelet
CC   production. The protein encoded by the full length sequence can be
CC   purified by using a gel affinity column where Mpl has been coupled to a
CC   resin. AAQ99551 and AAQ99553 also encode TPO proteins. The DNA sequences
CC   are inserted into vectors which are used to transform prokaryotic and
CC   eukaryotic host cells. Using the proteins encoded by these sequences, and
CC   derivatives of them, antibodies specifically immunoreactive with a TPO
CC   protein can be created. The antibodies, DNA sequences and vectors are
CC   used to isolate the protein sequences. The TPO proteins can then be used
CC   in the treatment of platelet disorders. These include thrombocytopenia,
CC   hypoplastic anaemia, AIDS, disseminated intravascular coagulation
CC   syndrome and thrombotic thrombocytopenia. (Updated on 25-MAR-2003 to
CC   correct PR field.)
XX
SQ   Sequence 31 BP; 1 A; 5 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.4;  DB 1;  Length 31;
  Best Local Similarity   95.5%;  Pred. No. 1.1e+03;
  Matches   21;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTT 2186
              ||||||||||||||||||| |||
Db         10 CTTTTTTTTTTTTTTTTTCTTT 31


RESULT 316
ABA97621
ID   ABA97621 standard; DNA; 31 BP.
XX
AC   ABA97621;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly j nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
```

PR 20-APR-1999; 99JP-00111601.
PR 24-AUG-1999; 99JP-00236666.
PR 30-AUG-1999; 99JP-00242693.
PR 01-FEB-2000; 2000JP-00028896.
XX
PA (BIOI-) BIOINDUSTRY KYOKAI SH.
PA (KANK-) KANKYO ENG KK.
PA (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR WPI; 2002-134193/18.
XX
PT Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT the obtained data.
XX
PS Example 5; Page 17; 34pp; Japanese.
XX
CC This invention relates to a method for measuring nucleic acids using a
CC nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC decreases the fluorescence of the fluorochrome when hybridised with a
CC target nucleic acid, the decrease in the fluorescence is measured. The
CC method can be used for measuring a target nucleic acid
XX
SQ Sequence 31 BP; 4 A; 1 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.4; DB 1; Length 31;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2157 TTTTTCTCCTTTTTTTTTTTTTTTTTTT 2186
| | | | |||||||||| ||||||||||
Db 2 TATATATTTTTTTTTTTTCTTTTTTTTT 31

RESULT 317
AAL50570
ID AAL50570 standard; DNA; 22 BP.
XX
AC AAL50570;
XX
DT 12-DEC-2002 (first entry)
XX
DE Molecular array production method-related PCR primer.
XX
KW Molecular array; ss; target molecule identification; genetic analysis;
KW gene expression; SNP detection; haplotyping; sequencing; PCR; primer.
XX
OS Unidentified.
XX
PN WO200274988-A2.
XX
PD 26-SEP-2002.
XX
PF 18-MAR-2002; 2002WO-GB001245.
XX
PR 16-MAR-2001; 2001GB-00006635.
PR 02-AUG-2001; 2001GB-00018879.
XX
PA (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXF.
XX
PI Mir K;
XX
DR WPI; 2002-732872/79.
XX
PT Producing a molecular array with a plurality of molecules immobilized to
PT a solid substrate, useful in genetic analysis, gene expression studies or
PT the detection or typing of single nucleotide polymorphisms in a sample of
PT nucleic acids.
XX
PS Example 15; Page 122; 166pp; English.
XX
CC The invention comprises a method for producing a molecular array, the
CC method involves immobilising molecules to a solid phase at a density
CC which allows individual immobilised molecules to be individually
CC resolved. The molecular array produced by the method of the invention is
CC useful for identifying one or more target molecules in a sample. The
CC molecular array is also useful in genetic analysis, gene expression
CC studies, identifying molecules which interact with a target molecule,
CC detection/typing of single nucleotide polymorphisms, haplotyping and
CC sequencing. The present DNA sequence represents a PCR primer that was
CC used in an example of the invention
XX
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 4.9e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2167 TTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||:
Db 1 TTTTTTTTTTTTTTTTTTTV 21

RESULT 318
ABX74887
ID ABX74887 standard; DNA; 22 BP.
XX
AC ABX74887;
XX
DT 21-MAR-2003 (first entry)
XX
DE Oligo-dT primer used in human CC-RCC invention.
XX
KW Microarray; solid surface; immobilised probe; CC-RCC;
KW differential expression profile; aggressive CC-RCC tumour type;
KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
KW gene expression profiling; tumour tissue; oligo-dT; primer; ss.
XX
OS Synthetic.
XX
PN WO200279411-A2.
XX
PD 10-OCT-2002.
XX
PF 29-MAR-2002; 2002WO-US009576.
XX
PR 29-MAR-2001; 2001US-0279411P.
XX
PA (VAND-) VAN ANDEL INST.
XX
PI Haab B, Rhodes D, Teh BT, Takashi M;
XX
DR WPI; 2003-040679/03.
XX
PT New microarray, comprising a matrix of cDNA probe from a set of probes
PT immobilized to a solid surface in predetermined order, useful in the
PT prognosis of patients with clear cell renal carcinoma.
XX
PS Example 2; Page 30; 179pp; English.
XX
CC The present invention relates to a microarray comprising a matrix of at
CC least one cDNA probe from a set of probes immobilised to a solid surface
CC in a predetermined order, where a row of pixels corresponds to replicates
CC of one distinct probe from the set. The probes are complementary to
CC nucleic acid sequences that are expressed differentially in aggressive as
CC compared to non-aggressive types of clear cell renal carcinoma (CC-RCC)
CC and that hybridise to the probes under high stringency conditions. The
CC microarray is useful for the prognosis of patients with CC-RCC, wherein
CC aggressive and non-aggressive CC-RCC tumour types are characterised by
CC differential expression profiles of genes that hybridise with one or more
CC probes immobilised on the microarray. The arrays are useful for gene
CC expression profiling of tumour and normal tissues. The present sequence
CC represents an oligo-dT primer used in the examples of the present
CC invention
XX
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

```
  Query Match             0.7%;  Score 20.2;  DB 1;  Length 22;
  Best Local Similarity   95.2%;  Pred. No. 4.9e+02;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTV 21


RESULT 319
ACC48484
ID   ACC48484 standard; DNA; 22 BP.
XX
AC   ACC48484;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Locked nucleic acid anchored oligo(I) primer ON14.
XX
KW   Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .21
FT                   /*tag=  m
FT                   /mod_base= um
FT                   /note= "2'-O-methyluridine"
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   3
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   5
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   7
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   9
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   11
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   13
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   15
FT                   /*tag=  h
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   17
FT                   /*tag=  i
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   19
FT                   /*tag=  j
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   21
FT                   /*tag=  k
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   22
FT                   /*tag=  l
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Compound 17d"
XX
PN   WO2003020739-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-IB003911.
XX
PR   04-SEP-2001; 2001US-0317034P.
PR   22-SEP-2001; 2001US-0323967P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J,  Kauppinen S;
XX
DR   WPI; 2003-363021/34.
XX
PT   Novel nucleic acid comprising a locked nucleic acid unit having a
PT   modified base that comprises an optionally substituted carbocyclic aryl
PT   moiety, or modified nucleobase or nucleosidic base other than
PT   oxazole/imidazole.
XX
PS   Example 24a; Page 90; 119pp; English.
XX
CC   The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC   oligo(dT) primer ON14, which was used in first-strand cDNA synthesis from
CC   eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC   on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC   one of a set of such primers (see also ACC48482-85) that were used in an
CC   example from the invention to demonstrate improved reverse transcription
CC   of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC   were observed: efficient priming on mRNAs with short poly(A) tails;
CC   efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC   units resulting in an improved T20-VN anchor primer and thus avoiding
CC   reverse transcription of long poly(A) tracts; and improved reverse
CC   transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC   due to increased specificity. The invention relates to modified LNA units
CC   that comprise unique base groups. Desirable nucleobase and nucleosidic
CC   base substitutions can mediate universal hybridisation when incorporated
CC   into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC   PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC   and in diagnostics
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 22;
  Best Local Similarity   95.2%;  Pred. No. 4.9e+02;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTV 21


RESULT 320
ACC48485
ID   ACC48485 standard; DNA; 22 BP.
XX
AC   ACC48485;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Locked nucleic acid anchored oligo(I) primer ON15.
XX
KW   Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   21
FT                   /*tag=  a
```

```
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   22
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Compound 17d"
XX
PN   WO2003020739-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-IB003911.
XX
PR   04-SEP-2001; 2001US-0317034P.
PR   22-SEP-2001; 2001US-0323967P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J,  Kauppinen S;
XX
DR   WPI; 2003-363021/34.
XX
PT   Novel nucleic acid comprising a locked nucleic acid unit having a
PT   modified base that comprises an optionally substituted carbocyclic aryl
PT   moiety, or modified nucleobase or nucleosidic base other than
PT   oxazole/imidazole.
XX
PS   Example 24a; Page 90; 119pp; English.
XX
CC   The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC   oligo(dT) primer ON15, which was used in first-strand cDNA synthesis from
CC   eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC   on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC   one of a set of such primers (see also ACC48482-84) that were used in an
CC   example from the invention to demonstrate improved reverse transcription
CC   of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC   were observed: efficient priming on mRNAs with short poly(A) tails;
CC   efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC   units resulting in an improved T20-VN anchor primer and thus avoiding
CC   reverse transcription of long poly(A) tracts; and improved reverse
CC   transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC   due to increased specificity. The invention relates to modified LNA units
CC   that comprise unique base groups. Desirable nucleobase and nucleosidic
CC   base substitutions can mediate universal hybridisation when incorporated
CC   into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC   PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC   and in diagnostics
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match              0.7%;  Score 20.2;  DB 1;  Length 22;
  Best Local Similarity   95.2%;  Pred. No. 4.9e+02;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTTV 21


RESULT 321
ACC48483
ID   ACC48483 standard; DNA; 22 BP.
XX
AC   ACC48483;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Locked nucleic acid anchored oligo(I) primer ON13.
XX
KW   Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   modified_base   2
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   8
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   11
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   14
FT                   /*tag=  e
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   17
FT                   /*tag=  f
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   21
FT                   /*tag=  g
FT                   /mod_base= OTHER
FT                   /note= "OTHER= locked nucleic acid"
FT   modified_base   22
FT                   /*tag=  h
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Compound 17d"
XX
PN   WO2003020739-A2.
XX
PD   13-MAR-2003.
XX
PF   04-SEP-2002; 2002WO-IB003911.
XX
PR   04-SEP-2001; 2001US-0317034P.
PR   22-SEP-2001; 2001US-0323967P.
XX
PA   (EXIQ-) EXIQON AS.
XX
PI   Wengel J,  Kauppinen S;
XX
DR   WPI; 2003-363021/34.
XX
PT   Novel nucleic acid comprising a locked nucleic acid unit having a
PT   modified base that comprises an optionally substituted carbocyclic aryl
PT   moiety, or modified nucleobase or nucleosidic base other than
PT   oxazole/imidazole.
XX
PS   Example 24a; Page 90; 119pp; English.
XX
CC   The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC   oligo(dT) primer ON13, which was used in first-strand cDNA synthesis from
CC   eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC   on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC   one of a set of such primers (see also ACC48482-85) that were used in an
CC   example from the invention to demonstrate improved reverse transcription
CC   of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC   were observed: efficient priming on mRNAs with short poly(A) tails;
CC   efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC   units resulting in an improved T20-VN anchor primer and thus avoiding
CC   reverse transcription of long poly(A) tracts; and improved reverse
CC   transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC   due to increased specificity. The invention relates to modified LNA units
CC   that comprise unique base groups. Desirable nucleobase and nucleosidic
CC   base substitutions can mediate universal hybridisation when incorporated
CC   into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC   PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
```

```
CC   and in diagnostics
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 22;
  Best Local Similarity   95.2%;  Pred. No. 4.9e+02;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTV 21


RESULT 322
AAD51324
ID   AAD51324 standard; DNA; 22 BP.
XX
AC   AAD51324;
XX
DT   16-APR-2003  (first entry)
XX
DE   Anchored oligo dT primer used to illustrate the method of the invention.
XX
KW   Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
KW   gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
KW   musculoskeletal damage; ss.
XX
OS   Unidentified.
XX
PN   WO200290579-A1.
XX
PD   14-NOV-2002.
XX
PF   03-MAY-2002; 2002WO-AU000553.
XX
PR   04-MAY-2001; 2001AU-00004809.
PR   29-JUN-2001; 2001US-00896941.
XX
PA   (GENO-) GENOMICS RES PARTNERS PTY LTD.
XX
PI   Brandon RB;
XX
DR   WPI; 2003-120558/11.
XX
PT   Assessing condition e.g. athletic ability, stage of disease, presence of
PT   drugs, response to exercise, response to vaccines, therapies, nutritional
PT   states, of performance animal involves analyzing nucleic acid expression.
XX
PS   Disclosure; Page 46; 87pp; English.
XX
CC   The invention relates to a method for assessing a condition of a
CC   performance animal. The method involves determining in sample abundance
CC   of expressed target nucleic acid; transmitting digital sample signal to
CC   remote diagnostic server; processing digital sample signal at remotely
CC   located database to correlate digital signal with digital information and
CC   returning report of particular condition of animal. The method is useful
CC   for assessing a condition of a performance animal preferably human, dog
CC   or camel. The condition can be an athletic ability and a condition that
CC   enhances, hinders, impedes or does not change an expected ability of the
CC   performance animal; and also normal, pre-clinical, overt progress and/or
CC   stage of disease, undiagnosed of unclassified conditions, presence of
CC   drugs, response to exercise, response to vaccines, therapies, nutritional
CC   states and response to environmental conditions. Diseases assessed by the
CC   invention include laminitis, lameless, viral or bacterial disease,
CC   gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
CC   musculoskeletal damage or disorders and joint diseases. The present
CC   sequence is a primer used to illustrate the method of the invention
XX
SQ   Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 22;
  Best Local Similarity   95.2%;  Pred. No. 4.9e+02;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTV 21


RESULT 323
ABK13916
ID   ABK13916 standard; DNA; 23 BP.
XX
AC   ABK13916;
XX
DT   21-MAY-2002  (first entry)
XX
DE   3'-PCR primer used in method of identifying transcribed genes.
XX
KW   Identification of transcribed gene; mRNA profile; gene expression;
KW   cellular process; fingerprinting; susceptibility to external factor;
KW   development; disease; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200208461-A2.
XX
PD   31-JAN-2002.
XX
PF   23-JUL-2001; 2001WO-IB001539.
XX
PR   21-JUL-2000; 2000GB-00018016.
PR   21-JUL-2000; 2000US-0219925P.
XX
PA   (GLOB-) GLOBAL GENOMICS AB.
XX
PI   Linnarsson S,  Ernfors P,  Bauren G;
XX
DR   WPI; 2002-217065/27.
XX
PT   Providing mRNA profile, by generating two independent patterns
PT   characteristic of sample mRNA population, analyzing patterns, comparing
PT   gene expression by cell types under varied conditions, and identifying
PT   genes.
XX
PS   Example 2; Page 45; 67pp; English.
XX
CC   The present invention relates to a method for providing a profile of mRNA
CC   molecules present in a sample. The method comprises generating two
CC   independent patterns characteristic of the population of mRNA molecules
CC   expressed in the sample and analysing the patterns using a combinatorial
CC   algorithm, comparing gene expression by different or same cell types
CC   under different conditions, and identifying genes having a role in
CC   various cellular processes. The method is useful for the analysis and
CC   identification of transcribed genes, and fingerprinting. The method can
CC   be used to identify genes which play a role in determining various
CC   cellular processes, including susceptibility to external factors,
CC   development, and disease. The present sequence for a PCR primer is used
CC   in the methods of the present invention
XX
SQ   Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 3 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 23;
  Best Local Similarity   95.2%;  Pred. No. 5.5e+02;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||:
Db          1 TTTTTTTTTTTTTTTTTTTV 21


RESULT 324
ABK86172
ID   ABK86172 standard; DNA; 24 BP.
XX
AC   ABK86172;
```

```
XX
DT   24-SEP-2002  (first entry)
XX
DE   Oligo dT primer #4 used in method to study gene expression.
XX
KW   Oligo dT primer; gene expression analysis; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200236828-A2.
XX
PD   10-MAY-2002.
XX
PF   01-NOV-2001; 2001WO-US045401.
XX
PR   01-NOV-2000; 2000US-0244933P.
XX
PA   (GENO-) GENOMIC SOLUTIONS INC.
XX
PI   Kane MD,  Dombkowski AA,  Nagel AC;
XX
DR   WPI; 2002-508123/54.
XX
PT   Identifying and characterizing gene expression in samples, for
PT   identifying mRNAs expressed at different levels, comprises employing an
PT   identimer having a oligo-dT primer of a specific sequence and a
PT   detectable marker at its 5' end.
XX
PS   Example 1; Page 15; 45pp; English.
XX
CC   The invention relates to systems for identification and characterisation
CC   of gene expression in one or more samples, comprising an identimer having
CC   a specific oligo-dT primer sequence, where the identimer comprises a
CC   detectable marker at its 5' end. The system is useful for identifying any
CC   or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC   as the relative differences in mRNA between 2 or more samples, where
CC   desired, for supporting discovery of new genes, and for identifying mRNAs
CC   that are expressed at different levels between 2 or more samples. The new
CC   system or method addresses limitations of prior methods by comprising
CC   compositions and systems that incorporate new strategies where molecular
CC   or biochemical assay compositions and systems are linked to DNA or RNA
CC   sequence databases for optimal resource efficiency in assaying gene
CC   expression. The system has the following advantages over existing
CC   methods: (a) prior sequence information or clone library construction is
CC   not needed to enable the assay; (b) provides immediate sequence
CC   information in addition to information concerning changes or differences
CC   in mRNA level, to determine mRNA expression level and mRNA identification
CC   in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC   sample for subsequent investigation by common molecular biology
CC   techniques; and (d) does not require prior knowledge of the sequence of
CC   the genome of the organism under investigation and can be employed in
CC   organisms lacking significant genomic sequence in formation. The present
CC   sequence represents an oligo dT primer used in the method of the
CC   invention
XX
SQ   Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 4 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 24;
  Best Local Similarity   95.2%;  Pred. No. 6.1e+02;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTT 2185
              :||||||||||||||||||||
Db          4 VTTTTTTTTTTTTTTTTTTT 24


RESULT 325
AAX84260/c
ID   AAX84260 standard; DNA; 25 BP.
XX
AC   AAX84260;
XX
DT   08-SEP-1999  (first entry)
XX
DE   PCR primer for human Nck associated protein 1 coding sequence.
XX
KW   Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;
KW   therapy; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9931239-A1.
XX
PD   24-JUN-1999.
XX
PF   14-DEC-1998;   98WO-JP005646.
XX
PR   15-DEC-1997;   97JP-00363183.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
PA   (SAKA/) SAKAKI Y.
XX
PI   Sakaki Y;
XX
DR   WPI; 1999-395181/33.
XX
PT   Protein inhibiting apoptosis, useful in the diagnosis and treatment of
PT   Alzheimer's disease.
XX
PS   Disclosure; Page 77; 90pp; Japanese.
XX
CC   This sequence represents a PCR primer used to isolate DNA encoding the
CC   human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
CC   apoptosis. The protein can be used in the investigation, diagnosis and
CC   treatment (e.g. by gene therapy) of Alzheimer's disease
XX
SQ   Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 6.8e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db         25 GAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 326
AAA47833
ID   AAA47833 standard; DNA; 25 BP.
XX
AC   AAA47833;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Adapter sequence for 3' end of lectin cDNA.
XX
KW   Lectin; mannose; sugar; trangenic plant; crop protection; resistance;
KW   bacteria; virus; fungus; insect; targetting; neutrophil glycoprotein;
KW   polymorphonuclear cell; blood typing; primer; ss.
XX
OS   Hernandia moerenhoutiana.
XX
PN   WO200044780-A1.
XX
PD   03-AUG-2000.
XX
PF   28-JAN-2000; 2000WO-AU000039.
XX
PR   29-JAN-1999;   99AU-00008395.
XX
PA   (AURE-) AUSTRALIAN RED CROSS BLOOD SERVICE.
XX
PI   Clark TR,  Minchinton RM;
XX
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```
DR   WPI; 2000-532807/48.
XX
PT   New polypeptide, capable of binding to mannose, isolated from the plant
PT   Hernandia is useful for the generation of transgenic plants which exhibit
PT   enhanced resistance to micro-organisms, fungi, viruses and insects.
XX
PS   Example 8; Page 35; 63pp; English.
XX
CC   The Hernandia lectin is capable of binding and/or interacting with
CC   mannose or a sugar chemically related to mannose. The genetic sequence
CC   encoding lectin can be used for the generation of transgenic plants which
CC   exhibit enhanced resistance to micro-organisms, fungi, viruses and
CC   insects. The lectin polypeptide is also useful for targetting neutrophil
CC   glycoproteins for diagnostic and therapeutic applications, including
CC   evaluating the nature of immune cells and can also be used in typing,
CC   e.g. blood group typing of polymorphonuclear cells
XX
SQ   Sequence 25 BP; 1 A; 3 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 6.8e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2162 CTCCTTTTTTTTTTTTTTTTTTTTT 2186
              | |||  ||||||||||||||||||||
Db          1 CGCCTAGTTTTTTTTTTTTTTTTTT 25


RESULT 327
AAD26900/c
ID   AAD26900 standard; DNA; 25 BP.
XX
AC   AAD26900;
XX
DT   09-APR-2002  (first entry)
XX
DE   Bacterial PNP DNA fragment with an in-frame polyA tract.
XX
KW   Hypermutable organism; dominant negative allele; mismatch repair gene;
KW   spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
KW   bacteria; ss.
XX
OS   Bacteria.
OS   Unidentified.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .5
FT                   /*tag=  a
FT                   /note= "Bacterial PNP gene"
FT   misc_feature    6. .25
FT                   /*tag=  a
FT                   /note= "In-frame polyA tract"
XX
PN   WO200188192-A2.
XX
PD   22-NOV-2001.
XX
PF   14-MAY-2001; 2001WO-US015376.
XX
PR   17-MAY-2000; 2000US-0204769P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (MORP-) MORPHOTEK INC.
PA   (NICO/) NICOLAIDES N C.
PA   (SASS/) SASS P M.
PA   (GRAS/) GRASSO L.
PA   (VOGE/) VOGELSTEIN B.
PA   (KINZ/) KINZLER K W.
XX
PI   Nicolaides NC,  Sass PM,  Grasso L,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2002-083004/11.
XX
PT   Generating mutation in gene using cells which contain defective mismatch
PT   repair gene, useful to generate genetically altered mutations with new
PT   output traits.
XX
PS   Example 5; Fig 7; 59pp; English.
XX
CC   The patent discloses a method for generating hypermutable organisms.
CC   Dominant negative alleles of human mismatch repair genes can be used to
CC   generate hypermutable cells and organisms. They increase the rate of
CC   spontaneous mutations by reducing the effectiveness of DNA repair and
CC   thereby render the cells or animals hypermutable. The method is used to
CC   produce genetically altered organisms to produce new output traits. The
CC   present sequence is a bacterial poly purine nucleotide phosphorylase
CC   (polyPNP) DNA fragment containing an in-frame polyA tract. This sequence
CC   is used in the exemplification of the invention
XX
SQ   Sequence 25 BP; 21 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 6.8e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||||||  | |
Db         25 TTTTTTTTTTTTTTTTTTTTGCCAT 1


RESULT 328
ABK86170
ID   ABK86170 standard; DNA; 25 BP.
XX
AC   ABK86170;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Oligo dT primer #3 used in method to study gene expression.
XX
KW   Oligo dT primer; gene expression analysis; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200236828-A2.
XX
PD   10-MAY-2002.
XX
PF   01-NOV-2001; 2001WO-US045401.
XX
PR   01-NOV-2000; 2000US-0244933P.
XX
PA   (GENO-) GENOMIC SOLUTIONS INC.
XX
PI   Kane MD,  Dombkowski AA,  Nagel AC;
XX
DR   WPI; 2002-508123/54.
XX
PT   Identifying and characterizing gene expression in samples, for
PT   identifying mRNAs expressed at different levels, comprises employing an
PT   identimer having a oligo-dT primer of a specific sequence and a
PT   detectable marker at its 5' end.
XX
PS   Example 2; Page 21; 45pp; English.
XX
CC   The invention relates to systems for identification and characterisation
CC   of gene expression in one or more samples, comprising an identimer having
CC   a specific oligo-dT primer sequence, where the identimer comprises a
CC   detectable marker at its 5' end. The system is useful for identifying any
CC   or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC   as the relative differences in mRNA between 2 or more samples, where
CC   desired, for supporting discovery of new genes, and for identifying mRNAs
CC   that are expressed at different levels between 2 or more samples. The new
CC   system or method addresses limitations of prior methods by comprising
CC   compositions and systems that incorporate new strategies where molecular
```

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CC   or biochemical assay compositions and systems are linked to DNA or RNA
CC   sequence databases for optimal resource efficiency in assaying gene
CC   expression. The system has the following advantages over existing
CC   methods: (a) prior sequence information or clone library construction is
CC   not needed to enable the assay; (b) provides immediate sequence
CC   information in addition to information concerning changes or differences
CC   in mRNA level, to determine mRNA expression level and mRNA identification
CC   in one assay; (c) generates cDNA fragments from all mRNAs present in the
CC   sample for subsequent investigation by common molecular biology
CC   techniques; and (d) does not require prior knowledge of the sequence of
CC   the genome of the organism under investigation and can be employed in
CC   organisms lacking significant genomic sequence in formation. The present
CC   sequence represents an oligo dT primer used in the method of the
CC   invention
XX
SQ   Sequence 25 BP; 0 A; 0 C; 2 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 25;
  Best Local Similarity   88.0%;  Pred. No. 6.8e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTAACTT 2191
                ||||||||||||||||||||  ||
Db          1 TTTTTTTTTTTTTTTTTTTTGGTTT 25


RESULT 329
AAI73048/c
ID   AAI73048 standard; DNA; 26 BP.
XX
AC   AAI73048;
XX
DT   24-OCT-2002  (first entry)
XX
DE   Scaffold oligonucleotide.
XX
KW   Molecular scaffold; fluorophore; fluorescence; energy transfer;
KW   emission wavelength; excitation wavelength; multiple; single nucleotide;
KW   polymorphism; ss.
XX
OS   Synthetic.
XX
PN   WO200222883-A1.
XX
PD   21-MAR-2002.
XX
PF   11-SEP-2001; 2001WO-US028967.
XX
PR   11-SEP-2000; 2000US-00658077.
PR   31-JUL-2001; 2001US-0309156P.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Ju J,  Li Z,  Tong A,  Russo JJ;
XX
DR   WPI; 2002-575158/61.
XX
PT   Composition of matter useful for multi-component analyses, comprises
PT   multiple fluorophores bound to molecular scaffold at preset positions to
PT   permit fluorescence energy transfer between two fluorophores.
XX
PS   Disclosure; Page 43; 113pp; English.
XX
CC   This sequence represents a molecular scaffold which may be used in a
CC   composition of matter comprising multiple fluorophores. The fluorophores
CC   are bound to the molecular scaffold at separate predetermined positions,
CC   to permit fluorescence energy transfer between two fluorophores. The
CC   fluorophores are characterized by maximum emission wavelength of one
CC   being greater than the minimum excitation wavelength of the other. The
CC   composition is useful for determining whether a preselected nucleotide
CC   residue is present at a predetermined position within a nucleic acid. It
CC   is also useful in multicomponent analysis including multiplex biological
CC   analysis, and identifying multiple single nucleotide polymorphisms. The
CC   presence of a number of given nucleotide residues is determined
CC   simultaneously by the composition of the invention
XX
SQ   Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 7.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                |||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 330
AAS20672/c
ID   AAS20672 standard; DNA; 26 BP.
XX
AC   AAS20672;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human zalpha11 Ligand sequencing primer ZC7764b.
XX
KW   Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW   natural killer cell proliferation; T-cell proliferation;
KW   B-cell proliferation; anti-tumour response; immune system;
KW   immunostimulant; cytostatic; human; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6307024-B1.
XX
PD   23-OCT-2001.
XX
PF   09-MAR-2000; 2000US-00522217.
XX
PR   09-MAR-1999;   99US-0123547P.
PR   11-MAR-1999;   99US-0123904P.
PR   01-JUL-1999;   99US-0142013P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Novak JE,  Presnell SR,  Sprecher CA,  Foster DC,  Holly RD;
PI   Gross JA,  Johnston JV,  Nelson AJ,  Dillon SR,  Hammond AK;
XX
DR   WPI; 2002-040208/05.
XX
PT   New zalpha11 ligand polypeptides and polynucleotides, useful for
PT   stimulating proliferation, activation, differentiation and/or induction
PT   of inhibition of specialized cell function, or for stimulating an
PT   antigenic response.
XX
PS   Example 7; Col 139; 105pp; English.
XX
CC   The present invention relates to the isolation of a novel cytokine,
CC   zalpha11 Ligand and the polynucleotide encoding it. The invention also
CC   gives the sequence for the zalpha11 receptor and the polynucleotide
CC   encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC   natural killer (NK) cells or NK cell progenitors, the activation of NK
CC   cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC   anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC   reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC   zalpha11 Ligand polypeptide is also useful in preparing antibodies that
CC   bind to zalpha11 Ligand epitopes. The zalpha11 Ligand polynucleotides can
CC   be used as probes or primers to clone regions of a zalpha11 Ligand gene,
CC   and in gene therapy. Zalpha11 Ligand may also be used to identify
CC   inhibitors of its activity, to enhance the generation of anti-tumour
CC   responses with or without the infusion of donor lymphocytes, and to
CC   activate or stimulate the immune system. The present sequence represents
CC   a sequencing primer used to sequence cDNA clones in the isolation of
CC   human zalpha11 Ligand
XX
```

```
SQ   Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 7.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                ||||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 331
ABX93461/c
ID   ABX93461 standard; DNA; 26 BP.
XX
AC   ABX93461;
XX
DT   27-MAY-2003  (first entry)
XX
DE   LS147-specific polynucleotide sequencing related universal primer #1.
XX
KW   LS147; cancer; lung cancer; gene therapy; cytostatic; ss; sequencing;
KW   primer; EST clone; expressed sequence tag clone.
XX
OS   Synthetic.
XX
PN   US2002188114-A1.
XX
PD   12-DEC-2002.
XX
PF   05-JUN-1998;   98US-00092296.
XX
PR   05-JUN-1997;   97US-0048810P.
XX
PA   (BILL/) BILLINGEL P.
PA   (COHE/) COHEN M.
PA   (COLP/) COLPITTS T L.
PA   (FRIE/) FRIEDMAN P N.
PA   (KLAS/) KLASS M R.
PA   (RUSS/) RUSSELL J C.
PA   (STRO/) STROUPE S.
XX
PI   Billingel P,  Cohen M,  Colpitts TL,  Friedman PN,  Klass MR;
PI   Russell JC,  Stroupe S;
XX
DR   WPI; 2003-341045/32.
XX
PT   New LS147 polypeptide, useful for preparing a composition for treating
PT   e.g., lung cancer.
XX
PS   Example 2; Page 39; 47pp; English.
XX
CC   The invention describes a purified polypeptide or its fragment derived
CC   from the LS147 gene capable of selectively hybridising to the nucleic
CC   acid of the gene and has at least 50% identity with the polynucleotide.
CC   The LS147 polypeptide is useful for preparing a composition for treating
CC   cancer, e.g. lung cancer using gene therapy. This sequence represents a
CC   universal primer used to sequence LS147 expressed sequence tag (EST)-
CC   clones
XX
SQ   Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 7.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                ||||   ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 332
AAA13806
ID   AAA13806 standard; DNA; 26 BP.
XX
AC   AAA13806;
XX
DT   27-JUL-2000  (first entry)
XX
DE   Yeast DOG2 stress responsive gene PCR primer SEQ ID NO:5.
XX
KW   Yeast; stress responsive gene; promoter; brewing; beer; wine; sake;
KW   bread; oxidative stress; osmotic pressure; stress; glucose starvation;
KW   PCR primer; ss.
XX
OS   Saccharomyces cerevisiae.
XX
PN   JP2000078977-A.
XX
PD   21-MAR-2000.
XX
PF   04-SEP-1998;   98JP-00251390.
XX
PR   04-SEP-1998;   98JP-00251390.
XX
PA   (TAIF ) MARUHA CORP.
XX
DR   WPI; 2000-285929/25.
XX
PT   A stress-responsive gene promotor.
XX
PS   Example 3; Page 10; 12pp; Japanese.
XX
CC   The present invention describes a stress responsive gene promoter
CC   isolated from Saccharomyces cerevisiae (yeast). Also described in the
CC   present invention are: (1) a promoter containing a DNA hybridising with
CC   the above DNA under a stringent condition and having stress-responsive
CC   promoter activity; (2) a gene expression cassette containing the above
CC   promoter; (3) an expression vector containing the above gene expression
CC   cassette; (4) a recombinant vector in which a gene encoding an optional
CC   polypeptide is recombined to the above expression vector; (5) a
CC   transformant containing the above recombinant vector; and (6) a method
CC   for the preparation of the above polypeptide in which the above
CC   transformant is cultured and the polypeptide is collected from the
CC   resultant culture. Saccharomyces cerevisiae is used for the brewing of
CC   beer, wine and sake and production of bread. The gene is responsive to
CC   the stresses such as oxidative stress, osmotic pressure stress and
CC   glucose starvation stress. The present sequence represents a PCR primer
CC   for the yeast DOG2 stress responsive gene, which is used in an example
CC   from the present invention
XX
SQ   Sequence 26 BP; 3 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 7.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAAC 2189
                | ||||||||||||| |||||||  ||
Db          1 CATTTTTTTTTTTATTTTTTGAC 25


RESULT 333
AAD12516
ID   AAD12516 standard; DNA; 26 BP.
XX
AC   AAD12516;
XX
DT   25-SEP-2001  (first entry)
XX
DE   Thuja sp. pinoresinol/lariciresinol reductase cDNA cloning linker primer.
XX
KW   Dirigent protein; pinoresinol/lariciresinol reductase; stereospecificity;
KW   lignan biosynthetic pathway; secoisolariciresinol; western red cedar;
KW   PCR primer; ss.
XX
```

```
OS   Thuja plicata.
XX
PN   WO200149833-A2.
XX
PD   12-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-US035265.
XX
PR   30-DEC-1999;   99US-00475316.
XX
PA   (UNIW ) UNIV WASHINGTON STATE RES FOUND.
PA   (MINU ) UNIV MINNESOTA.
XX
PI   Lewis NG,  Davin LB,  Dinkova-Kostova AT,  Fujita M,  Gang DR;
PI   Ford JD,  Sarkanen S;
XX
DR   WPI; 2001-465260/50.
XX
PT   Dirigent and/or pinoresinol/lariciresinol reductase proteins useful for
PT   producing optically-pure lignans.
XX
PS   Example 14; Page 56; 183pp; English.
XX
CC   The present invention relates to an isolated dirigent and/or pinoresinol
CC   /lariciresinol reductase protein from a lignan biosynthetic pathway.
CC   Dirigent and/or pinoresinol/lariciresinol reductase protein and the
CC   nucleic acids that encode it may be expressed either in vivo or in vitro
CC   to produce enzymes involved in the biosynthesis of lignans. The 78-kD
CC   dirigent protein confers stereospecificity in 8,8'-linked lignan
CC   formation and binds to and orients coniferyl alcohol-derived free
CC   radicals, which then under go stereospecific coupling to form (+)-
CC   pinoresinol. Pinoresinol/lariciresinol reductase catalyses the conversion
CC   of pinoresinol to lariciresinol and then to secoisolariciresinol. The
CC   present sequence is 3' linker PCR primer, XhoI-poly(dT) used in the
CC   cloning of Thuja plicata pinoresinol/ lariciresinol reductase cDNA
XX
SQ   Sequence 26 BP; 1 A; 2 C; 3 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 26;
  Best Local Similarity   88.0%;  Pred. No. 7.5e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
                ||||   ||||||||||||||||||
Db          2 TCTCGAGTTTTTTTTTTTTTTTTT 26


RESULT 334
AAH91554
ID   AAH91554 standard; DNA; 28 BP.
XX
AC   AAH91554;
XX
DT   09-OCT-2001  (first entry)
XX
DE   Human inflammatory bowel disease associated polymorphic site #629.
XX
KW   Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
KW   single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;
KW   chromosome 5q31-33; forensic test; gene therapy; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    20
FT                   /*tag=  a
FT                   /note= "SNP, optionally T or A at this position"
XX
PN   WO200142511-A2.
XX
PD   14-JUN-2001.
XX
PF   11-DEC-2000; 2000WO-US033632.
XX
PR   10-DEC-1999;   99US-0170257P.
PR   10-APR-2000; 2000US-0196046P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.
XX
PI   Daly M,  Hudson TJ,  Lander ES,  Rioux J,  Siminovitch K;
XX
DR   WPI; 2001-367874/38.
XX
PT   Testing for the presence of polymorphisms associated with inflammatory
PT   bowel disease, using a hybridization assay.
XX
PS   Claim 1; Page 65; 463pp; English.
XX
CC   The present invention describes a method for detecting the presence of
CC   polymorphisms associated with inflammatory bowel diseases such as
CC   ulcerative colitis and Crohn's disease. The methods can be used to detect
CC   the presence of genetic polymorphisms associated with inflammatory bowel
CC   disease and correlating their occurrence with disease states. They may be
CC   used in this way for phenotypic correlations, forensics, paternity
CC   testing, medicine and genetic analysis. The present sequence is a
CC   polymorphic site described in the exemplification of the invention
XX
SQ   Sequence 28 BP; 5 A; 3 C; 0 G; 19 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 28;
  Best Local Similarity   84.6%;  Pred. No. 8.9e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2150 ATTGATTTTTTTCTCCTTTTTTTTTT 2175
                 ||| |||||||||| |  ||||||||
Db          3 ATTAATTTTTTTCTTCCNTTTTTTTT 28


RESULT 335
ACC83476
ID   ACC83476 standard; DNA; 28 BP.
XX
AC   ACC83476;
XX
DT   08-SEP-2003  (first entry)
XX
DE   Oligo dT primer.
XX
KW   Rat; Czf-1; chondrocyte; zinc finger; osteopathic; antiarthritic;
KW   antirheumatic; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2003044159-A2.
XX
PD   30-MAY-2003.
XX
PF   20-NOV-2002; 2002WO-IL000925.
XX
PR   20-NOV-2001; 2001US-0331626P.
XX
PA   (PROC-) PROCHON BIOTECH LTD.
XX
PI   Yayon A,  Blumenstein S,  Harari D;
XX
DR   WPI; 2003-457599/43.
XX
PT   New chondrocyte-derived zinc finger polypeptides and encoding
PT   polynucleotides, useful for detecting, diagnosing and treating Czf-1
PT   protein-related diseases, such as osteoarthritis and rheumatoid
PT   arthritis.
XX
PS   Example 1; Page 27; 64pp; English.
XX
CC   The present sequence is that of an oligo-dT primer, which was used in the
```

```
CC   PCR amplification of cDNA (see ACC83474) encoding a novel rat zinc finger
CC   protein, designated Czf-1 (see ABR42912). Czf-1 is expressed in
CC   osteoblasts and chondrocytes, and serves as a marker for osteoarthritis.
CC   Czf-1 polynucleotides, polypeptides and antibodies can be used in the
CC   characterisation, diagnosis and treatment of fibroblast growth factor
CC   receptor-related and skeletal diseases and disorders, such as
CC   osteoarthritis, rheumatoid arthritis, and cartilage-related diseases
XX
SQ   Sequence 28 BP; 2 A; 3 C; 3 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 28;
  Best Local Similarity   88.0%;  Pred. No. 8.9e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTTTT 2185
              ||||   ||||||||||||||||||
Db          4 TCTCGAGTTTTTTTTTTTTTTTTT 28


RESULT 336
ABZ59816
ID   ABZ59816 standard; RNA; 28 BP.
XX
AC   ABZ59816;
XX
DT   01-APR-2003  (first entry)
XX
DE   Potato gene PCR primer DDT18AN.
XX
KW   Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
KW   transferrin binding protein; receptor-like protein kinase; helicase;
KW   non-long terminal repeat retroelement reverse transcriptase;
KW   overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   DE10114063-A1.
XX
PD   10-OCT-2002.
XX
PF   22-MAR-2001; 2001DE-01014063.
XX
PR   22-MAR-2001; 2001DE-01014063.
XX
PA   (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.
XX
PI   Buelow L,  Tscharntke M,  Haussuehl K;
XX
DR   WPI; 2003-041808/04.
XX
PT   New DNA sequences from potato, useful for producing plants with altered
PT   properties, e.g. tolerance of flooding, also related proteins, antibodies
PT   and inhibitory sequences.
XX
PS   Example 1; Page 8; 26pp; German.
XX
CC   The invention relates to DNA sequences (I) that encode six specific plant
CC   proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
CC   activity (IIa); (ii) a protein (ABP60426) with transferrin binding
CC   protein activity (IIb); (iii) a protein (ABP60427) with receptor-like
CC   protein kinase activity (IIc); (iv) a protein (ABP60428) with elongation
CC   factor EF-2 activity (IId); (v) a protein (ABP60429) with non-long
CC   terminal repeat retroelement reverse transcriptase activity (IIe); or
CC   (vi) a protein (ABP60430) with helicase activity (IIf). (I), also related
CC   sequences, derived ribozymes and antisense sequences, expression vectors,
CC   encoded proteins and antibodies against the proteins, are used to produce
CC   plants with altered properties, including tolerance of overwatering. The
CC   antibodies are also used for isolation of the proteins and in
CC   immunoassays. Also (I) or their primer or probe fragments are used to
CC   screen for terminators and constitutively, aerobically or anaerobically
CC   inducible plant promoters, specifically for use in potatoes and the
CC   sequence that encodes (IId) is used to alter the translation profile in
CC   plants. Since (I) are derived from potato, their promoters and
CC   terminators provide high level transgene expression in potato, with
CC   improved tissue specificity and inducibility, and can also be used to
CC   control endogenous genes. The present sequence is that of a PCR primer
CC   used in the first strand synthesis of cDNAs derived from Potato
XX
SQ   Sequence 28 BP; 3 A; 2 C; 2 G; 20 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 28;
  Best Local Similarity   88.0%;  Pred. No. 8.9e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTTTTTA 2187
              ||   | ||||||||||||||||||
Db          3 TCGATCTTTTTTTTTTTTTTTTTA 27


RESULT 337
ADD41445/c
ID   ADD41445 standard; DNA; 28 BP.
XX
AC   ADD41445;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Hepatitis C virus NS3 protease/helicase related PCR primer Seq ID26.
XX
KW   NS3 protease; NS3 helicase; hepatitis C virus; HCV; hepatitis C; ss; PCR;
KW   primer.
XX
OS   Unidentified.
XX
PN   JP2002345475-A.
XX
PD   03-DEC-2002.
XX
PF   25-MAY-2001; 2001JP-00156957.
XX
PR   25-MAY-2001; 2001JP-00156957.
XX
PA   (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
PA   (MITN ) MITSUBISHI GAS CHEM CO INC.
XX
DR   WPI; 2003-460881/44.
XX
PT   Functional nucleic acids targeting NS3 protease and/or helicase of
PT   hepatitis C virus (HCV) for prevention, diagnosis and treatment of
PT   hepatitis C.
XX
PS   Example 1; SEQ ID NO 26; 22pp; Japanese.
XX
CC   This invention relates to novel nucleic acids targeting the NS3 protease
CC   and/or helicase of hepatitis C virus (HCV). The invention provides RNA
CC   molecules having a base sequence with a structure given in the
CC   specification and capable of inhibition of NS3 protease and/or helicase
CC   of HCV, and capable of forming a secondary structure also given in the
CC   specification. The invention is useful for the effective prevention,
CC   diagnosis and treatment of hepatitis C. The present sequence is that of a
CC   PCR primer which was used during the exemplification of the invention.
XX
SQ   Sequence 28 BP; 20 A; 0 C; 8 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 28;
  Best Local Similarity   88.0%;  Pred. No. 8.9e+02;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTT 2179
              ||   | ||||||||||||||||||
Db         25 TTCCTCTCTCCTTTTTTTTTTTTT 1


RESULT 338
AAV15487/c
ID   AAV15487 standard; DNA; 29 BP.
```

XX
AC AAV15487;
XX
DT 20-JUL-1998 (first entry)
XX
DE PR-1 promoter primer P41+ for in vivo footprinting.
XX
KW Promoter PR-1; salicylic acid, 2,6-dichloroisonicotinic acid;
KW benzo(1,2,3)thiadiazole-7-carbothioic acid S-methyl ester;
KW transgenic plant; PCR; primer; ss.
XX
OS Synthetic.
OS Arabidopsis thaliana.
XX
PN WO9803536-A1.
XX
PD 29-JAN-1998.
XX
PF 18-JUL-1997; 97WO-US012626.
XX
PR 23-JUL-1996; 96US-0027228P.
XX
PA (NOVS) NOVARTIS CORP.
XX
PI Lebel EG, Ryals JA, Thorne L, Uknes SJ, Ward ER;
XX
DR WPI; 1998-120690/11.
XX
PT New chemically inducible promoter from Arabidopsis - used to regulate
PT gene expression in response to e.g. salicylic acid.
XX
PS Example 9; Page 32; 60pp; English.
XX
CC Primer P41+ corresponds to nucleotides -735 to -706 relative to the
CC transcription start site in the upstream region (see AAV15448) of the
CC Arabidopsis PR-1 gene (see AAV15448). It was used in non-coding strand
CC analysis of the PR-1 promoter region. In vivo footprinting analysis was
CC performed of the PR-1 promoter region. Inducible in vivo footprints are
CC located at positions -629 and -628 and at position -604 on the coding
CC strand and at position -641 on the non-coding strand. The use of PR-1
CC promoter fragments to regulate gene expression in plants in the presence
CC of chemical inducers is disclosed
XX
SQ Sequence 29 BP; 0 A; 2 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 29;
Best Local Similarity 88.0%; Pred. No. 9.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
||| |||||||||||||||||||
Db 29 GAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 339
AAV56638
ID AAV56638 standard; DNA; 30 BP.
XX
AC AAV56638;
XX
DT 23-NOV-1998 (first entry)
XX
DE Feline FLAF cDNA primer #9.
XX
KW Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW T lymphocyte cell; autoimmune disease; primer; ss.
XX
OS Synthetic.
OS Felis catus.
XX
PN WO9746583-A1.
XX
PD 11-DEC-1997.
XX
PF 29-MAY-1997; 97WO-JP001824.
XX
PR 04-JUN-1996; 96JP-00165249.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Imamura T, Maeda H, Fujiyasu T, Imagawa Y, Tokiyoshi S;
XX
DR WPI; 1998-042118/04.
XX
PT Novel feline cytokine protein - useful for treating feline auto:immune
PT diseases, e.g. those caused by feline herpes virus or feline calcivirus.
XX
PS Example 14; Page 66; 94pp; Japanese.
XX
CC AAV56637-V56640 are primers used in the amplification of novel feline
CC cytokine proteins, FLAFp40 and FLAFp35. This protein can be used in the
CC production of a FLAFp35/FLAFp40 heterodimer which can potentiate the
CC cytotoxic activity of feline cytotoxic T lymphocyte cells. Such proteins
CC are used for treatment of feline autoimmune diseases e.g. as caused by
CC feline herpes virus or feline calcivirus
XX
SQ Sequence 30 BP; 3 A; 3 C; 3 G; 21 T; 0 U; 0 Other;

Query Match 0.7%; Score 20.2; DB 1; Length 30;
Best Local Similarity 88.0%; Pred. No. 1.1e+03;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2161 TCTCCTTTTTTTTTTTTTTTTTT 2185
|||| ||||||||||||||||||
Db 6 TCTCGAGTTTTTTTTTTTTTTTTT 30

RESULT 340
AAV62858
ID AAV62858 standard; DNA; 30 BP.
XX
AC AAV62858;
XX
DT 05-MAR-1999 (first entry)
XX
DE Primer for PR-Q gene.
XX
KW Chemically regulatable DNA promoter; expression control; pesticide;
KW herbicide tolerance; pathogenesis-related gene; PR gene; primer; ss.
XX
OS Synthetic.
OS Nicotiana acuminata.
XX
PN US5851766-A.
XX
PD 22-DEC-1998.
XX
PF 31-MAY-1995; 95US-00456262.
XX
PR 31-MAY-1995; 95US-00456262.
XX
PA (NOVS) NOVARTIS FINANCE CORP.
XX
PI Harms C, Ryals JA;
XX
DR WPI; 1999-080396/07.
XX
PT Isolating chemically regulatable DNA sequences in plants - useful for
PT chemically controlling expression in transformed plants.
XX
PS Example 72; Col 96; 175pp; English.
XX
CC This sequence represents a primer used to isolate the tobacco
CC pathogenesis-related (PR) gene. The PR gene can be isolated using the
CC method of the invention. The method is for isolating a chemically
CC regulatable DNA promoter fragment from the 5' flanking region of a

```
CC   chemically regulatable gene in a plant tissue. The method allows
CC   isolation of sequences which will be useful for the controlled expression
CC   of genes, under the control of a non-coding regulatable sequence. This is
CC   useful in plants with a herbicide or pesticide detoxification mechanism
CC   under the control of a chemical regulator, the regulator being applied
CC   before or with the herbicide or pesticide to give optimal tolerance. The
CC   promoter fragment is useful for controlling sequences which encode traits
CC   such as height, shape, development, male or female sterility, and the
CC   ability of the plant to withstand cold, heat, salt and drought. The
CC   chemical induction of the promoter allows the regulation of production of
CC   compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
CC   industrial feedstocks, antimicrobials and pharmaceuticals, by
CC   biosynthesis or metabolite conversion, whose biosynthesis is controlled
CC   by endogenous or foreign genes. The method allows control over the time
CC   and rate of gene expression either throughout the whole plant, or in
CC   localized tissues, to achieve e.g. fungal or insect resistance by for
CC   instance dusting the leaves with the chemical regulator. Controlling the
CC   developmental processes by the application of a regulating chemical in
CC   e.g. the commercial production of cultivated crops allows processes such
CC   as germination, flower formation and fruit ripening to be synchronised at
CC   a given time
XX
SQ   Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 341
AAV81666
ID   AAV81666 standard; DNA; 30 BP.
XX
AC   AAV81666;
XX
DT   25-FEB-1999  (first entry)
XX
DE   Oligonucleotide SEQ ID NO:85 used in Example 72.
XX
KW   Regulation; transcription; plant tissue; chimeric construction; PR;
KW   pathogenesis-related protein; anti-pathogenic; transgenic plant;
KW   beta-1,3-glucanase activity; pest resistance; primer; ss.
XX
OS   Synthetic.
XX
PN   US5847258-A.
XX
PD   08-DEC-1998.
XX
PF   31-MAY-1995;   95US-00457364.
XX
PR   08-MAR-1988;   88US-00165667.
PR   06-FEB-1989;   89US-00305566.
PR   24-MAR-1989;   89US-00329018.
PR   20-JUN-1989;   89US-00368672.
PR   20-OCT-1989;   89US-00425504.
PR   07-SEP-1990;   90US-00580431.
PR   21-DEC-1990;   90US-00632441.
PR   01-APR-1991;   91US-00678378.
PR   27-SEP-1991;   91US-00768122.
PR   06-MAR-1992;   92US-00848506.
PR   06-NOV-1992;   92US-00973197.
PR   06-APR-1993;   93US-00042847.
PR   12-APR-1993;   93US-00045957.
PR   16-JUL-1993;   93US-00093301.
PR   13-JAN-1994;   94US-00181271.
PR   31-MAY-1995;   95US-00457364.
XX
PA   (NOVS ) NOVARTIS FINANCE CORP.
XX
PI   Payne GB,  Ward ER,  Moyer MB,  Ryals JA;
XX
DR   WPI; 1999-059180/05.
XX
PT   DNA encoding pathogenesis-related glucanase proteins - useful for
PT   producing transgenic plants with enhanced disease or pest resistance.
XX
PS   Example 72; Col 93; 169pp; English.
XX
CC   The present invention describes a DNA molecule encoding a pathogenesis-
CC   related (PR) protein having beta-1,3-glucanase activity selected from PR-
CC   2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described are: (i) a
CC   chimeric gene comprising the above DNA molecule linked to a heterologous
CC   promoter; (ii) a vector containing the chimeric gene; (iii) a host cell
CC   containing the chimeric gene; (iv) a transgenic plant containing the
CC   chimeric gene; and (v) a seed from the transgenic plant. The DNA molecule
CC   is used to produce transgenic plants with enhanced disease or pest
CC   resistance. The present sequence represents an oligonucleotide from the
CC   present invention
XX
SQ   Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAA 2804
              ||||| ||||||||||||||| | |
Db          4 GAATTCAAAAAAAAAAAAAAACATA 28


RESULT 342
AAF74908/c
ID   AAF74908 standard; DNA; 30 BP.
XX
AC   AAF74908;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CD40L poly-A tract sequence SEQ ID NO:5.
XX
KW   Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;
KW   diagnosis; antiarthritic; antirheumatic; immunosuppressive;
KW   antiinflammatory; inflammatory disease; autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200119844-A1.
XX
PD   22-MAR-2001.
XX
PF   13-SEP-2000; 2000WO-US024966.
XX
PR   13-SEP-1999;   99US-0153625P.
XX
PA   (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.
XX
PI   Crow MK,  Li Y;
XX
DR   WPI; 2001-244776/25.
XX
PT   New altered CD40L promoter for use in the study, diagnosis and treatment
PT   of a variety of inflammatory disorders and autoimmune diseases, such as
PT   rheumatoid arthritis.
XX
PS   Example 1; Fig 3; 90pp; English.
XX
CC   The present invention describes an isolated, purified nucleic acid, which
CC   is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having
CC   residues 331-455 of the sequence comprising 455 nucleotides given in
CC   AAF74905 where A in the wild type sequence at position 331 (corresponding
CC   to position -125) is replaced with C. (I) has antiarthritic,
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```
CC   antirheumatic, immunosuppressive and antiinflammatory activities, and can
CC   be used in gene therapy. (I) is useful in the study, diagnosis and
CC   treatment of inflammatory and autoimmune diseases, as well as diseases in
CC   which elevated expression of CD40L is a factor, e.g., rheumatoid
CC   arthritis. The present sequence represents a CD40L poly-A tract sequence
CC   which is used in an example from the present invention
XX
SQ   Sequence 30 BP; 24 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20.2;  DB 1;  Length 30;
  Best Local Similarity   88.0%;  Pred. No. 1.1e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTT 2180
              |||||| |  ||||||||||||||||
Db         25 TTTTTTGTTTTTTTTTTTTTTTTT 1


RESULT 343
AAA94322/c
ID   AAA94322 standard; DNA; 33 BP.
XX
AC   AAA94322;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 34-P.
XX
KW   RNA-protein fusion; protein library; protein isolation; DNA-RNA hybrid;
KW   gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        1. .13
FT                   /*tag=  a
FT                   /label= RNA
FT   modified_base   33
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US002589.
XX
PR   09-FEB-1999;   99US-00247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions.
XX
PS   Disclosure; Page 44; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides which were
CC   used for the generation of RNA-protein fusions, including fusions having
CC   a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form
XX
SQ   Sequence 33 BP; 22 A; 4 C; 6 G; 0 T; 1 U; 0 Other;

  Query Match              0.7%;  Score 20.2;  DB 1;  Length 33;
  Best Local Similarity   88.0%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||||||||| | || |
Db         31 TTTTTTTTTTTTTTTTTTCAGTTCG 7


RESULT 344
AAV48094/c
ID   AAV48094 standard; DNA; 34 BP.
XX
AC   AAV48094;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Oligonucleotide 34-P.
XX
KW   In situ translation; RNA-protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss; rRNA/DNA hybrid.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   34
FT                   /*tag=  a
FT                   /note= "Puromycin"
XX
PN   WO9831700-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;   98WO-US000807.
XX
PR   21-JAN-1997;   97US-0035963P.
PR   06-NOV-1997;   97US-0064491P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 1998-414032/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions generated
PT   in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
PT   with altered properties, potentially useful as catalysts or for therapy
PT   or diagnosis.
XX
PS   Disclosure; Page 40; 94pp; English.
XX
CC   The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
CC   variations were used to generate RNA-protein fusions. These were used in
CC   the selection of a specific protein or RNA, by in vitro or in situ
CC   translation of candidate RNA molecules to produce RNA-protein fusions,
CC   then selecting specific RNA protein fusions. The method is used to select
CC   proteins (or DNA encoding them) having altered properties, e.g. for
CC   identification of new binding reagents, to identify improved human
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The methods allow many
CC   rounds of selection and amplification to be performed, resulting in
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CC   enrichment of even very rare molecules and allowing isolation of proteins
CC   that bind specifically to almost any compound or catalyse almost any
CC   reaction
XX
SQ   Sequence 34 BP; 22 A; 4 C; 6 G; 0 T; 1 U; 1 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 34;
  Best Local Similarity   88.0%;  Pred. No. 1.4e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTG 2193
                ||||||||||||||||||  | ||| |
Db         31 TTTTTTTTTTTTTTTTTTCAGTTCG 7


RESULT 345
ABK99273
ID   ABK99273 standard; RNA; 36 BP.
XX
AC   ABK99273;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #3.
XX
KW   Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS   Synthetic.
XX
PN   US2002064771-A1.
XX
PD   30-MAY-2002.
XX
PF   06-APR-2001; 2001US-00828034.
XX
PR   07-APR-2000; 2000US-0195852P.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (FERR/) FERRARI E.
XX
PI   Zhong W,  Hong Z,  Ferrari E;
XX
DR   WPI; 2002-582330/62.
XX
PT   Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT   nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT   and template and primer which do not form a stable duplex in the absence
PT   of HCV NS5B.
XX
PS   Example; Page 6; 17pp; English.
XX
CC   The invention relates to a replicase complex comprising a hepatitis C
CC   virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC   complementary nucleic acid primer which is annealed to the 3' terminus of
CC   the template, where the template is at least three nucleotides and the
CC   primer is two or three nucleotides, and the template and primer do not
CC   form a stable duplex in solution in the absence of the HCV NS5B protein.
CC   The complex is useful for detecting HCV replicase activity and permits
CC   establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC   and evaluate antiviral inhibitors and to improve the specificity and
CC   efficacy of the inhibitors. The complex is also useful in the development
CC   of a reliable system for determining kinetic and thermodynamic constants
CC   of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC   mechanistic inhibitors for mis-incorporation or chain termination.
CC   Specifically, the short RNA template and primer pairs are useful in
CC   screening assays which are used for determining kinetic, thermodynamic
CC   and mechanistic properties of NS5B replication and ultimately in the
CC   development of inhibitors of NS5B. Newly identified inhibitors of
CC   replicase activity may be used for developing anti-HCV pharmaceuticals.
CC   Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC   templates
XX
SQ   Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 36;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                |||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 346
AAD27117
ID   AAD27117 standard; RNA; 36 BP.
XX
AC   AAD27117;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, AU used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 1A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, AU used to direct RNA synthesis by RNA
CC   polymerase proteins of HCV, BVDV and polivirus. This sequence is used in
CC   the exemplification of the invention
XX
SQ   Sequence 36 BP; 33 A; 0 C; 2 G; 0 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 36;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
```

```
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 347
ABK99272
ID   ABK99272 standard; RNA; 36 BP.
XX
AC   ABK99272;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #2.
XX
KW   Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS   Synthetic.
XX
PN   US2002064771-A1.
XX
PD   30-MAY-2002.
XX
PF   06-APR-2001; 2001US-00828034.
XX
PR   07-APR-2000; 2000US-0195852P.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (FERR/) FERRARI E.
XX
PI   Zhong W,  Hong Z,  Ferrari E;
XX
DR   WPI; 2002-582330/62.
XX
PT   Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT   nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT   and template and primer which do not form a stable duplex in the absence
PT   of HCV NS5B.
XX
PS   Example; Page 6; 17pp; English.
XX
CC   The invention relates to a replicase complex comprising a hepatitis C
CC   virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC   complementary nucleic acid primer which is annealed to the 3' terminus of
CC   the template, where the template is at least three nucleotides and the
CC   primer is two or three nucleotides, and the template and primer do not
CC   form a stable duplex in solution in the absence of the HCV NS5B protein.
CC   The complex is useful for detecting HCV replicase activity and permits
CC   establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC   and evaluate antiviral inhibitors and to improve the specificity and
CC   efficacy of the inhibitors. The complex is also useful in the development
CC   of a reliable system for determining kinetic and thermodynamic constants
CC   of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC   mechanistic inhibitors for mis-incorporation or chain termination.
CC   Specifically, the short RNA template and primer pairs are useful in
CC   screening assays which are used for determining kinetic, thermodynamic
CC   and mechanistic properties of NS5B replication and ultimately in the
CC   development of inhibitors of NS5B. Newly identified inhibitors of
CC   replicase activity may be used for developing anti-HCV pharmaceuticals.
CC   Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC   templates
XX
SQ   Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 36;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 348
AAD27116
ID   AAD27116 standard; RNA; 36 BP.
XX
AC   AAD27116;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, AA used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 1A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, AA used to direct RNA synthesis by RNA
CC   polymerase proteins of HCV, BVDV and polivirus. This sequence is used in
CC   the exemplification of the invention
XX
SQ   Sequence 36 BP; 34 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 36;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 349
```

```
AAD27121
ID   AAD27121 standard; RNA; 36 BP.
XX
AC   AAD27121;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, (AU)4 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 1C; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, (AU)4 used to direct RNA synthesis by
CC   RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used
CC   in the exemplification of the invention
XX
SQ   Sequence 36 BP; 30 A; 0 C; 2 G; 0 T; 4 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 36;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                |||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 350
ABK99274
ID   ABK99274 standard; RNA; 36 BP.
XX
AC   ABK99274;
XX
DT   21-OCT-2002  (first entry)
XX
DE   Hepatitis C virus (HCV) NS5B replicase RNA synthesis template #4.
XX
KW   Hepatitis C virus; HCV; NS5B replicase; ss; RNA polymerase.
XX
OS   Synthetic.
XX
PN   US2002064771-A1.
XX
PD   30-MAY-2002.
XX
PF   06-APR-2001; 2001US-00828034.
XX
PR   07-APR-2000; 2000US-0195852P.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (FERR/) FERRARI E.
XX
PI   Zhong W,  Hong Z,  Ferrari E;
XX
DR   WPI; 2002-582330/62.
XX
PT   Novel replicase complex comprising hepatitis C virus NS5B replicase, a 3
PT   nucleotide-long template to which a 2 nucleotide-long primer is annealed,
PT   and template and primer which do not form a stable duplex in the absence
PT   of HCV NS5B.
XX
PS   Example; Page 6; 17pp; English.
XX
CC   The invention relates to a replicase complex comprising a hepatitis C
CC   virus (HCV) NS5B replicase protein, a linear nucleic acid template and a
CC   complementary nucleic acid primer which is annealed to the 3' terminus of
CC   the template, where the template is at least three nucleotides and the
CC   primer is two or three nucleotides, and the template and primer do not
CC   form a stable duplex in solution in the absence of the HCV NS5B protein.
CC   The complex is useful for detecting HCV replicase activity and permits
CC   establishment of sensitive RNA-dependent RNA polymerase assays to screen
CC   and evaluate antiviral inhibitors and to improve the specificity and
CC   efficacy of the inhibitors. The complex is also useful in the development
CC   of a reliable system for determining kinetic and thermodynamic constants
CC   of HCV NS5B-catalysed nucleotide incorporation and investigation of
CC   mechanistic inhibitors for mis-incorporation or chain termination.
CC   Specifically, the short RNA template and primer pairs are useful in
CC   screening assays which are used for determining kinetic, thermodynamic
CC   and mechanistic properties of NS5B replication and ultimately in the
CC   development of inhibitors of NS5B. Newly identified inhibitors of
CC   replicase activity may be used for developing anti-HCV pharmaceuticals.
CC   Sequences ABK99271-ABK99296 represent HCV NS5B replicase RNA synthesis
CC   templates
XX
SQ   Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 36;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                |||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 351
AAD27118
ID   AAD27118 standard; RNA; 36 BP.
XX
AC   AAD27118;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, (AU)5 used to direct RNA synthesis by HCV RNA polymerase.
```

```
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 1A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, (AU)5 used to direct RNA synthesis by
CC   RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used
CC   in the exemplification of the invention
XX
SQ   Sequence 36 BP; 29 A; 0 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 36;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                ||||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 352
AAD27125
ID   AAD27125 standard; RNA; 37 BP.
XX
AC   AAD27125;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, (AU)2 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 2A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, (AU)2 used to direct RNA synthesis by
CC   RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used
CC   in the exemplification of the invention
XX
SQ   Sequence 37 BP; 33 A; 0 C; 2 G; 0 T; 2 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 37;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
                ||||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 353
AAD27124
ID   AAD27124 standard; RNA; 37 BP.
XX
AC   AAD27124;
XX
DT   09-APR-2002  (first entry)
XX
DE   RNA template, (AU)3 used to direct RNA synthesis by HCV RNA polymerase.
XX
KW   Hepatitis C virus; HCV replicase; non-structural protein 5B; NS5B;
KW   lead compound; RNA polymerase; ss.
XX
OS   Unidentified.
XX
PN   US6322966-B1.
XX
```

```
PD   27-NOV-2001.
XX
PF   11-MAY-1999;   99US-00309670.
XX
PR   11-MAY-1999;   99US-00309670.
XX
PA   (ZHON/) ZHONG W.
PA   (HONG/) HONG Z.
PA   (LAUJ/) LAU J Y N.
XX
PI   Zhong W,  Hong Z,  Lau JYN;
XX
DR   WPI; 2002-096587/13.
XX
PT   Assay system for hepatitis C virus replicase activity comprises RNA
PT   template with unstable, small stemloop capable of forming copy-back
PT   structure, viral non-structural protein 5B, nucleoside triphosphates,
PT   buffer.
XX
PS   Example 1; Fig 2A; 10pp; English.
XX
CC   The present invention relates to an assay system for hepatitis C virus
CC   (HCV) replicase activity. The assay system comprises an RNA template that
CC   has an unstable, small stemloop at the 3' end capable of forming a copy-
CC   back structure, a HCV non-structural protein 5B (NS5B), ATP, GTP, CTP,
CC   and UTP nucleoside triphosphates (NTPs), where one of the NTP is
CC   radiolabelled and an assay buffer that supports replication activity of
CC   NS5B. The invention also relates to the identification of optimal
CC   properties of an RNA template for copy-back self-priming RNA synthesis of
CC   HCV. This activity can be used to screen for anti-HCV replicase compounds
CC   or to characterise the biological relevance of lead compounds. The
CC   optimal RNA templates can be used for developing a system to characterise
CC   HCV NS5B polymerase mechanistically and kinetically and for designing
CC   small RNA molecules to co-crystallise with HCV NS5B polymerase. The assay
CC   system of the invention is useful for detecting HCV replicase activity.
CC   The nucleic acid synthesised by NS5B is detected by evaluating an
CC   autoradiograph of reaction products separated by gel electrophoresis. The
CC   present sequence is RNA template, (AU)3 used to direct RNA synthesis by
CC   RNA polymerase proteins of HCV, BVDV and polivirus. This sequence is used
CC   in the exemplification of the invention
XX
SQ   Sequence 37 BP; 32 A; 0 C; 2 G; 0 T; 3 U; 0 Other;

  Query Match             0.7%;  Score 20.2;  DB 1;  Length 37;
  Best Local Similarity   88.0%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       2780 GAATTGAAAAAAAAAAAAAAAAAAA 2804
              |||   ||||||||||||||||||||
Db          2 GAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 354
AAQ25565
ID   AAQ25565 standard; DNA; 20 BP.
XX
AC   AAQ25565;
XX
DT   25-MAR-2003  (revised)
DT   02-DEC-1992  (first entry)
XX
DE   Dye-coupled 3'-amino modified oligonucleotide.
XX
KW   DNA synthesis; RNA; antisense strands; detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    20
FT                    /*tag=  a
FT                    /note= "3-amino modified"
XX
PN   EP490281-A1.
XX
PD   17-JUN-1992.
XX
PF   06-DEC-1991;   91EP-00120935.
XX
PR   11-DEC-1990;   90DE-04039488.
XX
PA   (FARH ) HOECHST AG.
XX
PI   Engels J,  Herrlein M,  Konrad R,  Mag M;
XX
DR   WPI; 1992-201578/25.
XX
PT   New dye-coupled modified nucleosides, nucleotides and oligo:nucleotides -
PT   useful for synthesis of antisense DNA and RNA strands in presence of
PT   template, also for in=vivo and in=vitro detection of genetic material.
XX
PS   Example; Page 9; 17pp; German.
XX
CC   The sequence is an example of a dye coupled 3'-amino modified oligo-
CC   nucleotide, it can be used in the synthesis of DNA and RNA nucleosides,
CC   nucleotides and oligonucleotides and for the synthesis of opposite
CC   strands in the presence of a template strand and in fluorescence
CC   microscopic and macroscopic detection in vivo and in vitro of genetic
CC   material. It is labelled with a fluorescent dye. See also AAQ25566 and
CC   AAQ25567. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 355
AAQ33554
ID   AAQ33554 standard; DNA; 20 BP.
XX
AC   AAQ33554;
XX
DT   25-MAR-2003  (revised)
DT   02-FEB-1993  (first entry)
XX
DE   Microsatellite sequence from clone AGLA247.
XX
KW   PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW   genetic mapping; traits; amplification; ss.
XX
OS   Bos taurus.
XX
PN   WO9213102-A1.
XX
PD   06-AUG-1992.
XX
PF   15-JAN-1992;   92WO-US000340.
XX
PR   15-JAN-1991;   91US-00642342.
XX
PA   (GENM-) GENMARK.
XX
PI   Georges M,  Massey JM;
XX
DR   WPI; 1992-284684/34.
XX
PT   Polymorphic bovine DNA markers - used in genetic identification, gene
PT   mapping, and selective breeding.
XX
PS   Table 7; Page 150; 517pp; English.
XX
```

```
CC   The sequence is that of a bovine microsatellite sequence obtd. by
CC   screening a library of bovine MboI DNA fragments of between 250 and 500
CC   bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC   clones cross-hybridised. Assuming independent distribution of
CC   microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC   in the bovine genome is estimated at >100, 000. The sequence information
CC   for ca. 230 such bovine microsatellites is summarised in the
CC   specification and indexed herein (see below). The sequences upstream and
CC   downstream of the microsatellite sequence were used to generate the
CC   required PCR primers for in vitro amplification of the corresp.
CC   microsatellite (using the program OPTIPRIM). The microsatellites may be
CC   used to identify individuals, for parentage testing, and in the genetic
CC   mapping of economic trait loci, or genes involved the determinism of
CC   economically important traits esp. in cattle, to allow selective
CC   breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
CC   field.)
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 356
AAQ58578/c
ID   AAQ58578 standard; RNA; 20 BP.
XX
AC   AAQ58578;
XX
DT   25-MAR-2003  (revised)
DT   21-AUG-1994  (first entry)
XX
DE   Sequence of synthetic RNA oligo which is a target nucleotide for a novel
DE   receptor.
XX
KW   Novel receptor; nucleic acid; transport; oligo; ss.
XX
OS   Synthetic.
XX
PN   WO9404194-A1.
XX
PD   03-MAR-1994.
XX
PF   13-AUG-1993;   93WO-US007603.
XX
PR   14-AUG-1992;   92US-00930087.
XX
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI   Usman N,  Rebek J,  De Mendoza J;
XX
DR   WPI; 1994-082846/10.
XX
PT   Transport of nucleic acid derivs. across membranes - using new receptors
PT   which use salt bridging, aromatic stacking, hydrogen bonding and
PT   chelation.
XX
PS   Example; Table 1, page 38; 103pp; English.
XX
CC   The inventors claim a method of transporting a nucleic acid deriv. accros
CC   a membrane which comprises using a receptor that uses salt bridgin,
CC   aromatic stacking, H bonding and chelation to recognise the nucleic acid
CC   deriv. AAQ56305, AAQ58577-86 are nucleic acid derivs used in the
CC   examples. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 357
AAQ94205
ID   AAQ94205 standard; DNA; 20 BP.
XX
AC   AAQ94205;
XX
DT   25-MAR-2003  (revised)
DT   24-AUG-1995  (first entry)
XX
DE   Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
XX
KW   Oligonucleotide ligand; steroid hormone; hapten; immobilisation;
KW   immunodetection; estradiol; alpha-anomer; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .21
FT                   /*tag=  b
FT                   /note= "the glycosidic bonds between nucleotides are all
FT                   in the alpha-anomer form"
FT   modified_base   20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "carries a group derived ffrom aminopropanediol"
XX
PN   WO9429723-A1.
XX
PD   22-DEC-1994.
XX
PF   10-JUN-1994;   94WO-FR000689.
XX
PR   11-JUN-1993;   93FR-00007093.
XX
PA   (CROS/) CROS P.
PA   (KURF/) KURFURST R.
PA   (BATT/) BATTAIL N.
PA   (PIGA/) PIGA N.
XX
PI   Cros P,  Kurfurst R,  Battail N,  Piga N;
XX
DR   WPI; 1995-036665/05.
XX
PT   Assay device for hapten or its specific antibodies - comprises support
PT   having competitive reagent immobilised via nucleic acid ligand to improve
PT   orientation and accessibility.
XX
PS   Example 1; Page 10; 39pp; French.
XX
CC   Oligonucleotides (AAQ94201-Q94205) were synthesised for use as ligands.
CC   The ligands are covalently linked to a hapten (esp. a steroid hormone) to
CC   form a conjugate which is then immobilised on a solid support for
CC   interaction with antibodies against the hapten. Nucleic acid ligands are
CC   less likely to be recognised by the antibodies than are peptide ligands
CC   and nucleic acids are also less likely to undergo intramolecular
CC   organisation which interferes with accessibility of the hapten to the
CC   antibodies. For immunodiagnosis of oestradiol, the active hapten
CC   oestradiol-6-carboxymethoxime-N- hydroxysuccinimide ester was used.
CC   (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 358
AAQ75596/c
ID   AAQ75596 standard; DNA; 20 BP.
XX
AC   AAQ75596;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||||
Db         20 TTGAAAAAAAAAAAAAAAAA 1


RESULT 359
AAQ75582
ID   AAQ75582 standard; DNA; 20 BP.
XX
AC   AAQ75582;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 5; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAAC 20


RESULT 360
AAQ90405
ID   AAQ90405 standard; DNA; 20 BP.
XX
AC   AAQ90405;
XX
DT   08-JAN-1996  (first entry)
XX
DE   T2 (synthetic DNA probe with 5' amino terminal #4).
XX
KW   T2; HLA; dQa; self-addressable electronic device; SAED; hybridisation;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "3' aminolink2 Thymine; allows binding to any
FT                   amine"
XX
PN   WO9512808-A1.
XX
PD   11-MAY-1995.
XX
PF   26-OCT-1994;   94WO-US012270.
XX
PR   01-NOV-1993;   93US-00146504.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Heller MJ,  Tu E;
XX
DR   WPI; 1995-185870/24.
XX
PT   New self-addressable electronic devices - used for multi-step and
```

```
PT   multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT   and bio:polymer synthesis.
XX
PS   Example 1; Page 41; 86pp; English.
XX
CC   The sequences represented by, AAQ90402-15 are synthetic DNA probes
CC   containing 5' amino termini. The sequences shown in AAQ90390-401 are
CC   synthetic DNA probes with 3' ribonucleoside termini. These sequences were
CC   specific for the polymorphisms of HLA gene dQa. The sequences were used
CC   in the device of the invention. This is a self-addressable electronic
CC   device (SAED) that can be used to carry out multi-step and multiplex
CC   reactions, such as nucleic acid hybridisations. The advantages of this
CC   method are that these reactions can be carried out with complete and
CC   precise electronic control, and that the rate, specificity and
CC   sensitivity of these reactions are greatly improved at micro-locations
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 361
AAV07752
ID   AAV07752 standard; DNA; 20 BP.
XX
AC   AAV07752;
XX
DT   07-DEC-1998  (first entry)
XX
DE   Phosphorothioate oligonucleotide.
XX
KW   phosphorothioate; sulphurisation; heterocycle; automated synthesis;
KW   antisense; EDITH; Beaucage reagent; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .20
FT                   /*tag=  a
FT                   /note= "phosphorothioate internucleotide linkages"
XX
PN   WO9741130-A2.
XX
PD   06-NOV-1997.
XX
PF   29-APR-1997;   97WO-US007118.
XX
PR   30-APR-1996;   96US-00641920.
XX
PA   (MINU ) UNIV MINNESOTA.
PA   (LOUU ) UNIV LOUISIANA STATE & AGRIC.
XX
PI   Barany G,  Musier-Forsyth K,  Xu Q,  Chen L,  Hammer RP;
XX
DR   WPI; 1997-549671/50.
XX
PT   Sulphurisation of phosphorus-containing compounds, e.g.
PT   oligo:nucleotide(s) - by contacting the compound with a di:sulphide-
PT   containing five-membered heterocycle.
XX
PS   Example 7; Page 30; 51pp; English.
XX
CC   The present invention provides a method for sulphurising phosphorus-
CC   containing compounds. It comprises contacting the phosphorus-containing
CC   compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-
CC   substituted-1,2,4-dithiazolin-5-one compound. The method is especially
CC   useful for incorporation of phosphorothioate linkages into biologically
CC   important molecules such as DNA, RNA and phosphopeptides. Molecules
CC   containing such linkages are useful e.g. as antisense compounds for
CC   inhibiting gene expression, as reagents for studying DNA-protein or RNA-
CC   protein interactions, or as catalytic RNA. The present sequence
CC   represents an oligonucleotide with phosphorothioate linkages prepared by
CC   the method of the invention
XX
SQ   Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   5.0%;  Pred. No. 4.1e+02;
  Matches    1;  Conservative   19;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTA 2187
              ::::::::::::::::::|
Db          1 UUUUUUUUUUUUUUUUUUA 20


RESULT 362
AAT63649
ID   AAT63649 standard; DNA; 20 BP.
XX
AC   AAT63649;
XX
DT   06-JUN-1997  (first entry)
XX
DE   Anti-HTLV antisense reference oligonucleotide HT.
XX
KW   antisense; complementary; tax gene; inhibit; HTLV-1;
KW   human T-cell lymphotropic virus type 1; viral antigen expression; ss.
XX
OS   Synthetic.
XX
PN   JP09052898-A.
XX
PD   25-FEB-1997.
XX
PF   09-AUG-1995;   95JP-00224606.
XX
PR   09-AUG-1995;   95JP-00224606.
XX
PA   (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
XX
DR   WPI; 1997-197252/18.
XX
PT   Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region of
PT   tax gene from human T-cell lymphotropic virus type 1 and inhibits viral
PT   antigen expression.
XX
PS   Example 1; Page 8; 10pp; Japanese.
XX
CC   Oligonucleotides having a partial sequence consisting of at least 15
CC   bases of AAT63641 (an antisense oligo complementary to a region of the
CC   tax gene which can inhibit human T-cell lymphotropic virus type 1 (HTLV-
CC   1) viral antigen expression) are claimed. In an example, six antisense
CC   oligos were designed, T1-T6 (AAT63650-55) and were compared to six oligos
CC   derived from other regions of HTLV-1, i.e. SJ1 (splice junction), P1
CC   (p21), R1 (rex), RR1 (rex response element), E1 (env) and G1 (gag), four
CC   reference oligonucleotides TIS (tax-sense), HC (dC20), HT (dT20)
CC   (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen
CC   expression inhibiting test. Oligonucleotide T1 gave the best results
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20
```

```
RESULT 363
AAV34591/c
ID   AAV34591 standard; DNA; 20 BP.
XX
AC   AAV34591;
XX
DT   25-AUG-1998  (first entry)
XX
DE   M. vaccae antigenic sequence hybridising oligo AD12.
XX
KW   Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW   M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW   mycobacteria infection; vaccine; cancer; ss.
XX
OS   Synthetic.
OS   Mycobacterium vaccae.
XX
PN   WO9808542-A2.
XX
PD   05-MAR-1998.
XX
PF   28-AUG-1997;   97WO-NZ000105.
XX
PR   29-AUG-1996;   96US-00705347.
PR   12-JUN-1997;   97US-00873970.
XX
PA   (GENE-) GENESIS RES & DEV CORP.
XX
PI   Tan P,  Hiyama J,  Visser E,  Skinner MA,  Scott LM,  Prestidge RL;
XX
DR   WPI; 1998-216926/19.
XX
PT   Mycobacterium vaccae polypeptides - used to develop products for use in
PT   detection, therapy and prevention of mycobacteria infections or as immune
PT   response enhancers.
XX
PS   Example 8; Page 99; 153pp; English.
XX
CC   This oligonucleotide is used in the DNA cloning strategies of the
CC   Mycobacterium vaccae antigens. The invention provides M. vaccae
CC   polypeptides that comprise an immunogenic portion of a soluble M. vaccae
CC   antigen, or a variant, where the antigen induces an immune response in
CC   patients previously exposed to a mycobacterium. Such M. vaccae
CC   polypeptides can be used in methods for enhancing non-specific immune
CC   response. The methods and products can be used for the detection,
CC   treatment and prevention of infectious diseases caused by mycobacteria
CC   such as M. vaccae, M. avium or M. tuberculosis. The products also have
CC   the ability to induce cell proliferation and cytokine production (e.g.
CC   interferon-gamma and interleukin-12 production) in T cells, NK cells, B
CC   cells, or macrophages. They can be used for enhancing immune responses
CC   for use in vaccines or immunotherapy of infectious diseases and cancers
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 364
AAT86606
ID   AAT86606 standard; DNA; 20 BP.
XX
AC   AAT86606;
XX
DT   04-JUN-1998  (first entry)
XX
DE   Oligonucleotide separated by capillary affinity gel electrophoresis.
XX
KW   Capillary afinity gel electrophoresis; separation; polymer-gel;
KW   polyacrylamide; ss.
XX
OS   Synthetic.
XX
PN   WO9745721-A1.
XX
PD   04-DEC-1997.
XX
PF   23-MAY-1997;   97WO-EP002647.
XX
PR   24-MAY-1996;   96CH-00001320.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Muscate A,  Paulus A,  Natt F;
XX
DR   WPI; 1998-041763/04.
XX
PT   Separation of electrically charged target molecules - by capillary
PT   affinity gel electrophoresis using polymer-gel to which receptors for
PT   target molecules are bound.
XX
PS   Example D3; Page 25; 41pp; English.
XX
CC   A mixture of oligonucleotides (AAT86604-7) were separated by a new
CC   process using capillary affinity gel electrophoresis. The invention
CC   relates to selective separation of electrically charged target molecules
CC   in an analytical mixture. It comprises capillary affinity gel
CC   electrophoresis using a capillary tube which is at least partly filled
CC   with a polymer gel. Receptors for target molecules are covalently bound
CC   to the polymer. An electric field of at least 50 volts/cm is applied. The
CC   capillary tube is charged with the analytical mixture. In a first
CC   separation stage, the target molecules in the mixture are bound to the
CC   receptors and the remaining components are eluted, optionally whilst
CC   splitting open. In a second stage, the elution conditions are changed,
CC   optionally in stages, so that the affinity of the target molecules for
CC   the receptor is eliminated and the target molecules are eluted and
CC   detected, optionally whilst splitting open. The process is useful for
CC   selective separation and/or determination of charged organic compounds,
CC   such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
CC   for isolation of specific proteins and DNA molecules, purification of
CC   antibodies, analysis of antisense compounds or screening for enzyme
CC   inhibitors. The process achieves higher resolution and selectivity than
CC   prior art processes, especially in the case of complex biological
CC   analytical mixtures. It has high sensitivity, even with small amounts of
CC   samples. The derivatised polymers may be synthesised specifically using
CC   standard methods
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 365
AAX27533
ID   AAX27533 standard; RNA; 20 BP.
XX
AC   AAX27533;
XX
DT   27-MAY-1999  (first entry)
XX
DE   Synthetic RNA sequence produced by the method of the invention.
XX
KW   Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;
KW   cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.
XX
```

OS Synthetic.
XX
PN WO9909044-A1.
XX
PD 25-FEB-1999.
XX
PF 17-AUG-1998; 98WO-EP005215.
XX
PR 18-AUG-1997; 97CH-00001931.
XX
PA (PITS/) PITSCH S.
PA (WEIS/) WEISS P A.
PA (JENN/) JENNY L.
XX
PI Pitsch S, Weiss PA, Jenny L;
XX
DR WPI; 1999-180963/15.
XX
PT 2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have
PT high purity, use in machine synthesis of ribonucleic acids, enable longer
PT oligonucleotide chain construction, and larger amounts.
XX
PS Example 6; Page 25; 38pp; English.
XX
CC The invention relates to silyloxymethyl protected D- or L-ribonucleosides
CC and their phosphonates (I), and silyloxymethyl halides (II). (I) are
CC intermediates for synthesis of RNA-oligonucleotides with predetermined
CC nucleotide sequence, particularly by machine synthesis. The groups
CC specified above, apart from those on silyl, are those particularly for
CC the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide
CC products in diagnosis, therapy, and as research tools, are well known,
CC and are not dealt with in detail. (II) is an intermediate for (I). The
CC silyloxymethyl halide reagent is easy to prepare, and yields are high.
CC Introduction of the silyloxymethyl group into the ribonucleoside is
CC simple and rapid, and the acetal bond formed does not migrate,
CC eliminating particularly the prior art problem of 2' to 3' isomerisation.
CC The methylenedioxy group spacer between the silyl group and nucleoside
CC ring results in less steric hindrance than bulky direct silyloxy
CC linkages, enabling first, a range of choices for the silyl substituents,
CC to provide, e.g., acid or base stability; and second, higher yields in
CC coupling. Purer products are therefore obtained than in prior art,
CC enabling larger quantities and longer chains of oligoribonucleotides to
CC be synthesised successfully, and in shorter times
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 20 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 0.0%; Pred. No. 4.1e+02;
Matches 0; Conservative 20; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
:::::::::::::::::::
Db 1 UUUUUUUUUUUUUUUUUUUU 20

RESULT 366
AAZ11326/c
ID AAZ11326 standard; DNA; 20 BP.
XX
AC AAZ11326;
XX
DT 25-OCT-1999 (first entry)
XX
DE Mycobacterial 16S rRNA specific oligo AD12.
XX
KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; PCR primer; ss.
XX
OS Synthetic.

OS Mycobacterium vaccae.
XX
PN WO9932634-A2.
XX
PD 01-JUL-1999.
XX
PF 23-DEC-1998; 98WO-NZ000189.
XX
PR 23-DEC-1997; 97US-00996624.
PR 23-DEC-1997; 97US-00997080.
PR 23-DEC-1997; 97US-00997362.
PR 11-JUN-1998; 98US-00095855.
PR 17-SEP-1998; 98US-00156181.
PR 04-DEC-1998; 98US-00205426.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX
DR WPI; 1999-430163/36.
XX
PT Enhancing immune response to an antigen.
XX
PS Example 15; Page 177; 243pp; English.
XX
CC The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC to enhance the expression of co-stimulatory molecules on dendritic cells
CC and monocytes, and to enhance dendritic cell maturation and function. The
CC proteins can be expressed by standard recombinant methodology.
CC Pharmaceutical compositions comprising the proteins or nucleic acid
CC sequences encoding the proteins can be used for the treatment,
CC prevention, and detection of disorders including infectious diseases,
CC immune disorders and cancer. In particular, the compounds and methods are
CC used for treatment of diseases of the respiratory system, such as
CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
CC sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 367
AAA40449/c
ID AAA40449 standard; DNA; 20 BP.
XX
AC AAA40449;
XX
DT 13-NOV-2000 (first entry)
XX
DE Electochemical detection method sample DNA target.
XX
KW Electrochemical detection; glucose; cholesterol; urea nitrogen;
KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
KW plasma; serum; urine; lymph diagnosis; ss.
XX
OS Synthetic.
XX
PN EP1018646-A2.
XX
PD 12-JUL-2000.
XX

PF 07-JAN-2000; 2000EP-00100126.
XX
PR 06-JAN-1999; 99JP-00001111.
PR 24-MAY-1999; 99JP-00143599.
XX
PA (FUJF) FUJI PHOTO FILM CO LTD.
XX
PI Ogawa M, Takenaka S, Takagi M;
XX
DR WPI; 2000-444372/39.
XX
PT Quantitative analysis of a biochemical compound such as glucose, in body
PT a body fluid such as blood, comprising detecting enhanced electron
PT transfer between an oxidase and a DNA-immobilized electrode, useful for
PT diagnosis of disease.
XX
PS Example 1; Page 8; 14pp; English.
XX
CC This invention describes a novel method for quantitatively analysing a
CC biochemical compound (I) which comprises contacting (I) with double
CC stranded DNA fixed to the surface of an electrode at their terminals in
CC which electrochemically active threading intercalators are intercalated,
CC in an aqueous medium under application of electric potential to the
CC electrode in the presence of an oxidase which oxidizes the biochemical
CC compound and becomes reduced, and detecting electric current flowing
CC between the electrode and a second electrode in the aqueous medium. The
CC method is useful for detection of biochemical compounds such as glucose,
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
CC for diagnosis of various diseases. The method allows detection of
CC biochemical compounds quickly and easily with a high sensitivity using a
CC simple apparatus. This sequence represents DNA fragment used as a target
CC sample in the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 368
AAA40448
ID AAA40448 standard; DNA; 20 BP.
XX
AC AAA40448;
XX
DT 13-NOV-2000 (first entry)
XX
DE Electochemical detection method fixed probe DNA.
XX
KW Electrochemical detection; glucose; cholesterol; urea nitrogen;
KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
KW plasma; serum; urine; lymph diagnosis; probe; ss.
XX
OS Synthetic.
XX
PN EP1018646-A2.
XX
PD 12-JUL-2000.
XX
PF 07-JAN-2000; 2000EP-00100126.
XX
PR 06-JAN-1999; 99JP-00001111.
PR 24-MAY-1999; 99JP-00143599.
XX
PA (FUJF) FUJI PHOTO FILM CO LTD.
XX
PI Ogawa M, Takenaka S, Takagi M;
XX
DR WPI; 2000-444372/39.
XX
PT Quantitative analysis of a biochemical compound such as glucose, in body
PT a body fluid such as blood, comprising detecting enhanced electron
PT transfer between an oxidase and a DNA-immobilized electrode, useful for
PT diagnosis of disease.
XX
PS Example 1; Page 7; 14pp; English.
XX
CC This invention describes a novel method for quantitatively analysing a
CC biochemical compound (I) which comprises contacting (I) with double
CC stranded DNA fixed to the surface of an electrode at their terminals in
CC which electrochemically active threading intercalators are intercalated,
CC in an aqueous medium under application of electric potential to the
CC electrode in the presence of an oxidase which oxidizes the biochemical
CC compound and becomes reduced, and detecting electric current flowing
CC between the electrode and a second electrode in the aqueous medium. The
CC method is useful for detection of biochemical compounds such as glucose,
CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
CC for diagnosis of various diseases. The method allows detection of
CC biochemical compounds quickly and easily with a high sensitivity using a
CC simple apparatus. This sequence represents DNA fragment used as fixed
CC probe DNA in the method of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 369
AAZ91117
ID AAZ91117 standard; DNA; 20 BP.
XX
AC AAZ91117;
XX
DT 06-JUN-2000 (first entry)
XX
DE Oligonucleotide #5 for conjugation to abietane derivative.
XX
KW Abietane derivative; labelling; diagnostic test; biotin substitute; ss.
XX
OS Synthetic.
XX
PN FR2781802-A1.
XX
PD 04-FEB-2000.
XX
PF 31-JUL-1998; 98FR-00010084.
XX
PR 31-JUL-1998; 98FR-00010084.
XX
PA (INMR) BIO MERIEUX.
XX
PI Charles MH, Piga N, Battail PN, Veron L, Delair T, Mandrand B;
XX
DR WPI; 2000-239603/21.
XX
PT Saturated and unsaturated derivatives of abietic acid and their
PT conjugated derivatives with natural and synthetic polymers, having use in
PT diagnostics, chemical reactions and analysis.
XX
PS Example 5; Page 20; 39pp; French.
XX
CC The invention relates to novel saturated and unsaturated abietane
CC derivatives. The new compounds may be used directly or indirectly in the

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CC   development of new diagnostic tests, to follow infections, especially
CC   viral infections, to follow and/or measure chemical products, especially
CC   potential pollutants. In diagnostic tests they may be used as markers, or
CC   to form a universal solid phase after immobilization on a solid support,
CC   to produce monoclonal antibodies or polyclonal antibodies having
CC   diagnostic uses. The oligonucleotides AAZ91113-Z91117 represent examples
CC   of sequences that can be labeled with the new abietane derivatives. The
CC   new derivatives may be used to substitute for biotin in diagnostic tests,
CC   but because they are not found naturally in humans the risk of potential
CC   interactions with biological molecules is eliminated
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 370
AAA50193
ID   AAA50193 standard; DNA; 20 BP.
XX
AC   AAA50193;
XX
DT   07-NOV-2000  (first entry)
XX
DE   2'-Methoxyethoxy-modified oligonucleotide.
XX
KW   Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .19
FT                   /*tag=  a
FT                   /note= "2'-methoxyethoxy modified thymidine"
XX
PN   WO200047593-A1.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-US003543.
XX
PR   12-FEB-1999;   99US-00250075.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Manoharan M,  Maier MA;
XX
DR   WPI; 2000-558188/51.
XX
PT   Preparation of mixed backbone oligomeric compounds useful as e.g. primers
PT   for diagnostic tests, involves oxidation of H-phosphonate internucleoside
PT   linkages to phosphodiester internucleoside linkages.
XX
PS   Example 12; Page 34; 49pp; English.
XX
CC   The present sequence is that of a phosphodiester oligonucleotide
CC   containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group on its 5'
CC   ribosyl sugar moiety. It is an example of an oligomeric compound produced
CC   according to the methods of the invention. The invention provides
CC   compounds and methods for the preparation of mixed backbone oligomeric,
CC   or chimeric, compounds having phosphodiester internucleoside linkages in
CC   addition to phosphorothioate and/or phosphoramidate internucleoside
CC   linkages. The methods also include incorporation of boranophosphate
CC   internucleoside linkages. The methods utilise H-phosphonate intermediates
CC   that are coupled together forming contiguous regions of 1 or more H-
CC   phosphonate internucleoside linkages. Each contiguous region is
CC   subsequently oxidized to phosphodiester, phosphorothioate,
CC   phosphoroamidate or boranophosphate internucleoside linkages prior to
CC   further elongation. Mixed backbone oligomeric compounds are prepared in
CC   this manner by oxidizing adjacent regions with different reagents.
CC   Oligomeric compounds of the invention are prepared using novel oxidation
CC   steps that oxidize a region of 1 or more H-phosphonate internucleoside
CC   linkages without degrading existing linkages that have been previously
CC   oxidized. The oligonucleotides obtained are useful as primers in PCR,
CC   probes, linkers, gene fragments and for other diagnostic tests on e.g.
CC   biological tissue, fluid, cells etc., as research reagents, and as
CC   antiviral agents
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 371
AAC87238
ID   AAC87238 standard; DNA; 20 BP.
XX
AC   AAC87238;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.
XX
KW   Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW   immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW   hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW   antagonist; mimic; inhibitor; drug screening;
KW   cellular target identification; oligonucleotide optimisation;
KW   immunotherapy; ss.
XX
OS   Synthetic.
XX
PN   WO200067023-A1.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011697.
XX
PR   29-APR-1999;   99US-0131830P.
PR   03-MAR-2000; 2000US-0186845P.
XX
PA   (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Noll BO,  Schetter C,  Krieg AM;
XX
DR   WPI; 2001-016002/02.
XX
PT   Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT   functional modifiers, immunostimulatory DNA binding competitors and to
PT   optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
PS   Example 1; Page 45; 95pp; English.
XX
CC   The invention relates to the use of an immunostimulatory single-stranded
CC   DNA-binding protein in screening assays to identify compounds which bind
CC   to it and thereby act as functional modifiers of immunostimulatory
CC   oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC   consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC   DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC   Immunostimulatory DNA-binding proteins can also be used in screening
CC   methods to identify immunostimulatory DNA binding competitors, and to
CC   optimize an immunostimulatory ODN for immune stimulation. Isolated
CC   complexes of an immunostimulatory DNA-binding protein bound to an
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CC   immunostimulatory ODN can additionally be used to screen a panel of
CC   candidate target molecules to identify the cellular target molecules of
CC   the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC   used in the methods of the invention are the RNA-binding proteins
CC   nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC   methods are useful for identifying a compound that inhibits interaction
CC   between immunostimulatory DNA and an immunostimulatory DNA-binding
CC   protein and for identifying agonists useful in immunotherapy. The complex
CC   is useful in screening for immunostimulatory DNA cellular target
CC   molecules. The candidate immunostimulatory ODN competitors allow the
CC   investigation of structure/activity relationships of immunostimulatory
CC   DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC   represents an oligonucleotide used in an exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 372
AAC87230
ID   AAC87230 standard; DNA; 20 BP.
XX
AC   AAC87230;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.
XX
KW   Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW   immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW   hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW   antagonist; mimic; inhibitor; drug screening;
KW   cellular target identification; oligonucleotide optimisation;
KW   immunotherapy; ss.
XX
OS   Synthetic.
XX
PN   WO200067023-A1.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011697.
XX
PR   29-APR-1999;   99US-0131830P.
PR   03-MAR-2000; 2000US-0186845P.
XX
PA   (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Noll BO,  Schetter C,  Krieg AM;
XX
DR   WPI; 2001-016002/02.
XX
PT   Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT   functional modifiers, immunostimulatory DNA binding competitors and to
PT   optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
PS   Example 1; Page 45; 95pp; English.
XX
CC   The invention relates to the use of an immunostimulatory single-stranded
CC   DNA-binding protein in screening assays to identify compounds which bind
CC   to it and thereby act as functional modifiers of immunostimulatory
CC   oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC   consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC   DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC   Immunostimulatory DNA-binding proteins can also be used in screening
CC   methods to identify immunostimulatory DNA binding competitors, and to
CC   optimize an immunostimulatory ODN for immune stimulation. Isolated
CC   complexes of an immunostimulatory DNA-binding protein bound to an
CC   immunostimulatory ODN can additionally be used to screen a panel of
CC   candidate target molecules to identify the cellular target molecules of
CC   the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC   used in the methods of the invention are the RNA-binding proteins
CC   nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC   methods are useful for identifying a compound that inhibits interaction
CC   between immunostimulatory DNA and an immunostimulatory DNA-binding
CC   protein and for identifying agonists useful in immunotherapy. The complex
CC   is useful in screening for immunostimulatory DNA cellular target
CC   molecules. The candidate immunostimulatory ODN competitors allow the
CC   investigation of structure/activity relationships of immunostimulatory
CC   DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC   represents an oligonucleotide used in an exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 373
AAC87241
ID   AAC87241 standard; DNA; 20 BP.
XX
AC   AAC87241;
XX
DT   09-MAR-2001  (first entry)
XX
DE   Poly T oligonucleotide, SEQ ID NO:20.
XX
KW   Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW   immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW   hnRNP A1; lupus La protein; functional modifier identification; agonist;
KW   antagonist; mimic; inhibitor; drug screening;
KW   cellular target identification; oligonucleotide optimisation;
KW   immunotherapy; ss.
XX
OS   Synthetic.
XX
PN   WO200067023-A1.
XX
PD   09-NOV-2000.
XX
PF   28-APR-2000; 2000WO-US011697.
XX
PR   29-APR-1999;   99US-0131830P.
PR   03-MAR-2000; 2000US-0186845P.
XX
PA   (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Noll BO,  Schetter C,  Krieg AM;
XX
DR   WPI; 2001-016002/02.
XX
PT   Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT   functional modifiers, immunostimulatory DNA binding competitors and to
PT   optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
PS   Example 1; Page 45; 95pp; English.
XX
CC   The invention relates to the use of an immunostimulatory single-stranded
CC   DNA-binding protein in screening assays to identify compounds which bind
CC   to it and thereby act as functional modifiers of immunostimulatory
CC   oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
```

CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC Immunostimulatory DNA-binding proteins can also be used in screening
CC methods to identify immunostimulatory DNA binding competitors, and to
CC optimize an immunostimulatory ODN for immune stimulation. Isolated
CC complexes of an immunostimulatory DNA-binding protein bound to an
CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory DNA cellular target
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 374
AAS10402
ID AAS10402 standard; DNA; 20 BP.
XX
AC AAS10402;
XX
DT 24-OCT-2001 (first entry)
XX
DE DNA template for 3' end labeling of an RNA molecule, #14.
XX
KW 3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss.
XX
OS Synthetic.
XX
PN US6238865-B1.
XX
PD 29-MAY-2001.
XX
PF 16-OCT-1998; 98US-00173936.
XX
PR 17-OCT-1997; 97US-0063757P.
XX
PA (CHEN/) CHEN G.
PA (HUAN/) HUANG Z.
PA (SZOS/) SZOSTAK J W.
XX
PI Huang Z, Szostak JW;
XX
DR WPI; 2001-366470/38.
XX
PT Modifying a 3' terminus of a pre-selected DNA sequence, useful for
PT labeling and modifying 3'-termini of other nucleic acids, comprises using
PT a synthetic nucleotide template with a defined overhang nucleotide.
XX
PS Example 5; Col 13; 22pp; English.
XX
CC The sequence represents a synthetic DNA template molecule used to
CC demonstrate the method of the invention. The invention relates to a
CC method of modifying (e.g. 3' end labelling with 32P dATP) the 3' terminus
CC of an RNA molecule by providing a DNA oligonucleotide, complimentary to
CC the 3' end of the RNA molecule, with an overhang at the 5' end which
CC allows incorporation of the labeling nucleotide into the RNA molecule.
CC The method, based on the synthesis of Okazaki fragments, is useful for
CC labeling and modifying the 3'-termini of other nucleic acids such as DNA
CC fragments. The method is a simple and efficient way of labeling or
CC modifying RNA 3'-termini using DNA polymerase and a synthetic template
CC with defined overhang nucleotides
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 375
AAD16997
ID AAD16997 standard; DNA; 20 BP.
XX
AC AAD16997;
XX
DT 29-NOV-2001 (first entry)
XX
DE Capture probe CP5'.
XX
KW Scaffold protein; antibody mimic; fibronectin type III domain;
KW randomised loop; randomised beta-sheet; diagnostic purpose;
KW protein designing; probe; tenth module of human Fn3; 10Fn3;
KW fibronectin module of type III; Fn3; ss.
XX
OS Unidentified.
XX
PN WO200164942-A1.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006414.
XX
PR 29-FEB-2000; 2000US-00515260.
XX
PA (PHYL-) PHYLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX
DR WPI; 2001-557782/62.
XX
PT Fibronectin scaffold protein array for obtaining a protein/compound which
PT binds to a compound/protein, comprises a fibronectin type III domain
PT having a randomized loop, a randomized beta-sheet or their combination.
XX
PS Disclosure; Page 41; 67pp; English.
XX
CC The present invention relates to an array of proteins (antibody mimics)
CC comprising a fibronectin type III domain having a randomised loop, a
CC randomised beta-sheet, or their combination, and has the capacity to bind
CC to a compound that is not bound by a corresponding naturally- occurring
CC fibronectin, immobilised onto a solid support. The antibody mimics is
CC useful for detecting a compound preferably a protein, in a biological
CC sample. It is also useful to detect one or more different analytes
CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
CC is also useful for the purpose of designing proteins capable of binding
CC to virtually any compound of interest. The present sequence is a capture
CC probe used to self-assemble and anchor the tenth module of human
CC fibronectin module of type III (Fn3) (10Fn3) which is used in an
CC exemplification of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20
```

RESULT 376
AAF60896/c
ID AAF60896 standard; DNA; 20 BP.
XX
AC AAF60896;
XX
DT 15-MAY-2001 (first entry)
XX
DE Conjugate forming oligonucleotide ON5 SEQ ID 5.
XX
KW Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
KW antipsoriatic; antiasthmatic; gene therapy; tumor cell; antisense;
KW tumor therapy; drug; phosphodiester linkage; ss.
XX
OS Unidentified.
XX
PN DE19935302-A1.
XX
PD 08-FEB-2001.
XX
PF 28-JUL-1999; 99DE-01035302.
XX
PR 28-JUL-1999; 99DE-01035302.
XX
PA (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;
XX
DR WPI; 2001-203679/21.
XX
PT New substituted aryl conjugates of parent molecules, especially
PT oligonucleotides, having improved transmembrane and intracellular
PT transport properties, useful as medicaments or diagnostic agents.
XX
PS Disclosure; Page 9; 28pp; German.
XX
CC This invention describes a novel conjugate (I) which consists of (A) a
CC molecule to be transported and (B) at least one aryl residue of formula -
CC Ar-(X-C(Y)-R_1)_n (II). Ar = group containing at least one aromatic ring;
CC X = O or N (sic); Y = O, S or NH-R_2 (sic); R_1 = optionally substituted
CC 1-23C alkyl (optionally containing double and/or triple bonds); R_2 =
CC optionally substituted 1-18C alkyl (optionally containing double and/or
CC triple bonds); n = integer of 1 or more. (A) is bonded to (B) directly or
CC via a chemical group, provided that the chemical group is other than CH_2
CC -S if the bond is via a phosphodiester linkage of (A). The invention also
CC describes (i) the preparation of a conjugate (I') of (A') a molecule to
CC be transported and (B') at least one aryl residue (not restricted to
CC (II)), by preparing (A') containing a reactive function at the position
CC at which (B') is to be bonded, preparing (B') and reacting (A') and (B');
CC and (ii) the use of aryl groups (II) (optionally bonded via a chemical
CC group) for transporting (A) across biological membranes. The products of
CC the invention have cytostatic, virucide, vasotropic, dermatological,
CC antipsoriatic and antiasthmatic activity and can be used for gene
CC therapy. Conjugation of (A) with (B) is useful for transporting (A)
CC across biological membranes or into eukaryotic or prokaryotic cells
CC (specifically bacterial, yeast or mammalian cells, including human cells,
CC particularly tumor cells). Medicaments, diagnostic agents and test kits
CC containing (I) are also claimed. Typically (I) are antisense
CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
CC treating viral infections or diseases associated with integrins or cell-
CC cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma); or
CC labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
CC hybridization. Conjugation with (B) markedly improves the cellular uptake
CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
CC in which case the conjugates (I) are fluorescently labeled, allowing
CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
CC is superior to that obtained using other conjugated groups related to
CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
CC the scope of (B)) have superior uptake to corresponding fluorescein
CC conjugates
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1
```

RESULT 377
AAS63428/c
ID AAS63428 standard; DNA; 20 BP.
XX
AC AAS63428;
XX
DT 29-JAN-2002 (first entry)
XX
DE Oligonucleotide-nanoparticle probe #52.
XX
KW Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
KW ss.
XX
OS Synthetic.
XX
PN WO200173123-A2.
XX
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001WO-US010071.
XX
PR 28-MAR-2000; 2000US-0192699P.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
PR 26-JUN-2000; 2000US-0213906P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Park S, Li Z;
XX
DR WPI; 2001-656926/75.
XX
PT Detecting and separating nucleic acid, useful e.g. for diagnosis,
PT comprises reaction with nanoparticles that carry oligonucleotides
PT complementary to parts of the target.
XX
PS Example 18; Page 158; 404pp; English.
XX
CC The invention relates to a method for detection of nucleic acid (I)
CC having at least 2 portions, comprising treatment with nanoparticles that
CC carry oligonucleotides complementary to at least 2 parts of (I), where
CC detectable change caused by hybridisation of the oligonucleotide to (I)
CC is observed. The method is used to detect (or to separate) specific (I),
CC e.g. for diagnosing a wide variety of diseases, sequencing, in forensic
CC analysis etc., and generally to detect analytes other than (I). The
CC oligonucleotide-derivatised nanoparticles are also useful for preparing
CC nanostructures useful, for example, as biochips, biofilters, mechanical
CC devices, separation membranes, chemical sensors, in computers, and for
CC drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be
CC produced, allowing their direct use (as probes) in polymerase chain
CC reaction, i.e. they survive multiple heating/cooling cycles so do not
CC need to be added after amplification. (I) are detected by simple colour

```
CC   change, without the need for special equipment, making possible rapid
CC   field testing for e.g. pathogens. AAS63374-AAS63448 represent
CC   oligonucleotide-nanoparticle probes, and related sequences, used in the
CC   method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 378
AAF28481/c
ID   AAF28481 standard; DNA; 20 BP.
XX
AC   AAF28481;
XX
DT   03-APR-2001  (first entry)
XX
DE   Random oligonucleotide, SEQ ID NO: 53.
XX
KW   Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
KW   disease diagnosis; forensic analysis; DNA sequencing; paternity testing;
KW   cell line authentication; gene therapy; ss.
XX
OS   Synthetic.
XX
PN   WO200100876-A1.
XX
PD   04-JAN-2001.
XX
PF   26-JUN-2000; 2000WO-US017507.
XX
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
XX
PA   (MIRK/) MIRKIN C A.
PA   (LETS/) LETSINGER R L.
PA   (MUCI/) MUCIC R C.
PA   (STOR/) STORHOFF J J.
PA   (ELGH/) ELGHANIAN R.
PA   (TATO/) TATON T A.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2001-061976/07.
XX
PT   Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics
PT   and DNA sequencing, comprises observing detectable change brought about
PT   by hybridization of nucleic acid with substrate or particle bound
PT   oligonucleotides.
XX
PS   Disclosure; Page 199; 205pp; English.
XX
CC   The present sequence is an oligonucleotide used in a method for detecting
CC   a nucleic acid having at least 2 portions. The method comprises
CC   hybridising the nucleic acid with oligonucleotides, such as the present
CC   sequence, attached to a substrate and/or particle and detecting a change
CC   in colour, conductivity or optical density. The method is useful for the
CC   diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,
CC   for paternity testing, for cell line authentication and for monitoring
CC   gene therapy. Detecting nucleic acids based upon observing a colour
CC   change is cheap, fast, simple, and does not require specialised or
CC   expensive equipment. The nanoparticle oligonucleotide conjugates remain
CC   stable for at least 6 months. A single base mismatch and as little as 20
CC   femtomoles (fM) of target can be detected using the conjugates
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 379
AAS10371/c
ID   AAS10371 standard; DNA; 20 BP.
XX
AC   AAS10371;
XX
DT   24-OCT-2001  (first entry)
XX
DE   Oligonucleotide-cyclic disulphide linker, d.
XX
KW   Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
KW   DNA isolation; genetic disease; bacterial disease; viral disease;
KW   forensic science; paternity testing; gene therapy; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1
FT                   /*tag=  a
FT                   /note= "A is covalently linked to a cyclic-disulphide
FT                   moiety"
XX
PN   WO200151665-A2.
XX
PD   19-JUL-2001.
XX
PF   12-JAN-2001; 2001WO-US001190.
XX
PR   13-JAN-2000; 2000US-0176409P.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
PR   12-JAN-2001; 2001US-00760500.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Li Z;
XX
DR   WPI; 2001-451868/48.
XX
PT   Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
PT   viral diseases, by contacting the nucleic acid with oligonucleotides
PT   attached to nanoparticles and having sequences complementary a portion of
PT   the nucleic acid.
XX
PS   Example 24; Fig 44; 323pp; English.
XX
CC   The sequence represents a cyclic disulphide linked oligonucleotide which
CC   may be coupled with colloidal gold particles (nanoparticles) and used to
CC   demonstrate the method of the invention. The invention relates to
CC   isolating or detecting a nucleic acid of interest, in a mixture of
CC   nucleic acids, by binding it to 2 or more complimentary nucleotides which
CC   have a nanoparticle attached to their 5' ends. The nanoparticles (e.g.
CC   colloidal gold) are used to both isolate and detect (e.g. by linking the
CC   particle to a fluorescent probe) the resultant complex. The methods are
CC   useful for detecting nucleic acids, natural or synthetic, and modified or
CC   unmodified. The methods may also be applied in the diagnosis of genetic,
CC   bacterial and viral diseases, in forensics, in DNA sequencing, for
CC   paternity testing, for cell line authentication, and for monitoring gene
CC   therapy. The methods are further useful in research and analytical
CC   laboratories in DNA sequencing, in the field to detect the presence of
CC   specific pathogens, for quick identification of an infection to assist in
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CC   drug prescription, and in homes and health centres for inexpensive first-
CC   line screening. The methods, which are based on observing colour change
CC   with the naked eye, are cheap, fast, simple, robust (reagents are
CC   stable), do not require specialised or expensive equipment, and little or
CC   no instrumentation is required
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 380
AAF99427
ID   AAF99427 standard; DNA; 20 BP.
XX
AC   AAF99427;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #543.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 49; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 20


RESULT 381
AAF99099
ID   AAF99099 standard; DNA; 20 BP.
XX
AC   AAF99099;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #215.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 42; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 20
```

```
RESULT 382
AAF99431/c
ID   AAF99431 standard; DNA; 20 BP.
XX
AC   AAF99431;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #547.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 49; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 383
AAH46465
ID   AAH46465 standard; DNA; 20 BP.
XX
AC   AAH46465;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Oligonucleotide #13.
XX
KW   Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "All bases are phosphorothioate"
FT   modified_base   1
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Modified with 2'-O-methyl"
XX
PN   US6242591-B1.
XX
PD   05-JUN-2001.
XX
PF   11-JAN-2000; 2000US-00481486.
XX
PR   15-OCT-1997;   97US-00950779.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cole DL,  Ravikumar VT,  Cheruvallath ZS;
XX
DR   WPI; 2001-407218/43.
XX
PT   Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
PT   useful in biological research, comprises phosphitylating the 5'-hydroxyl
PT   of a nucleic acid having a nucleoside with a 2' modification.
XX
PS   Example 23; Col 11; 7pp; English.
XX
CC   The present invention relates to a method for preparing phosphorothioate
CC   oligonucleotides having at least one nucleoside with a 2' modification.
CC   The method comprises phosphitylating the 5'-hydroxyl of a nucleic acid
CC   group having at least one nucleoside with a 2' modification in an
CC   acetonitrile. The present sequence was used to illustrate the method of
CC   the present invention. The method is useful for synthesising sulphurised
CC   2' substituted phosphorothioate oligonucleotides, which may be used in
CC   molecular biological research, in applications such as anti-viral
CC   therapy, and for determining the stereochemical pathways of certain
CC   enzymes which recognise nucleic acids
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 384
AAH78547/c
ID   AAH78547 standard; cDNA; 20 BP.
XX
AC   AAH78547;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Nucleotide sequence of a cDNA sequence.
XX
KW   Nucleic acid identification; DNA library screening; ss.
XX
OS   Synthetic.
XX
```

PN US6274321-B1.
XX
PD 14-AUG-2001.
XX
PF 03-DEC-1999; 99US-00454704.
XX
PR 03-DEC-1999; 99US-00454704.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Blumberg B;
XX
DR WPI; 2001-588900/66.
XX
PT Screening nucleic acids (NA) in pool of interest comprises pooling,
PT expressing NA to form expression product pool and identifying NA in NA
PT pool corresponding to expression product pool having interaction with
PT target moiety.
XX
PS Disclosure; Col 22; 19pp; English.
XX
CC The specification describes a method for identifying a nucleic acid in a
CC pool of interest. The method comprises pooling individually identifiable
CC nucleic acids into at least two pools of one nucleic acid each;
CC expressing nucleic acid pools to obtain protein expression product pools;
CC assaying protein expression product pools for products having interaction
CC with target molecule; selecting nucleic acid pools corresponding to
CC identified protein expression product pools; and identifying individual
CC nucleic acids in identified nucleic acid pools. The method is useful for
CC identifying a nucleic acid (e.g. cDNA) in a pool of interest and for
CC functionally screening several nucleic acids. The method is also useful
CC for screening genomic DNA libraries or other source of individual cDNAs,
CC mRNAs, synthetic libraries of nucleic acids e.g. combinatorial libraries.
CC The present sequence was used in the course of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 385
AAF28351/c
ID AAF28351 standard; DNA; 20 BP.
XX
AC AAF28351;
XX
DT 02-APR-2001 (first entry)
XX
DE DNA oligomer #1.
XX
KW Deoxynucleic S-Methythiourea; DNmt; antisense therapy;
KW cardiovascular disease; inflammatory disease; neurocellular disease;
KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;
KW influenza; herpes; infection; ss.
XX
OS Unidentified.
XX
PN US6169176-B1.
XX
PD 02-JAN-2001.
XX
PF 28-SEP-1999; 99US-00407675.
XX
PR 02-JUL-1998; 98US-0091481P.
PR 11-DEC-1998; 98US-0111800P.
PR 02-JUL-1999; 99US-00347443.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Dev AP, Bruice TC;
XX
DR WPI; 2001-122276/13.
XX
PT Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
PT antisense therapy, by synthesizing oligonucleotides comprising backbone
PT of alkyl or alkoxy thiourea linkages in solution or on solid phase.
XX
PS Example 7; Fig 16; 48pp; English.
XX
CC The present sequence was used to demonstrate the ability of deoxynucleic
CC S-Methythiourea (DNmt) compounds to form triplexes with DNA oligomers. An
CC increase in the C content of the oligos resulted in a large decrease in
CC binding. This experiment was performed as an example of a method for
CC preparing oligonucleotides comprising a backbone of alkyl or alkoxy
CC thiourea linkages. The method is useful for preparing oligonucleotides
CC for use in antisense or antigene therapy, to inhibit production of
CC proteins associated with genetic diseases, cardiovascular, inflammatory
CC and neurocellular diseases, and for antiviral therapy, e.g. to treat
CC human immunodeficiency virus, human-cytomegalovirus, influenza and herpes
CC infections. The compounds are also useful as diagnostic reagents to
CC detect the presence or absence of the target DNA or RNA sequences to
CC which they specifically bind and by antagonising the normal biological
CC activity of a target protein, they can be used in the manipulation of
CC tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
CC cultures. The method provides an efficient and rapid solid-phase method
CC for the synthesis of thiourea and S-methylthiourea
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 386
ABS77742
ID ABS77742 standard; DNA; 20 BP.
XX
AC ABS77742;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #226.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;

XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 23; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 387
ABS78072
ID ABS78072 standard; DNA; 20 BP.
XX
AC ABS78072;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #556.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 29; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 388
ABS78076/c
ID ABS78076 standard; DNA; 20 BP.
XX
AC ABS78076;
XX
DT 13-DEC-2002 (first entry)
XX
DE Angiogenesis inhibitory oligonucleotide #560.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophiliac joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
PT Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 29; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,

```
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 389
ABL39402
ID   ABL39402 standard; DNA; 20 BP.
XX
AC   ABL39402;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 838.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 309; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTT 20


RESULT 390
ABL38648/c
ID   ABL38648 standard; DNA; 20 BP.
XX
AC   ABL38648;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 2.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; ss.
XX
OS   Synthetic.
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 95; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
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                    ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 391
ABL39403
ID   ABL39403 standard; DNA; 20 BP.
XX
AC   ABL39403;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 839.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; ss.
XX
OS   Synthetic.
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 309; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
                ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 392
ABL54775
ID   ABL54775 standard; DNA; 20 BP.
XX
AC   ABL54775;
XX
DT   10-JUN-2002  (first entry)
XX
DE   CD14 receptor PCR primer SEQ ID NO 9.
XX
KW   Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;
KW   single-nucleotide polymorphism; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   JP2002034599-A.
XX
PD   05-FEB-2002.
XX
PF   26-JUL-2000; 2000JP-00225354.
XX
PR   26-JUL-2000; 2000JP-00225354.
XX
PA   (TOYM ) TOYOBO KK.
XX
DR   WPI; 2002-275727/32.
XX
PT   Detecting 1 base polymorphism on a sequence of a chromosome or it's
PT   fragment.
XX
PS   Example 2; Page 10; 10pp; Japanese.
XX
CC   The invention relates to a method for detecting 1 base polymorphism on
CC   the sequence of a chromosome or its fragment in which a sample nucleic
CC   acid is reacted with a reaction liquor containing a nucleic acid primer
CC   having a base adjacent to the polymorphic base at its 3'-end, one
CC   dideoxynucleotide corresponding to a polymorphic base having a
CC   distinguishable feature or its mixture, DNA polymerase and a composition
CC   required for its activity expression to detect the presence of taking
CC   dideoxynucleotide in the nucleic acid primer and to detect the type of
CC   the base to be specified. The method is used for detecting 1 base
CC   polymorphism on the sequence of a chromosome or its fragment. The present
CC   sequence is that of a PCR primer, useful in examples of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
                ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 393
ABK65035/c
ID   ABK65035 standard; DNA; 20 BP.
XX
AC   ABK65035;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Nanoparticle-oligonucleotide #55.
XX
KW   Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200218643-A2.
XX
PD   07-MAR-2002.
XX
PF   10-AUG-2001; 2001WO-US025237.
XX
PR   11-AUG-2000; 2000US-0224631P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
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```
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-258024/30.
XX
PT   Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT   bacterial disease, comprises hybridizing nanoparticles with attached
PT   oligonucleotides to nucleic acid and detecting change brought about by
PT   hybridization.
XX
PS   Example 18; Page 410; 412pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid (NA) having
CC   at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC   attached oligonucleotides (OGN), where OGN has a sequence complementary
CC   to the sequence of NA; (b) contacting NA and NP under conditions
CC   effective to allow hybridisation of OGN with NA; and (c) observing a
CC   detectable change brought about by hybridisation of OGN with NA. The
CC   method is useful for detecting a nucleic acid, separating a selected
CC   nucleic acid from others and methods of nanofabrication. Detecting
CC   analytes such as nucleic acids and proteins are useful for the diagnosis
CC   of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC   cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC   In particular assays using OGN-NP conjugates prepared using linkers
CC   comprising a steroid residue attached to a cyclic disulphide have been
CC   found to be approximately 10 times more sensitive than assays employing
CC   conjugates prepared using alkanethiols or acyclic disulphides as the
CC   linker. The OGN-NP conjugates are stable allowing them to be used
CC   directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC   target to be PCR amplified can be carried through the 30 or 40 heating
CC   cooling cycles of the PCR and are still able to detect the amplicons
CC   without opening the tubes and causing contamination. ABK64981-ABK65055
CC   represent nanoparticle-oligonucleotides of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 394
ABK65050/c
ID   ABK65050 standard; DNA; 20 BP.
XX
AC   ABK65050;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Nanoparticle-oligonucleotide #70.
XX
KW   Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200218643-A2.
XX
PD   07-MAR-2002.
XX
PF   10-AUG-2001; 2001WO-US025237.
XX
PR   11-AUG-2000; 2000US-0224631P.
PR   08-DEC-2000; 2000US-0254392P.
PR   11-DEC-2000; 2000US-0255235P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-258024/30.
XX
PT   Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT   bacterial disease, comprises hybridizing nanoparticles with attached
PT   oligonucleotides to nucleic acid and detecting change brought about by
PT   hybridization.
XX
PS   Example 24; Fig 44; 412pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid (NA) having
CC   at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC   attached oligonucleotides (OGN), where OGN has a sequence complementary
CC   to the sequence of NA; (b) contacting NA and NP under conditions
CC   effective to allow hybridisation of OGN with NA; and (c) observing a
CC   detectable change brought about by hybridisation of OGN with NA. The
CC   method is useful for detecting a nucleic acid, separating a selected
CC   nucleic acid from others and methods of nanofabrication. Detecting
CC   analytes such as nucleic acids and proteins are useful for the diagnosis
CC   of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC   cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC   In particular assays using OGN-NP conjugates prepared using linkers
CC   comprising a steroid residue attached to a cyclic disulphide have been
CC   found to be approximately 10 times more sensitive than assays employing
CC   conjugates prepared using alkanethiols or acyclic disulphides as the
CC   linker. The OGN-NP conjugates are stable allowing them to be used
CC   directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC   target to be PCR amplified can be carried through the 30 or 40 heating
CC   cooling cycles of the PCR and are still able to detect the amplicons
CC   without opening the tubes and causing contamination. ABK64981-ABK65055
CC   represent nanoparticle-oligonucleotides of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 395
AAL45122
ID   AAL45122 standard; DNA; 20 BP.
XX
AC   AAL45122;
XX
DT   24-MAY-2002  (first entry)
XX
DE   Oligonucleotide synthesis method related DNA #1.
XX
KW   Oligonucleotide synthesis; polynucleotide array; protecting group;
KW   oxidation; ss.
XX
OS   Synthetic.
XX
PN   EP1176151-A1.
XX
PD   30-JAN-2002.
XX
PF   27-JUL-2001; 2001EP-00118360.
XX
PR   28-JUL-2000; 2000US-00627249.
XX
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PA   (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI   Dellinger DJ,  Perbost MGM,  Betley JR,  Caruthers M;
XX
DR   WPI; 2002-156732/21.
XX
PT   Synthesis of polynucleotide useful during fabrication of an array
PT   involves coupling nucleoside phosphoramidite and a solid-supported
PT   nucleoside and treating the product with an oxidation/deprotection
PT   composition.
XX
PS   Example 1; Page 15; 36pp; English.
XX
CC   The present invention relates to a method for the synthesis of a
CC   polynucleotide which involves coupling a second nucleoside to a first
CC   nucleoside through a phosphite linkage, where the second nucleoside has a
CC   non-carbonate protecting group protecting a hydroxyl, and exposing the
CC   product to a composition which concurrently oxidizes the phosphite formed
CC   to a phosphate and deprotects the protected hydroxyl of the second
CC   nucleoside. The method is useful for synthesizing the polynucleotides,
CC   for carrying out either 3' to 5' or 5' to 3' synthesis and for
CC   fabricating an addressable array of polynucleotides on a substrate. The
CC   present sequence is an oligonucleotide produced to demonstrate the method
CC   of the invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 396
ABL36232/c
ID   ABL36232 standard; DNA; 20 BP.
XX
AC   ABL36232;
XX
DT   08-APR-2002  (first entry)
XX
DE   M tuberculosis rRNA probe SEQ ID NO: 83.
XX
KW   Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW   alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW   antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW   Th2 immune response; immunomodulatory; probe; ss.
XX
OS   Mycobacterium tuberculosis.
XX
PN   US6328978-B1.
XX
PD   11-DEC-2001.
XX
PF   02-JUN-1999;   99US-00324542.
XX
PR   23-DEC-1997;   97US-00997080.
XX
PA   (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI   Watson JD,  Tan PLJ,  Prestidge R;
XX
DR   WPI; 2002-138361/18.
XX
PT   Inhibiting skin inflammation associated with skin disorder e.g.
PT   psoriasis, by administering composition comprising delipidated and
PT   deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT   culture filtrate.
XX
PS   Example 5; Col 99-100; 116pp; English.
XX
CC   The present invention relates to a method of inhibiting skin inflammation
CC   associated with a skin disorder selected from psoriasis, atopic
CC   dermatitis and allergic contact dermatitis, which involves administering
CC   a composition containing delipidated and deglycolipidated Mycobacterium
CC   vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC   treated may also include alopecia areata, and skin cancers such as basal
CC   cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC   acts by inhibiting the Th2 immune response. The present sequence is a
CC   probe described in the exemplification of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 397
ABS64673/c
ID   ABS64673 standard; DNA; 20 BP.
XX
AC   ABS64673;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Nucleic acid detection method associated polynucleotide #55.
XX
KW   Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW   nanoparticle; viral RNA detection; bacterial DNA detection;
KW   fungal DNA detection; nanoprobe conjugate; ss.
XX
OS   Synthetic.
XX
PN   WO200246472-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-US046418.
XX
PR   08-DEC-2000; 2000US-0254392P.
PR   08-DEC-2000; 2000US-0254418P.
PR   11-DEC-2000; 2000US-0255235P.
PR   11-DEC-2000; 2000US-0255236P.
PR   12-JAN-2001; 2001US-00760500.
PR   28-MAR-2001; 2001US-00820279.
PR   09-APR-2001; 2001US-0282640P.
PR   10-AUG-2001; 2001US-00927777.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA,  Garimella V,  Li Z,  Park S;
XX
DR   WPI; 2002-608256/65.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 18; Page 437; 442pp; English.
XX
CC   The invention describes a method of detecting (M1) a nucleic acid having
CC   two portions, involving providing nanoparticles having oligonucleotides
CC   attached to it, which has a sequence complementary to sequence of two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC   allow hybridisation of oligonucleotides with two or more portions of
CC   nucleic acid, and observing a detectable change brought about by
CC   hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
```

CC conjugates (II) and the aggregate probe are useful for detecting two or
CC more nucleic acids (from a biological source) having at least two
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC with a disease, synthetic, or structurally-modified natural or synthetic
CC RNA or DNA, or a product of a polymerase chain reaction amplification.
CC (II) is useful for preparing a nanoprobe conjugate for detecting an
CC analyte, and for detecting a nucleic acid bound to an electrode surface.
CC (I) and (II) are useful for fabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. (I), (II) and
CC the aggregate probe are useful for detecting an analyte (especially
CC polyvalent analyte) in a sample. This sequence represents a
CC polynucleotide used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 398
ABS64688/c
ID ABS64688 standard; DNA; 20 BP.
XX
AC ABS64688;
XX
DT 15-NOV-2002 (first entry)
XX
DE Nucleic acid detection method associated polynucleotide #70.
XX
KW Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
OS Synthetic.
XX
PN WO200246472-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-US046418.
XX
PR 08-DEC-2000; 2000US-0254392P.
PR 08-DEC-2000; 2000US-0254418P.
PR 11-DEC-2000; 2000US-0255235P.
PR 11-DEC-2000; 2000US-0255236P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
PR 09-APR-2001; 2001US-0282640P.
PR 10-AUG-2001; 2001US-00927777.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
DR WPI; 2002-608256/65.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change.
XX
PS Example 24; Fig 44; 442pp; English.
XX
CC The invention describes a method of detecting (M1) a nucleic acid having
CC two portions, involving providing nanoparticles having oligonucleotides
CC attached to it, which has a sequence complementary to sequence of two
CC portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC allow hybridisation of oligonucleotides with two or more portions of
CC nucleic acid, and observing a detectable change brought about by
CC hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC conjugates (II) and the aggregate probe are useful for detecting two or
CC more nucleic acids (from a biological source) having at least two
CC portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC with a disease, synthetic, or structurally-modified natural or synthetic
CC RNA or DNA, or a product of a polymerase chain reaction amplification.
CC (II) is useful for preparing a nanoprobe conjugate for detecting an
CC analyte, and for detecting a nucleic acid bound to an electrode surface.
CC (I) and (II) are useful for fabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. (I), (II) and
CC the aggregate probe are useful for detecting an analyte (especially
CC polyvalent analyte) in a sample. This sequence represents a
CC polynucleotide used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 399
ABN87103
ID ABN87103 standard; DNA; 20 BP.
XX
AC ABN87103;
XX
DT 30-JUL-2002 (first entry)
XX
DE Capture probe CP5' SEQ ID NO:23.
XX
KW Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.
XX
OS Synthetic.
XX
PN WO200232925-A2.
XX
PD 25-APR-2002.
XX
PF 16-OCT-2001; 2001WO-US032233.
XX
PR 16-OCT-2000; 2000US-00688566.
XX
PA (PHYL-) PHYLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX
DR WPI; 2002-444238/47.
XX
PT New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.
XX
PS Disclosure; Page 58; 94pp; English.
XX
CC The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present

CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 400
ABZ88267/c
ID ABZ88267 standard; DNA; 20 BP.
XX
AC ABZ88267;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3509; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 401
ABZ88565/c
ID ABZ88565 standard; DNA; 20 BP.
XX
AC ABZ88565;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3807; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 402
ABZ88619/c
ID   ABZ88619 standard; DNA; 20 BP.
XX
AC   ABZ88619;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 3861; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 403
ABZ89705/c
ID   ABZ89705 standard; DNA; 20 BP.
XX
AC   ABZ89705;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4947; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 404
ABZ85312/c
ID ABZ85312 standard; DNA; 20 BP.
XX
AC ABZ85312;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 554; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAAAA 2803
||||||||||||||||||||
Db 20 TGAAAAAAAAAAAAAAAAAA 1

RESULT 405
ABZ88816/c
ID ABZ88816 standard; DNA; 20 BP.
XX
AC ABZ88816;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4058; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 406
ABZ88881/c
ID   ABZ88881 standard; DNA; 20 BP.
XX
AC   ABZ88881;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4123; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 407
ABZ89546/c
ID   ABZ89546 standard; DNA; 20 BP.
XX
AC   ABZ89546;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4788; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2169 TTTTTTTTTTTTTTTTTTAA 2188
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTAA 1

RESULT 408
ABZ89706/c
ID ABZ89706 standard; DNA; 20 BP.
XX
AC ABZ89706;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4948; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 409
ABZ88620/c
ID ABZ88620 standard; DNA; 20 BP.
XX
AC ABZ88620;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3862; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 410
ABZ88880/c
ID   ABZ88880 standard; DNA; 20 BP.
XX
AC   ABZ88880;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4122; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTA 1


RESULT 411
ABZ89179/c
ID   ABZ89179 standard; DNA; 20 BP.
XX
AC   ABZ89179;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4421; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2168 TTTTTTTTTTTTTTTTTTTA 2187
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTA 1

RESULT 412
ABZ88814/c
ID ABZ88814 standard; DNA; 20 BP.
XX
AC ABZ88814;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4056; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 413
ABZ89241/c
ID ABZ89241 standard; DNA; 20 BP.
XX
AC ABZ89241;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4483; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 414
ABZ90650/c
ID   ABZ90650 standard; DNA; 20 BP.
XX
AC   ABZ90650;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 5892; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 415
ABZ99050/c
ID   ABZ99050 standard; DNA; 20 BP.
XX
AC   ABZ99050;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human PDE4C oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 14292; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
             ||||||||||||||||||||
Db         20 GAAAAAAAAAAAAAAAAAAA 1


RESULT 416
ABZ88815/c
ID   ABZ88815 standard; DNA; 20 BP.
XX
AC   ABZ88815;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4057; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
             ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 417
ABZ85311
ID   ABZ85311 standard; DNA; 20 BP.
XX
AC   ABZ85311;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 553; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 418
ABZ85435
ID   ABZ85435 standard; DNA; 20 BP.
XX
AC   ABZ85435;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 677; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 419
ABZ88817/c
ID   ABZ88817 standard; DNA; 20 BP.
XX
AC   ABZ88817;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4059; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 420
ABZ88939/c
ID ABZ88939 standard; DNA; 20 BP.
XX
AC ABZ88939;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4181; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 421
ABZ89302/c
ID ABZ89302 standard; DNA; 20 BP.
XX
AC ABZ89302;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4544; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTT 1


RESULT 422
ABZ87681/c
ID   ABZ87681 standard; DNA; 20 BP.
XX
AC   ABZ87681;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 2923; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         20 GAAAAAAAAAAAAAAAAAAA 1


RESULT 423
ABZ88566/c
ID   ABZ88566 standard; DNA; 20 BP.
XX
AC   ABZ88566;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 3808; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
```

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 424
ABZ89086/c
ID ABZ89086 standard; DNA; 20 BP.
XX
AC ABZ89086;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4328; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 425
ABZ85533/c
ID ABZ85533 standard; DNA; 20 BP.
XX
AC ABZ85533;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 775; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 426
ABZ89015/c
ID ABZ89015 standard; DNA; 20 BP.
XX
AC ABZ89015;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4257; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 427
ABZ89441/c
ID ABZ89441 standard; DNA; 20 BP.
XX
AC ABZ89441;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4683; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 428
ABZ89016/c
ID ABZ89016 standard; DNA; 20 BP.
XX
AC ABZ89016;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4258; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 429
ABZ89120/c
ID ABZ89120 standard; DNA; 20 BP.
XX
AC ABZ89120;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4362; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

```
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 430
ABZ89704/c
ID   ABZ89704 standard; DNA; 20 BP.
XX
AC   ABZ89704;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 4946; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 431
ACD27320/c
ID   ACD27320 standard; DNA; 20 BP.
XX
AC   ACD27320;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #54.
XX
KW   Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW   virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW   cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW   sexually transmitted disease; inherited disorder; forensic;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2002155461-A1.
XX
PD   24-OCT-2002.
XX
PF   12-OCT-2001; 2001US-00976378.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-228115/22.
XX
PT   Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT   comprises use of nanoparticles which have oligonucleotides attached to
PT   them that are complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 44; 130pp; English.
```

XX
CC This invention relates to a novel method for detecting a nucleic acid
CC having 2 portions. The method comprises providing nanoparticles having
CC oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC the oligonucleotide on the nanoparticle with two or more portions of
CC nucleic acid and observing a detectable change brought about by the
CC hybridisation. The method of the invention is useful for separating a
CC selected nucleic acid having 2 portions, from other nucleic acids, and
CC for detecting nucleic acids having 2 portions. The method of the
CC invention is useful for detecting any type of nucleic acids which may be
CC used for diagnosis of disease and in sequencing of nucleic acids.
CC Preferably, the method is useful for detecting nucleic acids for
CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC virus), bacterial diseases, sexually transmitted diseases, inherited
CC disorders, in forensics, in DNA sequencing, for paternity testing, for
CC cell line authentication, for monitoring gene therapy, etc. This method
CC involves detecting nucleic acids based on observing a colour change with
CC the naked eye so is cheap, fast, simple and robust, and does not require
CC specialised expensive equipment. The present sequence represents a thiol
CC modified oligonucleotide sequence used to demonstrate the method of the
CC invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 432
ACC58867
ID ACC58867 standard; DNA; 20 BP.
XX
AC ACC58867;
XX
DT 08-SEP-2003 (first entry)
XX
DE Doubly labelled DNA probe.
XX
KW Probe; nucleic acid detection; ss.
XX
OS Synthetic.
XX
PN WO2003043402-A2.
XX
PD 30-MAY-2003.
XX
PF 21-OCT-2002; 2002WO-US033699.
XX
PR 19-OCT-2001; 2001US-0336432P.
XX
PA (PROL-) PROLIGO LLC.
XX
PI Bruce I, Davies M, Wolter A;
XX
DR WPI; 2003-505122/47.
XX
PT Detection or quantification of nucleic acid analyte, by hybridizing a
PT nucleic acid probe having non-identical covalently attached dyes, with
PT nucleic acid analyte, and measuring change in fluorescence of the probes.
XX
PS Example 9; Page 32; 110pp; English.
XX
CC The present sequence is an example of nucleic acid probes of the
CC invention. The probe may be doubly labelled with non-identical covalently
CC attached dyes, e.g. the fluorescent intercalator ethidium, which serves
CC as the detector dye and the fluorescent dye fluorescein, which serves as
CC the donor dye of a fluorescent resonance energy transfer (FRET) system. A
CC bifunctional linker was used to attach the dyes to the oligonucleotide.
CC The probe generates a fluorescent signal upon hybridisation to a
CC complementary nucleic acid based on the interaction of the intercalator
CC with the formed double-stranded DNA. Nucleic acid probes of the invention
CC can be used in homogeneous assays, real-time PCR monitoring,
CC transcription assays, expression analysis on nucleic acid microarrays and
CC other microarray applications such as genotyping
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 433
ABZ22916
ID ABZ22916 standard; DNA; 20 BP.
XX
AC ABZ22916;
XX
DT 08-APR-2003 (first entry)
XX
DE Phosphorothioate 20-mer oligonucleotide #1.
XX
KW Chiral; phosphorothioate; oligonucleotide synthesis; enantiomer; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1. .20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages"
XX
PN WO2002102815-A2.
XX
PD 27-DEC-2002.
XX
PF 13-JUN-2002; 2002WO-US018581.
XX
PR 14-JUN-2001; 2001US-00881535.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ravikumar VT;
XX
DR WPI; 2003-157021/15.
XX
PT Preparing internucleotide phosphorothioate linkage enhanced in Sp/Rp
PT enantiomer, by coupling a synthon with 2'-substituted nucleoside in
PT presence of coupling agent having a pKa that enhances linkage in Sp/Rp
PT enantiomer.
XX
PS Example 1; Page 31; 65pp; English.
XX
CC The present invention describes a method (M1) for preparing an
CC internucleotide phosphorothioate linkage enriched in the Sp or Rp
CC enantiomer between a synthon having a hydroxyl moiety at the 5' position
CC and a 2'-substituted nucleoside having an activated phosphate moiety at
CC the 3'-position, comprising coupling a synthon with a 2'-substituted
CC nucleoside in the presence of coupling agent that is selected to enhance
CC either the Rp or Sp enantiomer according to its pKa. This method is
CC useful for preparing an oligonucleotide having at least one region of
CC internucleotide linkages that is enhanced in the Sp or Rp enantiomer,
CC which involves providing a nucleotide having a hydroxyl moiety at the 5'-
CC position or a growing oligonucleotide chain having a hydroxyl moiety at

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CC   the 5'-position, coupling the nucleotide or growing oligonucleotide chain
CC   to a 2'-substituted nucleoside having an activated phosphate moiety at
CC   the 3' position in the presence of the coupling agent, and repeating the
CC   coupling step until the desired number of linkages is established. The
CC   oligonucleotide having a region of internucleotide linkages that is
CC   enhanced in the Sp enantiomer is further processed to include another
CC   region of internucleotide linkages that is enhanced in the Sp and/or Rp
CC   enantiomer. Oligonucleotides prepared by the method lead to improved
CC   drugs, diagnostics and research reagents. The present sequence represents
CC   an oligonucleotide used in the exemplification of the present invention
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 434
AAL61645/c
ID   AAL61645 standard; DNA; 20 BP.
XX
AC   AAL61645;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Thiol-modified oligo #4 used in the nucleic acid detection method.
XX
KW   Nucleic acid detection; fabrication; ss.
XX
OS   Unidentified.
XX
PN   WO2003035829-A2.
XX
PD   01-MAY-2003.
XX
PF   08-OCT-2002; 2002WO-US032088.
XX
PR   09-OCT-2001; 2001US-0327864P.
PR   07-DEC-2001; 2001US-00008978.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Park S,  Taton TA,  Mirkin CA;
XX
DR   WPI; 2003-430409/40.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 18; Page 179; 467pp; English.
XX
CC   The invention relates to a method of detecting a nucleic acid having two
CC   portions. The method involves providing nanoparticles having
CC   oligonucleotides attached to it which has a sequence complementary to
CC   sequence of two portions of nucleic acid, contacting nucleic acid and
CC   nanoparticles to allow hybridisation of oligonucleotides with two or more
CC   portions of nucleic acid and observing a detectable change brought about
CC   by hybridisation. The method and aggregate probes are useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic or structurally modified natural or
CC   synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. The invention is useful for preparing a nanoprobe
CC   conjugate for detecting an analyte and for detecting a nucleic acid bound
CC   to an electrode surface. It is also useful for fabrication and for
CC   separating a selected nucleic acid having two portions from other nucleic
CC   acids. The present sequence is an oligo used to illustrate the method of
CC   the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 435
ABZ59815
ID   ABZ59815 standard; RNA; 20 BP.
XX
AC   ABZ59815;
XX
DT   01-APR-2003  (first entry)
XX
DE   Potato gene PCR primer dT20.
XX
KW   Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
KW   transferrin binding protein; receptor-like protein kinase; helicase;
KW   non-long terminal repeat retroelement reverse transcriptase;
KW   overwatering; transgenic; reverse transcriptase; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   DE10114063-A1.
XX
PD   10-OCT-2002.
XX
PF   22-MAR-2001; 2001DE-01014063.
XX
PR   22-MAR-2001; 2001DE-01014063.
XX
PA   (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.
XX
PI   Buelow L,  Tscharntke M,  Haussuehl K;
XX
DR   WPI; 2003-041808/04.
XX
PT   New DNA sequences from potato, useful for producing plants with altered
PT   properties, e.g. tolerance of flooding, also related proteins, antibodies
PT   and inhibitory sequences.
XX
PS   Example 1; Page 8; 26pp; German.
XX
CC   The invention relates to DNA sequences (I) that encode six specific plant
CC   proteins: (i) a protein (ABP60425) with mitochondrial carrier protein
CC   activity (IIa); (ii) a protein (ABP60426) with transferrin binding
CC   protein activity (IIb); (iii) a protein (ABP60427) with receptor-like
CC   protein kinase activity (IIc); (iv) a protein (ABP60428) with elongation
CC   factor EF-2 activity (IId); (v) a protein (ABP60429) with non-long
CC   terminal repeat retroelement reverse transcriptase activity (IIe); or
CC   (vi) a protein (ABP60430) with helicase activity (IIf). (I), also related
CC   sequences, derived ribozymes and antisense sequences, expression vectors,
CC   encoded proteins and antibodies against the proteins, are used to produce
CC   plants with altered properties, including tolerance of overwatering. The
CC   antibodies are also used for isolation of the proteins and in
CC   immunoassays. Also (I) or their primer or probe fragments are used to
CC   screen for terminators and constitutively, aerobically or anaerobically
CC   inducible plant promoters, specifically for use in potatoes and the
CC   sequence that encodes (IId) is used to alter the translation profile in
CC   plants. Since (I) are derived from potato, their promoters and
CC   terminators provide high level transgene expression in potato, with
CC   improved tissue specificity and inducibility, and can also be used to
CC   control endogenous genes. The present sequence is that of a PCR primer
CC   used in the first strand synthesis of cDNAs derived from Potato
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
```

```
  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 436
ABX79181/c
ID   ABX79181 standard; DNA; 20 BP.
XX
AC   ABX79181;
XX
DT   15-APR-2003  (first entry)
XX
DE   Thio-modified 20dA oligonucleotide.
XX
KW   Nanoparticle; ss; nucleic acid detection; viral disease; probe;
KW   human immunodeficiency virus infection; hepatitis virus infection;
KW   herpes virus infection; cytomegalovirus infection; forensic science;
KW   Epstein-Barr virus infection; bacterial disease; gene therapy;
KW   sexually transmitted disease; inherited disorder; DNA sequencing;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
PN   US2002155462-A1.
XX
PD   24-OCT-2002.
XX
PF   12-OCT-2001; 2001US-00976577.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-198491/19.
XX
PT   Detecting nucleic acids having at least 2 portions comprises use of
PT   nanoparticles which have oligonucleotides attached to them that are
PT   complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 44; 130pp; English.
XX
CC   The invention relates to detecting a nucleic acid (NA) having at least 2
CC   portions, comprises providing a type of nanoparticles (NP) having
CC   attached to oligonucleotides (O) ((O) on each NP has a sequence
CC   complementary to sequence of at least 2 portions of NA), contacting NA
CC   and NP to allow hybridisation of (O) on NP with 2 or more portions of NA,
CC   and observing a detectable change brought about by hybridisation of (O)
CC   on NP with NA. The nanoparticle is useful for separating a selected
CC   nucleic acid having at least 2 portions, from other nucleic acids, and
CC   for detecting nucleic acids having at least 2 portions. The method of
CC   using NP is useful for detecting any type of nucleic acids which may be
CC   used for diagnosis of disease and in sequencing of nucleic acids.
CC   Preferably, the method is useful for detecting nucleic acids for
CC   diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC   virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC   virus), bacterial diseases, sexually transmitted diseases, inherited
CC   disorders, in forensics, in DNA sequencing, for paternity testing, for
CC   cell line authentication and for monitoring gene therapy. The method is
CC   useful in research and analytical laboratories in DNA sequencing and in
CC   the field to detect the presence of specific pathogens. Detecting nucleic
CC   acids based on observing a colour change with the naked eye is cheap,
CC   fast, simple and robust, and do not require specialised expensive
CC   equipment. The present sequence is a nanoparticle (e.g. gold particles)
CC   labelled probe used to demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 437
ABX92177/c
ID   ABX92177 standard; DNA; 20 BP.
XX
AC   ABX92177;
XX
DT   12-MAY-2003  (first entry)
XX
DE   Nanoparticle-associated oligonucleotide SEQ ID 55.
XX
KW   Nonoparticle; nucleic acid detection; hybridisation; diagnosis;
KW   sequencing; viral infection; human immunodeficiency virus; HIV;
KW   hepatitis virus; herpes virus; cytomegalovirus; Epstein-Barr virus;
KW   bacterial infection; sexually transmitted disease; inherited disorder;
KW   forensic; paternity testing; cell line authentication; gene therapy; ss.
XX
OS   Synthetic.
XX
PN   US2002155458-A1.
XX
PD   24-OCT-2002.
XX
PF   28-SEP-2001; 2001US-00967409.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-182627/18.
XX
PT   Detecting nucleic acids having at least two portions involves use of
PT   nanoparticles which have oligonucleotides attached to them that are
PT   complementary to portions of the nucleic acid sequence.
XX
PS   Disclosure; Page 59; 130pp; English.
XX
CC   This invention describes a novel method of detecting nucleic acid having
CC   at least two portions. The method involves providing nanoparticles
CC   attached to oligonucleotides, where the oligonucleotide on each
CC   nanoparticle have a sequence complementary to a sequence of at least two
CC   portions of nucleic acid, contacting nucleic acid and nanoparticle to
CC   allow hybridisation of the oligonucleotide on the nanoparticle with two
CC   or more portions of nucleic acid and observing a detectable change
CC   brought about by hybridisation of the oligonucleotide nanoparticle with
CC   nucleic acid. The method is useful for separating a selected nucleic acid
CC   having at least two portions, from other nucleic acids and for detecting
CC   nucleic acids having at least two portions. The method is useful for
CC   detecting any type of nucleic acids which may be used for diagnosis of
```

```
CC   disease and in sequencing of nucleic acids. Preferably, the method is
CC   useful for detecting nucleic acids for diagnosis and/or monitoring of
CC   viral infections (human immunodeficiency virus (HIV), hepatitis virus,
CC   herpes virus, cytomegalovirus and Epstein-Barr virus), bacterial
CC   diseases, sexually transmitted diseases, inherited disorders, in
CC   forensics, in DNA sequencing, for paternity testing, for cell line
CC   authentication, and for monitoring gene therapy. The method is useful in
CC   research and analytical laboratories in DNA sequencing, in the field to
CC   detect the presence of specific pathogens. Detecting nucleic acids based
CC   on observing a colour change with the naked eye is cheap, fast, simple
CC   and robust and does not require specialised expensive equipment. ABX92123
CC   -ABX92186 and ABQ77356 represent oligonucleotides used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 438
ACD27255/c
ID   ACD27255 standard; DNA; 20 BP.
XX
AC   ACD27255;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method associated #54.
XX
KW   Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW   virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW   cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW   sexually transmitted disease; inherited disorder; forensic;
KW   paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2002155459-A1.
XX
PD   24-OCT-2002.
XX
PF   11-OCT-2001; 2001US-00975062.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-228114/22.
XX
PT   Detecting nucleic acids having 2 portions e.g. for detecting disease,
PT   comprises use of nanoparticles which have oligonucleotides attached to
PT   them that are complementary to portions of the nucleic acid sequence.
XX
PS   Example 18; Page 43; 129pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid
CC   having 2 portions. The method comprises providing nanoparticles having
CC   oligonucleotides attached, where the oligonucleotide on each nanoparticle
CC   has a sequence complementary to a sequence of 2 portions of nucleic acid.
CC   The nucleic acid and nanoparticle are contacted to allow hybridisation of
CC   the oligonucleotide on the nanoparticle with two or more portions of
CC   nucleic acid and observing a detectable change brought about by the
CC   hybridisation. The method of the invention is useful for separating a
CC   selected nucleic acid having 2 portions, from other nucleic acids, and
CC   for detecting nucleic acids having 2 portions. The method of the
CC   invention is useful for detecting any type of nucleic acids which may be
CC   used for diagnosis of disease and in sequencing of nucleic acids.
CC   Preferably, the method is useful for detecting nucleic acids for
CC   diagnosis and/or monitoring of viral diseases (human immunodeficiency
CC   virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
CC   virus), bacterial diseases, sexually transmitted diseases, inherited
CC   disorders, in forensics, in DNA sequencing, for paternity testing, for
CC   cell line authentication, for monitoring gene therapy, etc. This method
CC   involves detecting nucleic acids based on observing a colour change with
CC   the naked eye so is cheap, fast, simple and robust, and does not require
CC   specialised expensive equipment. The present sequence represents a thiol
CC   modified oligonucleotide sequence used to demonstrate the method of the
CC   invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 439
ACD27125/c
ID   ACD27125 standard; DNA; 20 BP.
XX
AC   ACD27125;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW   Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
KW   DNA sequencing; paternity testing; cell line authentication.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2002164605-A1.
XX
PD   07-NOV-2002.
XX
PF   28-SEP-2001; 2001US-00966312.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
```

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-247253/24.
XX
PT Detecting nucleic acid having two portions, by providing nanoparticles
PT having oligonucleotides attached to it, contacting nucleic acid and
PT nanoparticles to allow hybridization, and observing detectable change,
PT useful in forensics.
XX
PS Example 18; Page 44; 130pp; English.
XX
CC This invention relates to a novel method for detecting nucleic acid
CC sequences having two portions. The method involves providing
CC nanoparticles having oligonucleotides attached to them, which has a
CC sequence complementary to sequence of two portions of nucleic acid,
CC contacting nucleic acid and nanoparticles, to allow hybridisation of
CC oligonucleotides with two or more portions of nucleic acid, and observing
CC a detectable change brought about by hybridisation. The method of the
CC invention and the aggregate probes are useful for detecting two or more
CC nucleic acids (from a biological source) having at least two portions,
CC such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with
CC a disease, synthetic, or structurally- modified natural or synthetic RNA
CC or DNA, or a product of a polymerase chain reaction amplification.
CC Nanoparticles and nanoparticle- oligonucleotide conjugates of the
CC invention are useful for nanofabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. The method of
CC the invention is useful in forensics, DNA sequencing, for paternity
CC testing, cell line authentication, and monitoring gene therapy.
CC Diagnostic assays employing the nanoparticle-oligonucleotide conjugates
CC of the invention improve the sensitivity of the nucleic acid detection
CC assay. The present sequence represents a thiol modified oligonucleotide
CC sequence used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 440
ACD27385/c
ID ACD27385 standard; DNA; 20 BP.
XX
AC ACD27385;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KW pathogen detection.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "
XX
PN US2002182611-A1.
XX
PD 05-DEC-2002.
XX
PF 28-SEP-2001; 2001US-00966491.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-596264/56.
XX
PT Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.
XX
PS Example 18; Page 43; 109pp; English.
XX
CC This invention relates to a novel method for detecting a nucleic acid by
CC contacting a nucleic acid with at least two types of nanoparticles having
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides
CC on the nanoparticles, and observing a detectable change. The
CC oligonucleotides on each nanoparticle have a sequence complementary to
CC its respective portion of the sequence of the nucleic acid to be
CC detected. The method of the invention may be used for the detection of a
CC nucleic acid used in, e.g. research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens, in
CC the doctor's office for quick identification of an infection to assist in
CC prescribing a drug for treatment, and in homes and health centres for
CC inexpensive first-line screening. The method of the invention detects
CC nucleic acids based on observing a colour change with the naked eye. This
CC method is cheap, fast, simple, robust and does not require specialised or
CC expensive equipment. The present sequence represents a thiol modified
CC oligonucleotide sequence used to demonstrate the method of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
||||||||||||||||||||
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 441
ACD27190/c
ID ACD27190 standard; DNA; 20 BP.
XX
AC ACD27190;
XX
DT 15-OCT-2003 (first entry)
XX
DE Nanotechnology nucleic acid detection method associated #54.
XX
KW Nanoparticle; ss; nucleic acid detection; DNA sequencing.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "
XX
PN US2002182613-A1.
XX
PD 05-DEC-2002.
XX
PF 12-OCT-2001; 2001US-00976971.
XX

```
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-596265/56.
XX
PT   Detection of nucleic acid for, e.g. research and analytical laboratories
PT   in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT   with nanoparticles having oligonucleotides.
XX
PS   Example 18; Page 43; 107pp; English.
XX
CC   This invention relates to a novel method for detecting a nucleic acid by
CC   contacting nucleic acid with at least two types of nanoparticles having
CC   oligonucleotides, allowing hybridisation of the oligonucleotides on the
CC   nanoparticles, and observing a detectable change. The oligonucleotides on
CC   each nanoparticle have a sequence complementary to its respective portion
CC   of the sequence of the nucleic acid. The method of the invention may be
CC   used for the detection of a nucleic acid used in, e.g. research and
CC   analytical laboratories in DNA sequencing, in the field to detect the
CC   presence of specific pathogens, in the doctor's office for quick
CC   identification of an infection to assist in prescribing a drug for
CC   treatment, and in homes and health centres for inexpensive first-line
CC   screening. The inventive method of detecting nucleic acids based on
CC   observing a colour change with the naked eye are cheap, fast, simple,
CC   robust (the reagents are stable), do not require specialised or expensive
CC   equipment, and little or no instrumentation is required. The present
CC   sequence represents a thiol modified oligonucleotide sequence used to
CC   demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 442
ACD27060/c
ID   ACD27060 standard; DNA; 20 BP.
XX
AC   ACD27060;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2003044805-A1.
XX
PD   06-MAR-2003.
XX
PF   15-OCT-2001; 2001US-00981344.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-521746/49.
XX
PT   Detection of nucleic acid having -2 portions used to prepare biomaterials
PT   and in nanofabrication methods, comprises providing nanoparticles,
PT   contacting nucleic acid and nanoparticles, and observing change.
XX
PS   Example 18; Page 44; 130pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The invention also
CC   provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC   conjugates are stable with tailored hybridisation abilities. The present
CC   sequence represents a thiol modified oligonucleotide sequence used to
CC   demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 443
AAL62273/c
ID   AAL62273 standard; DNA; 20 BP.
XX
AC   AAL62273;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128127.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
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```
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 1 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 GTGACCCGGACAGCAAGGCC 45
              ||||||||||||||||||||
Db         20 GTGACCCGGACAGCAAGGCC 1


RESULT 444
AAL62303/c
ID   AAL62303 standard; DNA; 20 BP.
XX
AC   AAL62303;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128157.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1029 ATCTTCCGGCCGGGAGGCGG 1048
              ||||||||||||||||||||
Db         20 ATCTTCCGGCCGGGAGGCGG 1
```

```
RESULT 445
AAL62320/c
ID   AAL62320 standard; DNA; 20 BP.
XX
AC   AAL62320;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128174.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 6 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1733 TCAGAAGGTGACAAGTACTG 1752
              ||||||||||||||||||||
Db         20 TCAGAAGGTGACAAGTACTG 1

RESULT 446
AAL62343/c
ID   AAL62343 standard; DNA; 20 BP.
XX
AC   AAL62343;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128197.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
```

```
XX
SQ   Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2653 CTAAGGTGAGTGTGCAGTAC 2672
              ||||||||||||||||||||
Db         20 CTAAGGTGAGTGTGCAGTAC 1


RESULT 447
AAL62284/c
ID   AAL62284 standard; DNA; 20 BP.
XX
AC   AAL62284;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128138.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        390 CCTACTCGCATCTGGGGGAA 409
              ||||||||||||||||||||
Db         20 CCTACTCGCATCTGGGGGAA 1


RESULT 448
AAL62290/c
ID   AAL62290 standard; DNA; 20 BP.
XX
AC   AAL62290;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128144.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
```

```
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 8 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        630 CCCTGGATGCCGCGGGCCTG 649
              ||||||||||||||||||||
Db         20 CCCTGGATGCCGCGGGCCTG 1


RESULT 449
AAL62301/c
ID   AAL62301 standard; DNA; 20 BP.
XX
AC   AAL62301;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128155.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        981 AAAATGGAGGCCGGTCCTTG 1000
              ||||||||||||||||||||
Db         20 AAAATGGAGGCCGGTCCTTG 1


RESULT 450
AAL62306/c
ID   AAL62306 standard; DNA; 20 BP.
XX
AC   AAL62306;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128160.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
```

```
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1170 CCAGACCTCATCTTGGAGGA 1189
              ||||||||||||||||||||
Db         20 CCAGACCTCATCTTGGAGGA 1


RESULT 451
AAL62312/c
ID   AAL62312 standard; DNA; 20 BP.
XX
AC   AAL62312;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128166.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1393 GTCTGCCCTGCAGAACTACA 1412
              ||||||||||||||||||||
Db         20 GTCTGCCCTGCAGAACTACA 1


RESULT 452
AAL62325/c
ID   AAL62325 standard; DNA; 20 BP.
XX
AC   AAL62325;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128179.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
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FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2021 CCTCTGGTAGGAGGCAAAGG 2040
              ||||||||||||||||||||
Db         20 CCTCTGGTAGGAGGCAAAGG 1


RESULT 453
AAL62327/c
ID   AAL62327 standard; DNA; 20 BP.
XX
AC   AAL62327;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128181.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base    1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2068 AGTGGTATCTGACACACTCT 2087
              ||||||||||||||||||||
Db         20 AGTGGTATCTGACACACTCT 1


RESULT 454
AAL62341/c
ID   AAL62341 standard; DNA; 20 BP.
XX
AC   AAL62341;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128195.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
```

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FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2630 TCTCGTTCCTGTTGGGCTGA 2649
              ||||||||||||||||||||
Db         20 TCTCGTTCCTGTTGGGCTGA 1


RESULT 455
AAL62272/c
ID   AAL62272 standard; DNA; 20 BP.
XX
AC   AAL62272;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128126.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GTGTCCAGTGACCCGGACAG 38
              ||||||||||||||||||||
Db         20 GTGTCCAGTGACCCGGACAG 1


RESULT 456
AAL62288/c
ID   AAL62288 standard; DNA; 20 BP.
XX
AC   AAL62288;
XX
DT   06-OCT-2003  (first entry)
```

```
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128142.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        580 CCGCAGGGATGCCTACCGCC 599
              ||||||||||||||||||||
Db         20 CCGCAGGGATGCCTACCGCC 1


RESULT 457
AAL62292/c
ID   AAL62292 standard; DNA; 20 BP.
XX
AC   AAL62292;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128146.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy        677 CCTCACCAGATGGACGAGGT 696
              ||||||||||||||||||||
Db         20 CCTCACCAGATGGACGAGGT 1


RESULT 458
AAL62307/c
ID   AAL62307 standard; DNA; 20 BP.
XX
AC   AAL62307;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128161.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 7 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1188 GACGAAATGAGATGGCAGCT 1207
             ||||||||||||||||||||
Db        20 GACGAAATGAGATGGCAGCT 1


RESULT 459
AAL62314/c
ID   AAL62314 standard; DNA; 20 BP.
XX
AC   AAL62314;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128168.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
```

```
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1426 GATTGTCATAGACAAATCCT 1445
              ||||||||||||||||||||
Db         20 GATTGTCATAGACAAATCCT 1


RESULT 460
AAL62313/c
ID   AAL62313 standard; DNA; 20 BP.
XX
AC   AAL62313;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128167.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 5 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1419 AAGCCCTGATTGTCATAGAC 1438
              ||||||||||||||||||||
Db         20 AAGCCCTGATTGTCATAGAC 1


RESULT 461
AAL62331/c
ID   AAL62331 standard; DNA; 20 BP.
XX
AC   AAL62331;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128185.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
```

```
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2231 CATGTTCCCTTAAGGTACTG 2250
              ||||||||||||||||||||
Db         20 CATGTTCCCTTAAGGTACTG 1


RESULT 462
AAL62286/c
ID   AAL62286 standard; DNA; 20 BP.
XX
AC   AAL62286;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128140.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 0 A; 7 C; 9 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        441 AGCCGGCGCCCACAGGCAGC 460
              ||||||||||||||||||||
Db         20 AGCCGGCGCCCACAGGCAGC 1


RESULT 463
AAL62339/c
ID   AAL62339 standard; DNA; 20 BP.
XX
AC   AAL62339;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128193.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
```

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PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 7 A; 2 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2504 TAACACATCATAAGGTTTTA 2523
              ||||||||||||||||||||
Db         20 TAACACATCATAAGGTTTTA 1


RESULT 464
AAL62340/c
ID   AAL62340 standard; DNA; 20 BP.
XX
AC   AAL62340;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128194.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 9 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2593 TTAATTGAAACTCTCTGTTC 2612
              ||||||||||||||||||||
Db         20 TTAATTGAAACTCTCTGTTC 1


RESULT 465
AAL62348/c
ID   AAL62348 standard; DNA; 20 BP.
XX
AC   AAL62348;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128202.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
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FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 81; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 9 A; 2 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2756 TGTATAATAAAAGTATTCTT 2775
              ||||||||||||||||||||
Db         20 TGTATAATAAAAGTATTCTT 1


RESULT 466
AAL62293/c
ID   AAL62293 standard; DNA; 20 BP.
XX
AC   AAL62293;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128147.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 2 G; 7 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        684 AGATGGACGAGGTGCAGAAT 703
              ||||||||||||||||||||
Db         20 AGATGGACGAGGTGCAGAAT 1


RESULT 467
AAL62308/c
ID   AAL62308 standard; DNA; 20 BP.
XX
AC   AAL62308;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128162.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
```

```
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1308 TCTTGGAGACGAACATACAG 1327
              ||||||||||||||||||||
Db         20 TCTTGGAGACGAACATACAG 1

RESULT 468
AAL62316/c
ID   AAL62316 standard; DNA; 20 BP.
XX
AC   AAL62316;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128170.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 0 G; 9 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1529 GAAGAAAGGTTAGGAGAGTA 1548
              ||||||||||||||||||||
Db         20 GAAGAAAGGTTAGGAGAGTA 1

RESULT 469
AAL62294/c
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```
ID   AAL62294 standard; DNA; 20 BP.
XX
AC   AAL62294;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128148.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
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CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        701 AATGTCGACGACCAGCACCT 720
              ||||||||||||||||||||
Db         20 AATGTCGACGACCAGCACCT 1


RESULT 470
AAL62298/c
ID   AAL62298 standard; DNA; 20 BP.
XX
AC   AAL62298;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128152.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
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  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        839 TGCTCAGTCCCTGGAAGATT 858
              ||||||||||||||||||||
Db         20 TGCTCAGTCCCTGGAAGATT 1


RESULT 471
AAL62305/c
ID   AAL62305 standard; DNA; 20 BP.
XX
AC   AAL62305;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128159.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 7 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1093 AGCTGTTCATTTGGCTAGGG 1112
              ||||||||||||||||||||
Db         20 AGCTGTTCATTTGGCTAGGG 1


RESULT 472
AAL62309/c
ID   AAL62309 standard; DNA; 20 BP.
XX
AC   AAL62309;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128163.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
```

```
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1365 TTGGCAGCCAGGCCATCTGT 1384
              ||||||||||||||||||||
Db         20 TTGGCAGCCAGGCCATCTGT 1


RESULT 473
AAL62315/c
ID   AAL62315 standard; DNA; 20 BP.
XX
AC   AAL62315;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128169.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
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CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 4 C; 2 G; 11 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1509 ACAGGAAATAAAATTGGAAC 1528
              ||||||||||||||||||||
Db         20 ACAGGAAATAAAATTGGAAC 1


RESULT 474
AAL62333/c
ID   AAL62333 standard; DNA; 20 BP.
XX
AC   AAL62333;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128187.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
```

```
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 1 G; 8 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2286 GTAAACTTGAAAAGGGTAGG 2305
              ||||||||||||||||||||
Db         20 GTAAACTTGAAAAGGGTAGG 1


RESULT 475
AAL62278/c
ID   AAL62278 standard; DNA; 20 BP.
XX
AC   AAL62278;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128132.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        125 CCTGGATTTAACTGGCGACT 144
              ||||||||||||||||||||
Db         20 CCTGGATTTAACTGGCGACT 1


RESULT 476
AAL62310/c
ID   AAL62310 standard; DNA; 20 BP.
XX
AC   AAL62310;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128164.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1375 GGCCATCTGTGCCGCGGTGT 1394
              ||||||||||||||||||||
Db         20 GGCCATCTGTGCCGCGGTGT 1

RESULT 477
AAL62319/c
ID   AAL62319 standard; DNA; 20 BP.
XX
AC   AAL62319;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128173.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
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CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
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CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 8 A; 2 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1712 CTCCTAACTTTGGACCTATT 1731
              ||||||||||||||||||||
Db         20 CTCCTAACTTTGGACCTATT 1

RESULT 478
AAL62336/c
ID   AAL62336 standard; DNA; 20 BP.
XX
AC   AAL62336;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128190.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
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FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
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CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 8 A; 6 C; 1 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2397 TATGCGTAATTTAATGGGGT 2416
              ||||||||||||||||||||
Db         20 TATGCGTAATTTAATGGGGT 1


RESULT 479
AAL62276/c
ID   AAL62276 standard; DNA; 20 BP.
XX
AC   AAL62276;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128130.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 9 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 GATTTTGGATTTACCGCTTG 110
              ||||||||||||||||||||
Db         20 GATTTTGGATTTACCGCTTG 1


RESULT 480
AAL62282/c
ID   AAL62282 standard; DNA; 20 BP.
XX
AC   AAL62282;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128136.
```

```
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 5 A; 5 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        167 ATGTTGTGGAAAATAACCGA 186
              ||||||||||||||||||||
Db         20 ATGTTGTGGAAAATAACCGA 1


RESULT 481
AAL62285/c
ID   AAL62285 standard; DNA; 20 BP.
XX
AC   AAL62285;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128139.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 1 A; 8 C; 8 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        405 GGGAAGCGTACGCCGCCGCC 424
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```
Db         20 GGGAAGCGTACGCCGCCGCC 1

RESULT 482
AAL62302/c
ID   AAL62302 standard; DNA; 20 BP.
XX
AC   AAL62302;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128156.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1013 GACAAGATCGGGTTGAATCT 1032
              ||||||||||||||||||||
Db         20 GACAAGATCGGGTTGAATCT 1

RESULT 483
AAL62347/c
ID   AAL62347 standard; DNA; 20 BP.
XX
AC   AAL62347;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128201.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 81; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
```

```
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 7 A; 3 C; 2 G; 8 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2754 CGTGTATAATAAAAGTATTC 2773
              ||||||||||||||||||||
Db         20 CGTGTATAATAAAAGTATTC 1


RESULT 484
AAL62283/c
ID   AAL62283 standard; DNA; 20 BP.
XX
AC   AAL62283;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128137.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        352 TCCCTACCAGCAGCTGGCCT 371
              ||||||||||||||||||||
Db         20 TCCCTACCAGCAGCTGGCCT 1


RESULT 485
AAL62323/c
ID   AAL62323 standard; DNA; 20 BP.
XX
AC   AAL62323;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128177.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
```

```
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 3 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1864 ACACTTAGCCATTGAAATGT 1883
              ||||||||||||||||||||
Db         20 ACACTTAGCCATTGAAATGT 1

RESULT 486
AAL62330/c
ID   AAL62330 standard; DNA; 20 BP.
XX
AC   AAL62330;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128184.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2220 CTTTGAAATGACATGTTCCC 2239
              ||||||||||||||||||||
Db         20 CTTTGAAATGACATGTTCCC 1

RESULT 487
AAL62342/c
ID   AAL62342 standard; DNA; 20 BP.
XX
AC   AAL62342;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128196.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
```

```
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2638 CTGTTGGGCTGAACCCTAAG 2657
              ||||||||||||||||||||
Db         20 CTGTTGGGCTGAACCCTAAG 1


RESULT 488
AAL62346/c
ID   AAL62346 standard; DNA; 20 BP.
XX
AC   AAL62346;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128200.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 81; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2709 TCTCTGCCTGTAAATGTTCC 2728
              ||||||||||||||||||||
Db         20 TCTCTGCCTGTAAATGTTCC 1


RESULT 489
AAL62277/c
ID   AAL62277 standard; DNA; 20 BP.
XX
AC   AAL62277;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128131.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
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FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         98 GATTTACCGCTTGGGGGCTG 117
              ||||||||||||||||||||
Db         20 GATTTACCGCTTGGGGGCTG 1


RESULT 490
AAL62287/c
ID   AAL62287 standard; DNA; 20 BP.
XX
AC   AAL62287;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128141.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        544 CCACCTCTCCGGGCTGGAGG 563
              ||||||||||||||||||||
Db         20 CCACCTCTCCGGGCTGGAGG 1


RESULT 491
AAL62300/c
ID   AAL62300 standard; DNA; 20 BP.
XX
AC   AAL62300;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128154.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
```

```
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        928 TGAATGCTTAAATGCCTCGT 947
              ||||||||||||||||||||
Db         20 TGAATGCTTAAATGCCTCGT 1


RESULT 492
AAL62304/c
ID   AAL62304 standard; DNA; 20 BP.
XX
AC   AAL62304;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128158.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 7 A; 2 C; 7 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1064 ACTCTCCTGACATCCTTAGT 1083
              ||||||||||||||||||||
Db         20 ACTCTCCTGACATCCTTAGT 1


RESULT 493
AAL62317/c
ID   AAL62317 standard; DNA; 20 BP.
XX
```

```
AC   AAL62317;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128171.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 5 A; 1 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1564 TGCAAAAATCCTTCTCCACC 1583
              ||||||||||||||||||||
Db         20 TGCAAAAATCCTTCTCCACC 1

RESULT 494
AAL62334/c
ID   AAL62334 standard; DNA; 20 BP.
XX
AC   AAL62334;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128188.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 9 A; 6 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
```

```
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2346 GTGGAGGTTCTGTATTTTAA 2365
              ||||||||||||||||||||
Db         20 GTGGAGGTTCTGTATTTTAA 1


RESULT 495
AAL62337/c
ID   AAL62337 standard; DNA; 20 BP.
XX
AC   AAL62337;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128191.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 9 A; 4 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2474 ATTAACTTTTAATGGTGATG 2493
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Db         20 ATTAACTTTTAATGGTGATG 1


RESULT 496
AAL62289/c
ID   AAL62289 standard; DNA; 20 BP.
XX
AC   AAL62289;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128143.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
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FT                    /*tag=  c
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FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
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PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
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CC   The invention is useful for inhibiting the expression of TFAP2C in cells
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CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
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XX
SQ   Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        624 CACACGCCCTGGATGCCGCG 643
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Db         20 CACACGCCCTGGATGCCGCG 1


RESULT 497
AAL62291/c
ID   AAL62291 standard; DNA; 20 BP.
XX
AC   AAL62291;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128145.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
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PI   Cowsert LM,  Freier SM;
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DR   WPI; 2003-569107/53.
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SQ   Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        669 ACGACATGCCTCACCAGATG 688
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Db         20 ACGACATGCCTCACCAGATG 1


RESULT 498
AAL62296/c
ID   AAL62296 standard; DNA; 20 BP.
XX
AC   AAL62296;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128150.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
```

```
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XX
SQ   Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        753 GTCCCATTTCCATGACCAAG 772
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Db         20 GTCCCATTTCCATGACCAAG 1


RESULT 499
AAL62321/c
ID   AAL62321 standard; DNA; 20 BP.
XX
AC   AAL62321;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128175.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
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SQ   Sequence 20 BP; 9 A; 3 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1751 TGGCTCTTTATTCATTAAGC 1770
              ||||||||||||||||||||
Db         20 TGGCTCTTTATTCATTAAGC 1


RESULT 500
AAL62324/c
ID   AAL62324 standard; DNA; 20 BP.
XX
AC   AAL62324;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128178.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
```

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XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
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PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
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  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1877 GAAATGTCAAATTGATGTGC 1896
              ||||||||||||||||||||
Db         20 GAAATGTCAAATTGATGTGC 1


RESULT 501
AAL62326/c
ID   AAL62326 standard; DNA; 20 BP.
XX
AC   AAL62326;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128180.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
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  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2029 AGGAGGCAAAGGTTCTATCT 2048
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Db         20 AGGAGGCAAAGGTTCTATCT 1


RESULT 502
AAL62329/c
ID   AAL62329 standard; DNA; 20 BP.
XX
AC   AAL62329;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128183.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
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FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
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XX
PN   WO2003051308-A2.
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PD   26-JUN-2003.
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PF   12-DEC-2002; 2002WO-US040100.
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PR   17-DEC-2001; 2001US-00023782.
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XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
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Qy       2195 AAGTTAACTCTTCAAATGGG 2214
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Db         20 AAGTTAACTCTTCAAATGGG 1


RESULT 503
AAL62344/c
ID   AAL62344 standard; DNA; 20 BP.
XX
AC   AAL62344;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128198.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
```

```
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
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CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2672 CAGTGTGTGTGGGTGAAATG 2691
              ||||||||||||||||||||
Db         20 CAGTGTGTGTGGGTGAAATG 1


RESULT 504
AAL62279/c
ID   AAL62279 standard; DNA; 20 BP.
XX
AC   AAL62279;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128133.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
```

```
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 9 C; 6 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        147 TTTGGGGGACGCCGGACGCC 166
              ||||||||||||||||||||
Db         20 TTTGGGGGACGCCGGACGCC 1


RESULT 505
AAL62280/c
ID   AAL62280 standard; DNA; 20 BP.
XX
AC   AAL62280;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128134.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        158 CCGGACGCCATGTTGTGGAA 177
              ||||||||||||||||||||
Db         20 CCGGACGCCATGTTGTGGAA 1
```

```
RESULT 506
AAL62281/c
ID   AAL62281 standard; DNA; 20 BP.
XX
AC   AAL62281;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128135.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        159 CGGACGCCATGTTGTGGAAA 178
              ||||||||||||||||||||
Db         20 CGGACGCCATGTTGTGGAAA 1


RESULT 507
AAL62297/c
ID   AAL62297 standard; DNA; 20 BP.
XX
AC   AAL62297;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128151.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
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FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
```

```
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        789 CCTGTCAGAAGGAGCTGGTG 808
              ||||||||||||||||||||
Db         20 CCTGTCAGAAGGAGCTGGTG 1


RESULT 508
AAL62318/c
ID   AAL62318 standard; DNA; 20 BP.
XX
AC   AAL62318;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128172.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1645 AGAGCCTTCACTGGTTCTGC 1664
              ||||||||||||||||||||
Db         20 AGAGCCTTCACTGGTTCTGC 1


RESULT 509
AAL62322/c
ID   AAL62322 standard; DNA; 20 BP.
XX
AC   AAL62322;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128176.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
```

```
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 8 A; 0 C; 5 G; 7 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1827 AATCTTTTAAATACATTCCC 1846
              ||||||||||||||||||||
Db         20 AATCTTTTAAATACATTCCC 1

RESULT 510
AAL62274/c
ID   AAL62274 standard; DNA; 20 BP.
XX
AC   AAL62274;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128128.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 2 A; 9 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         60 GCGGCGGCAGACGCCTGGTC 79
              ||||||||||||||||||||
Db         20 GCGGCGGCAGACGCCTGGTC 1

RESULT 511
AAL62299/c
ID   AAL62299 standard; DNA; 20 BP.
XX
AC   AAL62299;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128153.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
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XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
```

```
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 7 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        856 ATTGTCGCTCCTCAGCTCTA 875
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Db         20 ATTGTCGCTCCTCAGCTCTA 1


RESULT 512
AAL62332/c
ID   AAL62332 standard; DNA; 20 BP.
XX
AC   AAL62332;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128186.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2241 TAAGGTACTGAAGCTTTATT 2260
              ||||||||||||||||||||
Db         20 TAAGGTACTGAAGCTTTATT 1


RESULT 513
AAL62338/c
ID   AAL62338 standard; DNA; 20 BP.
XX
AC   AAL62338;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128192.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
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FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2491 ATGGGGTAATCTATAACACA 2510
              ||||||||||||||||||||
Db         20 ATGGGGTAATCTATAACACA 1


RESULT 514
AAL62271/c
ID   AAL62271 standard; DNA; 20 BP.
XX
AC   AAL62271;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128125.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base    1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 GCCGCCGATGCGTGTCCAGT 27
              ||||||||||||||||||||
Db         20 GCCGCCGATGCGTGTCCAGT 1


RESULT 515
AAL62275/c
ID   AAL62275 standard; DNA; 20 BP.
XX
AC   AAL62275;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128129.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
```

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XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 79; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 3 A; 5 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         70 ACGCCTGGTCACCGTGACCC 89
              ||||||||||||||||||||
Db         20 ACGCCTGGTCACCGTGACCC 1


RESULT 516
AAL62295/c
ID   AAL62295 standard; DNA; 20 BP.
XX
AC   AAL62295;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128149.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
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CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        727 GCACGATCAGACAGTCATTC 746
              ||||||||||||||||||||
Db         20 GCACGATCAGACAGTCATTC 1


RESULT 517
AAL62311/c
ID   AAL62311 standard; DNA; 20 BP.
XX
AC   AAL62311;
XX
```

```
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128165.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 6 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1377 CCATCTGTGCCGCGGTGTCT 1396
              ||||||||||||||||||||
Db         20 CCATCTGTGCCGCGGTGTCT 1

RESULT 518
AAL62328/c
ID   AAL62328 standard; DNA; 20 BP.
XX
AC   AAL62328;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128182.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Phosphorothioate backbone; All cytidines are 5-
FT                    methylcytidines"
FT   modified_base    1. .5
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
FT   modified_base    16. .20
FT                    /*tag=  c
FT                    /mod_base= OTHER
FT                    /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 8 A; 2 C; 3 G; 7 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       2186 TAACTTTGAAAGTTAACTCT 2205
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Db         20 TAACTTTGAAAGTTAACTCT 1


RESULT 519
AAL62335/c
ID   AAL62335 standard; DNA; 20 BP.
XX
AC   AAL62335;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128189.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Example 15; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 9 A; 4 C; 1 G; 6 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2379 GAGTGTACAGATTTTATTTA 2398
              ||||||||||||||||||||
Db         20 GAGTGTACAGATTTTATTTA 1


RESULT 520
AAL62345/c
ID   AAL62345 standard; DNA; 20 BP.
XX
AC   AAL62345;
XX
DT   06-OCT-2003  (first entry)
XX
DE   Human transcription factor-2 gamma antisense oligo, ISIS 128199.
XX
KW   Transcription factor-2 gamma; TFAP2C; AP-2 gamma; AP2-gamma; AP-2.2;
KW   Stra2; activating enhancer-binding protein 2 gamma; antisense therapy;
KW   oestrogen receptor factor-1; ERF-1; hyperproliferative disorder; cancer;
KW   breast; colon; developmental disorder; human; phosphorothioate backbone;
KW   antisense; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'methoxyethyl nucleotides"
XX
PN   WO2003051308-A2.
XX
PD   26-JUN-2003.
XX
PF   12-DEC-2002; 2002WO-US040100.
XX
PR   17-DEC-2001; 2001US-00023782.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Cowsert LM,  Freier SM;
XX
DR   WPI; 2003-569107/53.
XX
PT   New antisense compound targeted to a nucleic acid molecule encoding
PT   transcription factor-2 gamma, useful for inhibiting expression of the
PT   nucleic acid, and for treating cancer e.g. breast cancer or colon cancer.
XX
PS   Claim 3; Page 80; 107pp; English.
XX
CC   The invention relates to antisense compounds, compositions and methods
CC   for modulating the expression of transcription factor-2 gamma (TFAP2C).
CC   TFAP2C is also known as AP-2 gamma, AP2-gamma, AP-2.2, Stra2, activating
CC   enhancer-binding protein 2 gamma, oestrogen receptor factor-1 and ERF-1.
CC   The invention is useful for inhibiting the expression of TFAP2C in cells
CC   or tissues. It is useful for treating an animal having a disease or
CC   condition associated with TFAP2C, e.g., a hyperproliferative disorder
```

```
CC   such as cancer e.g. breast cancer or colon cancer and a developmental
CC   disorder. The invention is also useful for diagnostics, therapeutics,
CC   prophylaxis and as research reagents and kits. It is also used in
CC   antisense therapy. The present sequence is an antisense oligonucleotide
CC   targetted to human TFAP2C DNA. This sequence is used to illustrate the
CC   method of the invention
XX
SQ   Sequence 20 BP; 6 A; 6 C; 1 G; 7 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2689 ATGGAGATTTGGAATTGAAC 2708
              ||||||||||||||||||||
Db         20 ATGGAGATTTGGAATTGAAC 1


RESULT 521
ACH00064/c
ID   ACH00064 standard; DNA; 20 BP.
XX
AC   ACH00064;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Thiol modified" "
XX
PN   US2003049631-A1.
XX
PD   13-MAR-2003.
XX
PF   10-OCT-2001; 2001US-00974500.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-634854/60.
XX
PT   Detection of nucleic acid having at least two portions, by contacting
PT   nucleic acid and nanoparticles under conditions, which allows
PT   hybridization of oligonucleotides on nanoparticles with at least two
PT   portions of nucleic acid.
XX
PS   Example 18; Page 44; 108pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The invention also
CC   provides highly desirable nanoparticle-oligonucleotide conjugates. These
CC   conjugates are stable with tailored hybridisation abilities. The present
CC   sequence represents a thiol modified oligonucleotide sequence used to
CC   demonstrate the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 522
ACD99851/c
ID   ACD99851 standard; DNA; 20 BP.
XX
AC   ACD99851;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #537.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 23; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
```

```
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 523
ACD99847
ID   ACD99847 standard; DNA; 20 BP.
XX
AC   ACD99847;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #533.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 23; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 524
ACD99532
ID   ACD99532 standard; DNA; 20 BP.
XX
AC   ACD99532;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #218.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 14; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 525
ADA14838/c
ID   ADA14838 standard; DNA; 20 BP.
XX
AC   ADA14838;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hairpin target sequence, #2, used in an example of the invention.
XX
KW   Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW   quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW   rhodamine B-labelled dye; detection; gold support; ss.
XX
```

OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 1. .20
FT /*tag= a
FT /bound_moiety= "Hairpin oligonucleotide #2"
FT /note= "Forms a doube-stranded region with the hairpin
FT oligonucleotide shown in examples 3, 4 and 5"
XX
PN US2003013109-A1.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002US-00176055.
XX
PR 21-JUN-2001; 2001US-0299460P.
XX
PA (BALL/) BALLINGER C T.
PA (LOCA/) LOCASCIO M.
PA (LAND/) LANDRY D P.
XX
PI Ballinger CT, Locascio M, Landry DP;
XX
DR WPI; 2003-596312/56.
XX
PT Hairpin sensor useful for detecting a target nucleotide sequence in a
PT sample, comprises a hairpin loop assembly including a complementary probe
PT and a quenchable fluorescing agent.
XX
PS Example 3; Page 11; 16pp; English.
XX
CC The invention discloses a hairpin sensor comprising a hairpin loop
CC assembly including a complementary probe positioned between a first
CC inverse repeat arm and a second inverse repeat arm, and a quenchable
CC fluorescing agent joined, directly or indirectly, to the end of the
CC second inverse repeat arm of the hairpin loop assembly opposite the
CC complementary probe. Also claimed is a microarray comprising the hairpin
CC sensor, where the end of the first inverse repeat arm opposite the
CC complementary probe is bound, directly or indirectly, to a support, a kit
CC for detecting a target nucleotide sequence in a sample comprising the
CC hairpin sensor, and a support, and a hairpin sensor system, in which the
CC particle is conductive or semi-conductive, including at least one of the
CC above hairpin sensor assemblies. The hairpin sensor further comprises a
CC functional group joined to the end of the first inverse repeat arm
CC opposite the complementary probe, or first spacer opposite the first
CC inverse repeat arm, the functional group selected from amino, carboxyl,
CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC between the second inverse repeat arm and the quenchable fluorescing
CC agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC second spacer is positioned between the second inverse repeat arm and the
CC quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC or rhodamine B-labelled dye. Within the microarray the support is capable
CC of accepting a charge. At least one hairpin sensor comprises two or more
CC hairpin sensors. The two or more hairpin sensors include complementary
CC probes that are the same or different and respective quenchable
CC fluorescing agents that are the same or different. The two or more
CC hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC and system are useful for detecting a target nucleotide sequence in a
CC sample. Further, the method involves identifying the target nucleotide
CC sequence by the location of the complementary probe to which the target
CC nucleotide sequence binds. The two or more hairpin sensors include
CC complementary probes or quenchable fluorescing agents, that are
CC different. The sequence presented is the hairpin oligonucleotide target
CC sequence, #2, used in an example of the invention.
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTTTTTTTTTT 2185
Db 20 TTTTTTTTTTTTTTTTTTTT 1

RESULT 526
ADA06159/c
ID ADA06159 standard; DNA; 20 BP.
XX
AC ADA06159;
XX
DT 06-NOV-2003 (first entry)
XX
DE Nanoparticle labelled oligonucleotides, spacer DNA #2.
XX
KW ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;
KW nanostructure; viral disease; human immunodeficiency virus infection;
KW hepatitis virus infection; herpes virus infection;
KW cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;
KW sexually transmitted disease; inherited disorders; paternity testing;
KW cell line authentication; gene therapy.
XX
OS Synthetic.
XX
PN US2003068622-A1.
XX
PD 10-APR-2003.
XX
PF 12-OCT-2001; 2001US-00976863.
XX
PR 29-JUL-1996; 96US-0031809P.
PR 21-JUL-1997; 97WO-US012783.
PR 29-JAN-1999; 99US-00240755.
PR 25-JUN-1999; 99US-00344667.
PR 26-APR-2000; 2000US-0200161P.
PR 26-JUN-2000; 2000US-00603830.
XX
PA (NANO-) NANOSPHERE INC.
XX
PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;
XX
DR WPI; 2003-576420/54.
XX
PT Detecting nucleic acids having at least 2 portions comprises use of
PT nanoparticles which have oligonucleotides attached to them that are
PT complementary to portions of the target nucleic acid sequence.
XX
PS Example 18; Page 44; 130pp; English.
XX
CC The invention relates to detecting a nucleic acid (NA) having at least 2
CC portions comprises providing a type of nanoparticles (NP. e.g. colloidal
CC gold) having oligonucleotides (O) attached (where (O) on each NP has a
CC sequence complementary to sequence of at least two portions of NA),
CC contacting NA and NP to allow hybridisation of (O) on NP with 2 or more
CC portions of NA, and observing a detectable change brought about by
CC hybridization of (O) on NP with NA. Also included are aggregate probes,
CC core probes, substrate having NP attached to it, a metallic or
CC semiconductor NP having (O) attached to it, nanomaterials/nanostructures
CC comprising nanoparticles and methods of nanofabrication utilising
CC nanoparticles and satellite probes. The methods, probes nucleic acids,
CC nanoparticles and oligonucleotides are useful for separating a selected
CC nucleic acid having at least two portions, from other nucleic acids, and
CC for detecting nucleic acids having at least two portions, for detecting
CC NA having at least two portions. The method is useful for detecting any
CC type of nucleic acids which may be used for diagnosis of disease and in
CC sequencing of nucleic acids. Preferably, the method is useful for
CC detecting nucleic acids for diagnosis and/or monitoring of viral diseases
CC (human immunodeficiency virus, hepatitis virus, herpes virus,
CC cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually
CC transmitted diseases, inherited disorders, in forensics, in DNA
CC sequencing, for paternity testing, for cell line authentication, for
CC monitoring gene therapy, etc. The method is useful in research and
CC analytical laboratories in DNA sequencing, in the field to detect the

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CC   presence of specific pathogens, etc. Detecting nucleic acids based on
CC   observing a colour change with the naked eye is cheap, fast, simple and
CC   robust, and do not require specialised expensive equipment. The present
CC   sequence is a spacer oligonucleotide used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 527
ACD26995/c
ID   ACD26995 standard; DNA; 20 BP.
XX
AC   ACD26995;
XX
DT   15-OCT-2003  (first entry)
XX
DE   Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
KW   Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= Thiol modified" "
XX
PN   US2003049630-A1.
XX
PD   13-MAR-2003.
XX
PF   20-SEP-2001; 2001US-00957318.
XX
PR   29-JUL-1996;   96US-0031809P.
PR   21-JUL-1997;   97WO-US012783.
PR   29-JAN-1999;   99US-00240755.
PR   25-JUN-1999;   99US-00344667.
PR   26-APR-2000; 2000US-0200161P.
PR   26-JUN-2000; 2000US-00603830.
XX
PA   (NANO-) NANOSPHERE INC.
XX
PI   Mirkin CA,  Letsinger RL,  Mucic RC,  Storhoff JJ,  Elghanian R;
PI   Taton TA;
XX
DR   WPI; 2003-615795/58.
XX
PT   Detecting nucleic acid having two portions, by providing nanoparticles
PT   having oligonucleotides attached to it, contacting nucleic acid and
PT   nanoparticles to allow hybridization, and observing detectable change.
XX
PS   Example 18; Page 43; 129pp; English.
XX
CC   This invention relates to a novel method for detecting nucleic acids. The
CC   method comprises providing nanoparticles with oligonucleotides attached
CC   to them, which have a sequence complementary to a sequence of two
CC   portions of nucleic acid, contacting the nucleic acid and nanoparticles
CC   to allow hybridisation of the oligonucleotides with two or more portions
CC   of the nucleic acid, and observing a detectable change brought about by
CC   the hybridisation. The nucleic acid to be detected must have at least two
CC   portions and the distances between these are chosen so that when the
CC   nanoparticle-oligonucleotide conjugate binds the target sequence a
CC   detectable change occurs. The method of the invention is useful for
CC   detecting two or more nucleic acids (from a biological source) having at
CC   least two portions, such as viral RNA, bacterial or fungal DNA, a gene
CC   associated with a disease, synthetic, or structurally- modified natural
CC   or synthetic RNA or DNA, or a product of a polymerase chain reaction
CC   amplification. Nanoparticle-oligonucleotide conjugates of the invention
CC   are useful for preparing a nanoprobe conjugate for detecting an analyte,
CC   and for detecting a nucleic acid bound to an electrode surface.
CC   Nanoparticles and nanoparticle conjugates of the invention are useful for
CC   nanofabrication and for separating a selected nucleic acid having two
CC   portions from other nucleic acids. Diagnostic assays employing
CC   nanoparticle-oligonucleotide conjugates improve the sensitivity of
CC   nucleic acid detection methods and can be used to detect nucleic acids
CC   that are present in only small amounts in a sample. The present sequence
CC   represents a thiol modified oligonucleotide sequence used to demonstrate
CC   the method of the invention
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 528
ADB36933/c
ID   ADB36933 standard; DNA; 20 BP.
XX
AC   ADB36933;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #547.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 13; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
```

```
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 529
ADB36601
ID   ADB36601 standard; DNA; 20 BP.
XX
AC   ADB36601;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #215.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 8; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 530
ADB36929
ID   ADB36929 standard; DNA; 20 BP.
XX
AC   ADB36929;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #543.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 13; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.1e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTTTT 20


RESULT 531
AAQ75732
ID   AAQ75732 standard; DNA; 21 BP.
XX
AC   AAQ75732;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
```

```
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAAC 20


RESULT 532
AAQ75758/c
ID   AAQ75758 standard; DNA; 21 BP.
XX
AC   AAQ75758;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||||
Db         20 TTGAAAAAAAAAAAAAAAAA 1


RESULT 533
AAQ75756/c
ID   AAQ75756 standard; DNA; 21 BP.
XX
AC   AAQ75756;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||||
Db         20 TTGAAAAAAAAAAAAAAAAA 1


RESULT 534
AAQ75731
ID   AAQ75731 standard; DNA; 21 BP.
XX
AC   AAQ75731;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
```

```
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAAC 20


RESULT 535
AAQ75734
ID   AAQ75734 standard; DNA; 21 BP.
XX
AC   AAQ75734;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||||
Db          1 TTTTTTTTTTTTTTTTTAAC 20


RESULT 536
AAQ75755/c
ID   AAQ75755 standard; DNA; 21 BP.
XX
AC   AAQ75755;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2802
              ||||||||||||||||||||
Db         20 TTGAAAAAAAAAAAAAAAAA 1


RESULT 537
AAQ90391/c
ID   AAQ90391 standard; DNA; 21 BP.
XX
AC   AAQ90391;
XX
DT   08-JAN-1996  (first entry)
XX
DE   CP-1 (synthetic DNA probe with 3'ribonucleoside terminal #2).
XX
```

```
KW   CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;
KW   SAED; hybridisation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    21
FT                   /*tag=  a
FT                   /note= "3' ribonucleoside terminal"
XX
PN   WO9512808-A1.
XX
PD   11-MAY-1995.
XX
PF   26-OCT-1994;   94WO-US012270.
XX
PR   01-NOV-1993;   93US-00146504.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Heller MJ,  Tu E;
XX
DR   WPI; 1995-185870/24.
XX
PT   New self-addressable electronic devices - used for multi-step and
PT   multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT   and bio:polymer synthesis.
XX
PS   Example 1; Page 40; 86pp; English.
XX
CC   The sequences represented by, AAQ90390-90401 are synthetic DNA probes
CC   containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15
CC   are synthetic DNA probes with 5' amino termini. These sequences were
CC   specific for the polymorphisms of HLA gene dQa. The sequences were used
CC   in the device of the invention. This is a self-addressable electronic
CC   device (SAED) that can be used to carry out multi-step and multiplex
CC   reactions, such as nucleic acid hybridisations. The advantages of this
CC   method are that these reactions can be carried out with complete and
CC   precise electronic control, and that the rate, specificity and
CC   sensitivity of these reactions are greatly improved at micro-locations
XX
SQ   Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 538
AAT10743/c
ID   AAT10743 standard; RNA; 21 BP.
XX
AC   AAT10743;
XX
DT   09-SEP-1996  (first entry)
XX
DE   Oligonucleotide probe, CP-1.
XX
KW   Electronically self-addressable device; ED; electrode; current source;
KW   attachment layer; permeable; counterion; genetic typing; probe;
KW   detection; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   21
FT                   /*tag=  a
FT                   /note= "3'-ribonucleoside terminus"
XX
PN   WO9601836-A1.
XX
PD   25-JAN-1996.
XX
PF   05-JUL-1995;   95WO-US008570.
XX
PR   07-JUL-1994;   94US-00271882.
XX
PA   (NANO-) NANOGEN INC.
XX
PI   Heller MJ,  Tu E,  Evans GA,  Sosnowski RG;
XX
DR   WPI; 1996-097582/10.
XX
PT   Electronically self-addressable device - used for electronic control of,
PT   e.g. nucleic acid hybridisation.
XX
PS   Example 1; Page 60; 155pp; English.
XX
CC   The sequences given in AAT10742-67 are synthetic oligonucleotides which
CC   are used in the construction of the electronically self- addressable
CC   device (ED) of the invention. The ED comprises a substrate, an electrode
CC   or opt. a number of electrodes supported by the substrate, a current
CC   source operatively connected to the electrode and an attachment layer
CC   adjacent to the electrode which is permeable to a counterion but not
CC   permeable to a molecule capable of insulating or binding to the
CC   electrode. The attachment layer is capable of attaching a macromolecule.
CC   The ED is used for genetic typing and comprises a number of
CC   electronically addressable locations each comprising an electrode, and a
CC   binding entity, such as one of these probes, attached to each of the
CC   locations capable of detecting the presence of a genetic sequence
XX
SQ   Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 539
AAX81302/c
ID   AAX81302 standard; DNA; 21 BP.
XX
AC   AAX81302;
XX
DT   20-AUG-1999  (first entry)
XX
DE   3' ribonucleoside oligonucleotide probe CP-1.
XX
KW   Microelectronic device; multi-step reaction; microscopic format;
KW   ion-permeable permeation layer; electrode; electrical control; transport;
KW   attachment; binding; DNA/RNA hybrid; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_RNA        21
FT                   /*tag=  a
XX
PN   WO9929711-A1.
XX
PD   17-JUN-1999.
XX
PF   01-DEC-1998;   98WO-US025475.
XX
PR   05-DEC-1997;   97US-00986065.
XX
PA   (NANO-) NANOGEN INC.
XX
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PI   Sosnowski RG,  Butler WF,  Tu E,  Nerenberg MI,  Heller MJ,  Edman CF;
XX
DR   WPI; 1999-385567/32.
XX
PT   New microelectronic device designed to carry out and control multi-step
PT   and multiplex molecular biological reactions in microscopic format.
XX
PS   Example 1; Page 89; 179pp; English.
XX
CC   The specification describes a self-addressable, self-assembling
CC   microelectronic device which is designed to actively carry out and
CC   control multi-step and multiplex molecular biological reactions in
CC   microscopic formats. A key aspect of this inventions is played by the ion
CC   -permeable permeation layer which overlies the electrode. This permeation
CC   layer allows attachment of nucleic acids to permit immobilization but
CC   also separates the attached oligonucleotides and hybridized target DNA
CC   sequences from the highly reactive electrochemical environment generated
CC   immediately at the electrode surface. The microelectronic device is
CC   designed and fabricated to actively carry out and control reactions such
CC   as nucleic acid hybridizations, antibody/antigen reactions, sample
CC   preparation, diagnostics and biopolymer synthesis. The device can
CC   electronically control the transport and attachment of specific binding
CC   entities, such as nucleic acids and polypeptides, to specific micro-
CC   locations. The device can subsequently control the transport and reaction
CC   of analytes or reactants at the addressed specific micro-locations. The
CC   device is able to concentrate analytes and reactants, remove non-
CC   specifically bound molecules, provide stringency control for DNA
CC   hybridization reactions and improve the detection of analytes. The
CC   present sequence represents a probe used to exemplify the invention
XX
SQ   Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 4.7e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db         20 TTTTTTTTTTTTTTTTTTTT 1


RESULT 540
AAQ30432/c
ID   AAQ30432 standard; DNA; 23 BP.
XX
AC   AAQ30432;
XX
DT   25-MAR-2003  (revised)
DT   07-DEC-1992  (first entry)
XX
DE   Oligomer IL6805 for forming triplex with HUMIL6 target duplex.
XX
KW   Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW   malignancy; hepatitis; inflammation; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
FT   misc_feature     11. .12
FT                    /*tag=  d
FT                    /note= "o-xyloso dimer synthon linkage"
FT   misc_feature     12. .23
FT                    /*tag=  c
FT                    /label= inverted_polarity_region
FT                    /note= "see comments"
FT   modified_base    23
FT                    /*tag=  b
FT                    /mod_base= OTHER
FT                    /note= "OTHER= N4 N4 ethanocytosine"
XX
PN   WO9209705-A1.
XX
PD   11-JUN-1992.
XX
PF   25-NOV-1991;   91WO-US008811.
XX
PR   23-NOV-1990;   90US-00617907.
PR   18-JAN-1991;   91US-00643382.
PR   08-APR-1991;   91US-00683420.
PR   17-APR-1991;   91US-00686544.
PR   17-APR-1991;   91US-00686546.
PR   17-APR-1991;   91US-00686547.
PR   27-SEP-1991;   91US-00766733.
XX
PA   (GILE-) GILEAD SCI INC.
XX
PI   Froehler B,  Krawczyk S,  Matteucci MD,  Milligan J;
XX
DR   WPI; 1992-217083/26.
XX
PT   New oligomers contg. modified bases - which form a triplex with G-C
PT   doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT   herpes malignancy and inflammation.
XX
PS   Claim 12; Page 71; 77pp; English.
XX
CC   The synthetic oligomer is capable of forming a triplex at physiological
CC   pH with a purine rich target sequence by coupling into the major groove
CC   of the duplex. The specific target sequence of this oligomer is the human
CC   interleukin 6 gene untranslated sequence contg. a purine rich sequence
CC   concd. on one strand of the duplex. The oligomer, and others like it are
CC   useful in diagnosis and therapy of diseases characterised by specific DNA
CC   duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC   tumours and inflammation. The triple helices form under mild conditions
CC   thus assays may be carried out without subjecting the test specimen to
CC   harsh conditions. The oligomer contains an inverted polarity region
CC   formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC   (nucleotides have the 3'positions of xylose sugars linked via the o-
CC   xylene ring). Two nucleotides are coupled through a xylene residue to
CC   form the dimer synthon. This additional modifications may render the
CC   oligomer stable to nuclease activity. The oligomer is able to inhibit
CC   gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC   and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         23 GAAAAAAAAAAAAAAAAAAA 4


RESULT 541
ABX79809/c
ID   ABX79809 standard; cDNA; 24 BP.
XX
AC   ABX79809;
XX
DT   17-APR-2003  (first entry)
XX
DE   EST polymorphic DNA repeat polynucleotide #134.
XX
KW   EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW   polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW   Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW   Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW   Fredreich's ataxis; myotonic dystrophy; hyperandrogenaemia;
KW   spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
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OS   Homo sapiens.
XX
PN   US6472154-B1.
XX
PD   29-OCT-2002.
XX
PF   31-DEC-1999;   99US-00475947.
XX
PR   31-DEC-1999;   99US-00475947.
XX
PA   (TEXA ) UNIV TEXAS SYSTEM.
XX
PI   Garner HR,  Wren JD,  Minna JD,  Fondon JW;
XX
DR   WPI; 2003-208818/20.
XX
PT   Identifying a candidate polymorphic repeat within a coding sequence, for
PT   understanding or treating genetic disease, comprises detecting tandem
PT   repeats in a target coding sequence and scoring the repeats for
PT   polymorphic probability.
XX
PS   Example; Col 579; 588pp; English.
XX
CC   The invention discloses a method for identifying a candidate polymorphic
CC   repeat within a coding sequence (expressed sequence tag, EST), which
CC   comprises detecting tandem repeats in a target coding sequence, scoring
CC   the repeats for polymorphic probability and generating a dataset
CC   correlating the repeats with polymorphic probability to identify a
CC   candidate polymorphic repeat. The computational methods (polymorphic
CC   marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC   useful for identifying and detecting candidate polymorphic repeats in
CC   human genes, which can be used to understand, treat or eliminate genetic
CC   diseases, predispositions or adverse drug-treatment reactions. Examples
CC   of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC   syndrome, Huntington's disease, fragile-X syndrome, Fredreich's ataxis,
CC   myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC   spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC   the polymorphic repeats identified for a search of human ESTs
XX
SQ   Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         24 GAAAAAAAAAAAAAAAAAAA 5


RESULT 542
AAT68615/c
ID   AAT68615 standard; DNA; 24 BP.
XX
AC   AAT68615;
XX
DT   20-FEB-1998  (first entry)
XX
DE   DNA probe used in fingerprinting technique.
XX
KW   probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.
XX
OS   Synthetic.
XX
PN   EP778351-A2.
XX
PD   11-JUN-1997.
XX
PF   26-NOV-1996;   96EP-00118921.
XX
PR   30-NOV-1995;   95JP-00311949.
XX
PA   (HITA ) HITACHI LTD.
XX
PI   Kambara H,  Okano K,  Uematsu C;
XX
DR   WPI; 1997-300347/28.
XX
PT   Nucleic acid assay methods - based on restriction fragment length
PT   determination.
XX
PS   Example 1; Page 7; 21pp; English.
XX
CC   The present sequence is a DNA probe used in a novel method of analysis or
CC   assay for nucleotides, which comprises: (i) digesting DNA with a
CC   restriction enzyme; (ii) discriminating a difference in sequences of the
CC   DNA fragments obtained around the 3' termini with a DNA probe and
CC   extending the DNA probe by a complementary strand synthesis to
CC   fractionate the DNA fragments into groups; and (iii) measuring lengths of
CC   the DNA fragments which belong to the groups, or length of the extended
CC   DNA probe, and using the lengths obtained for the fragments around the 3'
CC   termini as fingerprints. Where polyA is present, the presence of
CC   recognition sequence GCG is critical for clarifying the terminal site,
CC   this is because the length of polyA cannot be controlled. The method is
CC   useful for assaying a large number of cDNA molecules or DNA fragments and
CC   for assaying long DNA sequences
XX
SQ   Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         20 GAAAAAAAAAAAAAAAAAAA 1


RESULT 543
ABK12409/c
ID   ABK12409 standard; DNA; 24 BP.
XX
AC   ABK12409;
XX
DT   18-JUN-2002  (first entry)
XX
DE   RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.
XX
KW   Polypeptide-laminin B210.67; embryo development teratogenesis;
KW   cytostatic; reverse transcriptase-PCR; RT-PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   CN1328013-A.
XX
PD   26-DEC-2001.
XX
PF   14-JUN-2000; 2000CN-00116514.
XX
PR   14-JUN-2000; 2000CN-00116514.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-270054/32.
XX
PT   Polypeptide-laminin B210.67, useful for treating diseases such as embryo
PT   development teratogenesis.
XX
PS   Example 2; Page 18 (disclosure); 33pp; Chinese.
XX
CC   The present invention relates to the isolation of polypeptide-laminin
CC   B210.67, and the polynucleotide encoding it. Also described is the
CC   process for preparing the protein by DNA recombination. The polypeptide
CC   is useful for treating diseases such as embryo development teratogenesis.
```

```
CC   The present sequence for reverse transcriptase (RT)-PCR primer #1 is used
CC   with RT-PCR primer #2 (ABK12410) for isolating cDNA encoding polypeptide-
CC   laminin B210.67
XX
SQ   Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 6.6e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAA 2188
              ||||||||||||||||||||
Db         24 TTTTTTTTTTTTTTTTTTAA 5


RESULT 544
AAZ99741
ID   AAZ99741 standard; DNA; 25 BP.
XX
AC   AAZ99741;
XX
DT   12-JUL-2000  (first entry)
XX
DE   Primer used to reverse transcribe barley 17 kDa foam protein mRNA.
XX
KW   Barley; 17 kDa foam protein; foam; prolamin storage protein;
KW   foaming beverage; beer; brewed product; foam head; primer; ss.
XX
OS   Hordeum vulgare.
XX
PN   WO200014237-A2.
XX
PD   16-MAR-2000.
XX
PF   02-SEP-1999;   99WO-IB001597.
XX
PR   03-SEP-1998;   98US-00146703.
PR   13-JAN-1999;   99US-0115756P.
XX
PA   (VAAG/) VAAG P.
PA   (BECH/) BECH L M.
PA   (CAME/) CAMERON-MILLS V.
PA   (SORE/) SORENSEN M B.
XX
PI   Vaag P,  Bech LM,  Cameron-Mills V,  Sorensen MB;
XX
DR   WPI; 2000-317103/27.
XX
PT   New foam protein from cereals useful for improving foam formation,
PT   stability and half-life in foaming products such as beverages and
PT   especially beer.
XX
PS   Example 6; Page 22; 82pp; English.
XX
CC   The present sequence represents a primer used to reverse transcribe mRNA
CC   encoding the barley 17 kDa foam protein. The protein has foam enhancing
CC   properties, and belongs to the prolamin storage protein family. It is
CC   found in the endosperm tissue of mature cereal grain, and is synthesised
CC   during grain development. The 17 kDa foam protein can be added to
CC   products, e.g. foaming beverages such as beer, to enhance the foaming
CC   quality of the product. The protein can be used to produce improved
CC   brewed products. The proteins and polynucleotides are especially useful
CC   for improving the formation, stability and half-life of the foam head on
CC   beer. The antibodies are useful to detect, measure and purify the
CC   proteins in samples such as transgenic cells/plants and foaming products
XX
SQ   Sequence 25 BP; 2 A; 2 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 7.3e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2163 TCCTTTTTTTTTTTTTTTTT 2182
              ||||||||||||||||||||
Db          6 TCCTTTTTTTTTTTTTTTTT 25


RESULT 545
ABZ23535/c
ID   ABZ23535 standard; DNA; 25 BP.
XX
AC   ABZ23535;
XX
DT   07-APR-2003  (first entry)
XX
DE   fragment of a plasmid used to detect somatic instability.
XX
KW   Replication error; drug development; somatic instability; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "this base represents an unspecified number of
FT                   bases"
FT   misc_feature    22
FT                   /*tag=  b
FT                   /note= "this base represents an unspecified number of
FT                   bases"
XX
PN   WO200295071-A2.
XX
PD   28-NOV-2002.
XX
PF   22-MAY-2002; 2002WO-NL000322.
XX
PR   22-MAY-2001; 2001EP-00201936.
XX
PA   (NEVW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.
PA   (TIJS/) TIJSTERMAN M.
XX
PI   Plasterk RHA,  Tijsterman M;
XX
DR   WPI; 2003-129440/12.
XX
PT   Determining whether a product of a gene is involved in preventing a
PT   replication error in a cell comprises providing a specific inhibitor for
PT   the product and determining the level of expression of a marker gene.
XX
PS   Example 1; Fig 3; 47pp; English.
XX
CC   The specification describes a method for determining whether a product of
CC   a gene is involved in preventing a replication error in a cell. The
CC   method comprises providing the cell with a specific inhibitor for the
CC   product and determining the level of functional expression of a marker
CC   gene in the cell, where the level of expression of the marker gene is
CC   dependent on the occurrence of the replication error. The method is used
CC   for determining whether a product of a gene is involved in preventing a
CC   replication error in a cell. The identified genes are useful for
CC   developing diagnostic tools, or as targets for drug development to
CC   manipulate cells on the basis of the presence or absence of function of
CC   the gene. ABZ23535-36 represents fragments of plasmids used to detect
CC   somatic instability, in the course of the invention
XX
SQ   Sequence 25 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 25;
  Best Local Similarity   95.2%;  Pred. No. 7.3e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              ||| ||||||||||||||||
Db         25 TTTNTTTTTTTTTTTTTTTT 5
```

```
RESULT 546
ACF79235
ID   ACF79235 standard; DNA; 25 BP.
XX
AC   ACF79235;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Calix(a)arene-oligonucleotide hybrid.
XX
KW   Calix(4)arene; triplex; gene therapy; DNA sensor; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   stem_loop       1. .25
FT                   /*tag=  a
FT   modified_base   13
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= calix(4)arene nucleoside"
XX
PN   WO2003059925-A1.
XX
PD   24-JUL-2003.
XX
PF   19-JUN-2002; 2002WO-KR001160.
XX
PR   15-JAN-2002; 2002KR-00002316.
XX
PA   (POST-) POSTECH FOUND.
XX
PI   Kim BH,  Kim SJ;
XX
DR   WPI; 2003-627375/59.
XX
PT   New calix(4)arene-nucleoside hybrid useful in gene therapy has at least
PT   one nucleoside attached to a calix(4)arene group through amide bonding,
PT   and is derived from a calix(4)arene having amino groups.
XX
PS   Claim 7; Page 20; 16pp; English.
XX
CC   The present sequence is that of a calix(4)arene-oligonucleotide hybrid of
CC   the invention, which includes a calix(4)arene-nucleoside (preferably
CC   thymidine) derivative. The calix(4)arene-oligonucleotide hybrid functions
CC   as a DNA hairpin structure mimic. It effectively recognises DNA or RNA
CC   through triplex formation by bonding between the calix(4)arene-containing
CC   cavity and a biologically active substance. The hybrid has a certain
CC   level of both rigidity and flexibility, is stable in vivo, has high cell
CC   permeability and can be mass-produced. It can be used as a DNA sensor or
CC   for gene therapy
XX
SQ   Sequence 25 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 25;
  Best Local Similarity   95.2%;  Pred. No. 7.3e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||| ||||||||
Db          1 TTTTTTTTTTTTNTTTTTTTT 21


RESULT 547
AAT94842
ID   AAT94842 standard; DNA; 27 BP.
XX
AC   AAT94842;
XX
DT   27-MAR-1998  (first entry)
XX
DE   Human ESF I 3' PCR primer.
XX
KW   Endometrial specific steroid-binding factor I; ESF I; human;
KW   inflammation; asthma; rhinitis; cystic fibrosis; airway disease;
KW   neoplasia; atopy; therapy; diagnosis; primer; PCR; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9734997-A1.
XX
PD   25-SEP-1997.
XX
PF   21-MAR-1996;   96WO-US003857.
XX
PR   21-MAR-1996;   96WO-US003857.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ni J,  Yu G,  Gentz RL;
XX
DR   WPI; 1997-480206/44.
XX
PT   Human endometrial specific steroid-binding factor I, II and III - used to
PT   treat inflammation, asthma, rhinitis, cystic fibrosis, airway disease,
PT   neoplasia, atopy etc.
XX
PS   Example 2; Page 52-53; 92pp; English.
XX
CC   This oligonucleotide contains an Asp718 site followed by 18 nucleotides
CC   complementary to a polyA tail. It was used with a 5' primer (see
CC   AAT94839), containing a BamHI site and 20 bases of the human endometrial
CC   specific steroid binding factor I (ESF I) coding sequence (see AAT94830),
CC   to amplify ESF I cDNA deposited as ATCC 97401. The PCR product was
CC   incorporated into baculovirus vector pRG1 and recombinant ESF I was
CC   expressed in Spodoptera frugiperda Sf9 cells. Human ESF I (see AAW35802)
CC   can be used to treat inflammation, asthma, rhinitis, cystic fibrosis,
CC   airway disease, neoplasia, atopy etc
XX
SQ   Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 8.9e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2164 CCTTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||
Db          8 CCTTTTTTTTTTTTTTTTTT 27


RESULT 548
AAA59740
ID   AAA59740 standard; DNA; 27 BP.
XX
AC   AAA59740;
XX
DT   06-OCT-2000  (first entry)
XX
DE   PCR primer for hESF I cDNA sequence amplification.
XX
KW   Endometrial specific steroid-binding factor; human; hESF; inflammation;
KW   asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy;
KW   eicosanoid level regulator; chemotaxis inhibitor; endometrial cancer;
KW   PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6066724-A.
XX
PD   23-MAY-2000.
XX
PF   21-MAR-1997;   97US-00821451.
XX
PR   21-MAR-1996;   96US-0014724P.
XX
```

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Gentz R, Ni J;
XX
DR WPI; 2000-375600/32.
XX
PT Novel gene encoding human endometrial specific steroid-binding factor I,
PT II and III which is useful for treating asthma, rhinitis, cystic
PT fibrosis, airway disease and neoplasia.
XX
PS Example 2; Col 34; 36pp; English.
XX
CC This invention relates to nucleic acid molecules encoding portions of the
CC human endometrial specific steroid-binding factors I, II, and III. Also
CC included in the invention are hESF I, II, and III polypeptide sequences.
CC The nucleotide sequence exhibit antiasthmatic, antiinflammatory,
CC antiallergic, and cytostatic properties. The polynucleotides are used in
CC gene therapy to express hESF I, II and III polypeptides in vivo to treat
CC and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way
CC disease, neoplasia and atopy. The polynucleotides are also used to
CC inhibit phospholipase A2 activity, bind polychlorinated biphenyls, reduce
CC foreign protein antigenicity, inhibit monocyte and neutrophil chemotaxis
CC and phagocytosis, inhibit platelet aggregation, regulate eicosanoid
CC levels in the human uterus and control the growth of endometrial cells.
CC The polynucleotides are also useful for detecting complementary
CC polynucleotides as a diagnostic reagent. The hESF I, II and III
CC polynucleotides are used to detect complementary polynucleotides such as
CC a diagnostic reagent. Detection of a mutated form of hESF I, II and III
CC associated with a dysfunction will provide a diagnostic tool that can
CC define diagnosis of a disease or susceptibility to a disease which
CC results from under-expression, over-expression or altered expression of
CC hESF I, II and III e.g. a susceptibility to inherited asthma and
CC endometrial cancer. They are also useful for chromosome identification.
CC The present sequence represents a PCR primer used to amplify the hESF I
CC cDNA sequence
XX
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||||
Db 8 CCTTTTTTTTTTTTTTTTTT 27

RESULT 549
AAF25224
ID AAF25224 standard; DNA; 27 BP.
XX
AC AAF25224;
XX
DT 30-APR-2001 (first entry)
XX
DE 3' primer for an endometrial specific steroid binding factor I cDNA.
XX
KW Human; endometrial specific steroid binding factor; hESF; hESFI; hESFII;
KW hESFIII; inflammation; asthma; rhinitis; cystic fibrosis; airway disease;
KW neoplasia; atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis;
KW phagocytosis; platelet aggregation; eicosanoid; endometrial cell;
KW PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6174992-B1.
XX
PD 16-JAN-2001.
XX
PF 08-MAR-1999; 99US-00263810.
XX
PR 21-MAR-1996; 96US-0014724P.
PR 21-MAR-1997; 97US-00821451.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz R;
XX
DR WPI; 2001-158477/16.
XX
PT New human endometrial specific steroid binding factors, useful for
PT treating and preventing inflammation, asthma, rhinitis, cystic fibrosis,
PT airway disease, neoplasia and atopy.
XX
PS Example 2; Col 33; 36pp; English.
XX
CC PCR primers AAF25221 and AAF25224 were used to amplify cDNA encoding a
CC human endometrial specific steroid binding factor (hESF). The
CC specification describes hESFI, hESFII, and hESFIII. hESFI, II and III
CC polypeptides, and polynucleotides encoding them are useful for treating
CC and preventing inflammation, asthma, rhinitis, cystic fibrosis, airway
CC disease, neoplasia and atopy, inhibiting phospholipase A2 activity,
CC binding polychlorinated biphenyls, reducing foreign protein antigenicity,
CC inhibiting monocyte and neutrophil chemotaxis and phagocytosis,
CC inhibiting platelet aggregation, regulating eicosanoid levels in the
CC human uterus, and for controlling the growth of endometrial cells. hESF
CC polypeptides and nucleotides are also useful for research, biological,
CC clinical or therapeutic purposes
XX
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||||
Db 8 CCTTTTTTTTTTTTTTTTTT 27

RESULT 550
ABL41793
ID ABL41793 standard; DNA; 27 BP.
XX
AC ABL41793;
XX
DT 29-MAY-2002 (first entry)
XX
DE Primer for human endometrial specific steroid-binding factor I cDNA.
XX
KW Human; endometrial specific steroid-binding factor; ESF;
KW prostatic steroid-binding protein; hESF I; hESF II; hESF III; asthma;
KW PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6338948-B1.
XX
PD 15-JAN-2002.
XX
PF 30-MAY-2000; 2000US-00583169.
XX
PR 21-MAR-1996; 96US-0014724P.
PR 21-MAR-1997; 97US-00821451.
PR 08-MAR-1999; 99US-00263810.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz R;
XX
DR WPI; 2002-215019/27.
XX
PT New antibody specific for human endometrial specific steroid-binding
PT factor (hESF) III, useful for detecting hESF III protein in biological
PT sample and to isolate or identify clones expressing the protein.

XX
PS Example 2; Col 33; 36pp; English.
XX
CC PCR primers ABL41790 and ABL41793 were used to amplify cDNA encoding
CC human endometrial specific steroid-binding factor (hESF) I. The primers
CC were used to introduce restriction sites for cloning. The full length
CC hESF I protein has a molecular weight of 9.8 kDa. The protein has
CC homology to rat prostatic steroid-binding protein. Antibodies which bind
CC hESF proteins, such as hESF I, hESF II, and hESF III are useful for
CC isolating or to identify clones expressing the polypeptides or to purify
CC the polypeptides by affinity chromatography. Agonists and antagonists of
CC hESF proteins are useful for treating and/or preventing susceptibility to
CC asthma
XX
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||||
Db 8 CCTTTTTTTTTTTTTTTTTT 27

RESULT 551
ABX14927
ID ABX14927 standard; DNA; 27 BP.
XX
AC ABX14927;
XX
DT 08-APR-2003 (first entry)
XX
DE hESF I amplifying 3' PCR primer for expression using baculovirus.
XX
KW Human; PCR; ss; endometrial specific steroid-binding factor; hESF;
KW Clara cell 10 kDa; CC10; secretory protein; asthma; primer;
KW prostatic steroid-binding protein; hormone; lung; uterus; gene therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002151012-A1.
XX
PD 17-OCT-2002.
XX
PF 06-NOV-2001; 2001US-00985911.
XX
PR 21-MAR-1996; 96US-0014724P.
PR 21-MAR-1997; 97US-00821451.
PR 08-MAR-1999; 99US-00263810.
PR 30-MAY-2000; 2000US-00583169.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Yu G, Gentz R;
XX
DR WPI; 2003-182506/18.
XX
PT New human endometrial specific steroid-binding factor (hESF) proteins and
PT genes, useful for treating or diagnosing a disease or susceptibility to a
PT disease, particularly asthma.
XX
PS Example 2; Page 18; 37pp; English.
XX
CC The invention discloses isolated polypeptides, which comprise human
CC endometrial specific steroid-binding factors I, II and III (hESF I, II
CC and III), and the nucleic acids encoding them. The hESF polypeptide has
CC homologies to mammalian Clara cell 10 kDa (CC10) secretory protein and
CC rat prostatic steroid-binding protein which are factors which modulate or
CC mediate the action of hormones involved in the regulation of functions of
CC the lung and uterus. The nucleic acids and polypeptides can be used to
CC identify compounds that bind to and inhibit activation, raise antibodies
CC or develop antagonists against the isolated hESF polypeptide. The
CC polypeptides or polynucleotides are useful for treating a patient having
CC a need of hESF I, hESF II, hESF III or for treating a patient having a
CC need to inhibit hESF. The polypeptide is administered by providing to the
CC patient the DNA encoding the hESF polypeptide in vivo (gene therapy). In
CC particular, the disease is asthma. The hESF polypeptides or
CC polynucleotides are also useful for diagnosing a disease or a
CC susceptibility to the disease. The sequence presented is the 3' PCR
CC primer which was used to amplify hESF I cDNA for expression using
CC baculovirus expression system T
XX
SQ Sequence 27 BP; 1 A; 5 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2164 CCTTTTTTTTTTTTTTTTTT 2183
||||||||||||||||||||
Db 8 CCTTTTTTTTTTTTTTTTTT 27

RESULT 552
ADD35234
ID ADD35234 standard; DNA; 28 BP.
XX
AC ADD35234;
XX
DT 15-JAN-2004 (first entry)
XX
DE Mouse mitochondrial DNA sequence SEQ ID NO:3014.
XX
KW ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
KW mitochondrial disease; oxidative phosphorylation dysfunction;
KW oxidative stress; apoptosis; aging.
XX
OS Mus musculus.
XX
PN WO2003020220-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-US027886.
XX
PR 30-AUG-2001; 2001US-0316323P.
PR 31-AUG-2001; 2001CA-02356540.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Wallace DC, Levy S, Kerstann K, Procaccio V;
XX
DR WPI; 2003-300821/29.
XX
PT Array containing probes for genes involved in mitochondrial biology,
PT useful for determining mitochondrial biology gene expression profiles for
PT use in diagnosing pathologies and identifying biochemical pathways.
XX
PS Claim 2; SEQ ID NO 3014; 201pp; English.
XX
CC The invention relates to a novel array comprising at least two isolated
CC nucleotide molecules, each molecule having a sequence capable of uniquely
CC hybridising to a nucleic acid molecule which is an expression product of
CC a gene involved in mitochondrial biology. The array comprises two or more
CC isolated nucleic acid molecules or spots, each molecule having a sequence
CC chosen from sequence of 994 human probes and 2046 mouse probes. An array
CC of the invention is useful for determining an expression profile of a
CC mouse or human sample containing nucleic acid, by contacting the array
CC with the sample under conditions allowing selective hybridisation, and
CC measuring hybridisation of nucleic acid in the sample to the array to
CC produce an expression profile. The array is also useful for determining
CC an expression profile of a first labelled sample containing nucleic acid
CC relative to a second, differently labelled sample containing nucleic
CC acid. The second sample is a reference or a standard. An array is useful

CC for determining an expression profile diagnostic of an energy-metabolism-
CC related physiological condition. An array of the invention is useful for
CC determining mitochondrial biology gene expression profiles of organisms,
CC such as human, mice and closely related species, tissue and organs of
CC such organisms, which are useful for determining expression profiles
CC diagnostic of energy metabolism-related physiological conditions,
CC diagnosing such physiological conditions, identifying biochemical
CC pathways, genes, and mutations involved in such physiological conditions,
CC identifying therapeutic agents useful for preventing and/or treating such
CC physiological conditions, evaluating and/or monitoring the efficacy of
CC such therapies, and creating and identifying animal models of human
CC energy metabolism-related physiological conditions. An array is also
CC useful for defining expression signatures or profiles for mitochondrial
CC diseases, as well as distinguishing clinical disorders that result from
CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
CC apoptosis and aging. An array of the invention contains probes of genes
CC not previously recognised to participate in mitochondrial biology. The
CC sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA
CC clones used to make the probes of the invention. Some sequences are not
CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
CC 1906, 2408 and 2643.
XX
SQ Sequence 28 BP; 0 A; 6 C; 4 G; 18 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       2164 CCTTTTTTTTTTTTTTTTTT 2183
              ||||||||||||||||||||
Db          9 CCTTTTTTTTTTTTTTTTTT 28
```

RESULT 553
AAA71190/c
ID AAA71190 standard; RNA; 29 BP.
XX
AC AAA71190;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site RNA #227.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Canis familiaris.
XX
PN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Example 8; Fig 135; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds
CC predicted or calculated to interact with the molecular interaction site;
CC and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC with members of the virtual library of compounds to generate a hierarchy
CC of the compounds ranked in accordance with their respective ability to
CC form physical interactions with the molecular interaction site. The
CC method also describes (1) RNA comprising a joined sequence of at least 24
CC nucleotides but not more than 70 nucleotides and having secondary
CC structure defined by: (a) 3 nucleotides forming a first side of a first
CC double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC internal loop region; (c) 4 nucleotides forming a first side of a second
CC ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC nucleotides forming a second side of the second ds region; (f) 4
CC nucleotides forming a second side of the internal loop region; and (g) 3
CC nucleotides forming a second side of the first ds region; (2) a purified
CC and isolated RNA fragment comprising the human sequence
CC UUUACAACAUAAUCUAGUUUACAGAAAAAUC (II). The methods and products can be
CC used for identifying agents which modulate the activity of biomolecules,
CC particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC or industrial compounds
XX
SQ Sequence 29 BP; 22 A; 1 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 29;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy       2169 TTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              |||||||||||||||||| | ||  | |
Db         29 TTTTTTTTTTTTTTTTTTCAGTTCTACA 2
```

RESULT 554
AAA71173/c
ID AAA71173 standard; DNA; 29 BP.
XX
AC AAA71173;
XX
DT 27-APR-2001 (first entry)
XX
DE Molecular interaction site DNA #154.
XX
KW Modulator; identification; molecular interaction; virtual library; ss.
XX
OS Canis familiaris.
XX
PN WO9958947-A2.
XX
PD 18-NOV-1999.
XX
PF 12-MAY-1999; 99WO-US010361.
XX
PR 12-MAY-1998; 98US-00076404.
PR 12-MAY-1998; 98US-0085092P.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ecker DJ, Griffey R, Crooke ST, Sampath R, Swayze E, Mohan V;
PI Hofstadler S, Mcneil J;
XX
DR WPI; 2000-086439/07.
XX
PT Identifying compounds which modulate activity of target biomolecules,
PT used to provide compounds which can be used as pharmacological,
PT agricultural and industrial compounds.
XX
PS Example 8; Fig 134; 405pp; English.
XX
CC This invention describes a novel method for identifying compounds which
CC modulate the activity of a target biomolecule. The method uses 3-
CC dimensional representations of the biomolecule and a library of compounds
CC and comprises (a) identifying at least one molecular interaction site of
CC the target RNA; (b) generating in silico a virtual library of compounds

```
CC   predicted or calculated to interact with the molecular interaction site;
CC   and (c) comparing 3-dimensional (3-D) representations of the target RNA
CC   with members of the virtual library of compounds to generate a hierarchy
CC   of the compounds ranked in accordance with their respective ability to
CC   form physical interactions with the molecular interaction site. The
CC   method also describes (1) RNA comprising a joined sequence of at least 24
CC   nucleotides but not more than 70 nucleotides and having secondary
CC   structure defined by: (a) 3 nucleotides forming a first side of a first
CC   double stranded (ds) region; (b) 2 nucleotides forming a first side of an
CC   internal loop region; (c) 4 nucleotides forming a first side of a second
CC   ds region; (d) 4 or 5 nucleotides forming an end loop region; (e) 4
CC   nucleotides forming a second side of the second ds region; (f) 4
CC   nucleotides forming a second side of the internal loop region; and (g) 3
CC   nucleotides forming a second side of the first ds region; (2) a purified
CC   and isolated RNA fragment comprising the human sequence
CC   UUUACAACAUAAUCUAGUUUACAGAAAAAUC (II). The methods and products can be
CC   used for identifying agents which modulate the activity of biomolecules,
CC   particularly RNA. Such agents can be used as pharmaceutical, agricultural
CC   or industrial compounds
XX
SQ   Sequence 29 BP; 22 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 29;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTTAACTTTGAAA 2196
              |||||||||||||||||| | ||  | |
Db         29 TTTTTTTTTTTTTTTTTTCAGTTCTACA 2

RESULT 555
AAQ85070
ID   AAQ85070 standard; DNA; 29 BP.
XX
AC   AAQ85070;
XX
DT   25-MAR-2003  (revised)
DT   28-SEP-1995  (first entry)
XX
DE   Oligonucleotide clamp.
XX
KW   Oligonucleotide clamp; diagnosis; therapeutic agents; herpes virus;
KW   cytomegalovirus; human papilloma virus; HIV; oncogenes;
KW   bromoacetylamidated; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "covalently bound cholesterol group"
FT   misc_feature    15. .16
FT                   /*tag=  b
FT                   /note= "linkage or monomer containing a bromoacetylamino
FT                   functionality"
FT   modified_base   29
FT                   /*tag=  c
FT                   /note= "covalently bound cholesterol group"
XX
PN   WO9501456-A1.
XX
PD   12-JAN-1995.
XX
PF   01-JUL-1994;   94WO-US007541.
XX
PR   02-JUL-1993;   93US-00087387.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM,  Lloyd DH;
XX
DR   WPI; 1995-061019/08.
XX
PT   New oligo:nucleotide clamps that stably bind to target polynucleotide(s)
PT   - may be used in diagnosis and therapy to inhibit genes or mRNA of, e.g.,
PT   herpes:virus, HIV, oncogene(s), etc.
XX
PS   Example 10; Page 28; 44pp; English.
XX
CC   The oligonucleotide clamps AAQ85069 and AAQ85070 are specific for a ss,
CC   or ds target nucleotide. When bound to the target sequence the two
CC   oligonucleotides form a stable non-covalent link, clamping the target
CC   sequence. This technique may be used to inhibit the expression, or
CC   function of an exogenous gene in a host (pref. human). The gene may be
CC   from herpes virus, cytomegalovirus, human papilloma virus, HIV or an
CC   oncogene. Therefore the clamps may be used in the treatment and diagnosis
CC   of human viral diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 29 BP; 2 A; 3 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 29;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTT 2178
              ||  |||||||| |  |||||||||||
Db          2 TTTTTTTTTTCACACTTTTTTTTTTT 29

RESULT 556
AAQ83933
ID   AAQ83933 standard; DNA; 29 BP.
XX
AC   AAQ83933;
XX
DT   25-MAR-2003  (revised)
DT   04-OCT-1995  (first entry)
XX
DE   Oligonucleotide clamp containing free amines in the hinge region.
XX
KW   HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Modified with cholesterol"
FT   modified_base   15. .16
FT                   /*tag=  b
FT                   /note= "C(pnp)A, pnp = a linkage or monomer containing a
FT                   bromoacetylamino functionality, and p = phosphodiester
FT                   linkage"
FT   modified_base   29
FT                   /*tag=  c
FT                   /note= "Modified with cholesterol"
XX
PN   WO9501365-A1.
XX
PD   12-JAN-1995.
XX
PF   05-JUL-1994;   94WO-US007557.
XX
PR   02-JUL-1993;   93US-00087386.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM;
XX
DR   WPI; 1995-060944/08.
XX
PT   Synthesis of branched polymers and novel branched polymeric structures -
PT   used as molecular probes esp. for detecting poly-nucleotide(s).
XX
PS   Example 5; Page 31; 52pp; English.
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```
XX
CC   This sequence represents an oligonucleotide clamp which was used to bind
CC   a target sequence comprising a segment of the HIV pol and nef genes in
CC   single stranded or double stranded forms. An oligonucleotide clamp is a
CC   compound capable of forming a covalently closed macromolecule or a stable
CC   circular complex after specifically binding to the target polynucleotide.
CC   The hinge region of this molecule comprises free amines. Oligonucleotide
CC   clamps generally comprise one or more oligonucleotide moieties capable of
CC   specific binding to the target molecule and one or more pairs of binding
CC   moieties covalently linked to the oligonucleotide moieties. Upon
CC   annealing of the oligonucleotides moieties to the target polynucleotide,
CC   the binding moieties of a pair are bought into juxtaposition so that they
CC   form a stable covalent or non-covalent linkage or complex. The
CC   interaction of the binding moieties effectively clamps the specifically
CC   annealed oligonucleotide moieties to the target polynucleotide. (Updated
CC   on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 29 BP; 2 A; 3 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 29;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2151 TTGATTTTTTTCTCCTTTTTTTTTTTTT 2178
                ||  |||||||| |  ||||||||||||
Db          2 TTTTTTTTTTTCACACTTTTTTTTTTT 29


RESULT 557
ACD18468/c
ID   ACD18468 standard; DNA; 29 BP.
XX
AC   ACD18468;
XX
DT   25-AUG-2003  (first entry)
XX
DE   Human zinc finger binding motif DNA #17.
XX
KW   Composite binding polypeptide; zinc finger nucleic acid binding domain;
KW   autoimmune disorder; immunosuppressive; zinc finger binding motif; human;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200299084-A2.
XX
PD   12-DEC-2002.
XX
PF   04-APR-2002; 2002WO-US022272.
XX
PR   04-APR-2001; 2001GB-00008491.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Moore M,  Sepp A,  Isalan M,  Choo Y;
XX
DR   WPI; 2003-278214/27.
XX
PT   New composite binding zinc finger polypeptide, useful for designing
PT   sequence-specific binding proteins regulating gene expression in the
PT   fields of molecular biology, and for the diagnosis and treatment of
PT   autoimmune disorders.
XX
PS   Example 4; Page 121; 157pp; English.
XX
CC   The invention relates to a composite binding polypeptide comprising a
CC   first natural binding domain derived from a first natural binding
CC   polypeptide and a second natural binding domain derived from a second
CC   natural binding polypeptide, where the first and second natural binding
CC   polypeptides may be the same or different and where the polypeptide binds
CC   to a target differing from the natural target of both the first and
CC   second binding polypeptides. The invention also relates to a chimeric
CC   polypeptide comprising a binding polypeptide cited above and a biological
CC   effector domain, a library of natural binding domains, a library of
CC   natural zinc finger nucleic acid binding domains comprising a linker
CC   attached to it, a method for selecting a binding polypeptide capable of
CC   binding to a target site and a method for designing a composite binding
CC   polypeptide. The methods and compositions of the present invention are
CC   useful for designing sequence-specific binding proteins for regulation of
CC   gene expression in the fields of molecular biology. They can also be used
CC   for the diagnosis and treatment of autoimmune disorders, and as research
CC   tools and in transgenic animals. This sequence represents human zinc
CC   finger binding motif DNA used in the scope of the invention
XX
SQ   Sequence 29 BP; 23 A; 4 C; 2 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 29;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTT 2182
                |||||||  ||| ||  ||||||||||
Db         28 TTTTTTTTGCCTGTTGGTTTTTTTTTT 1


RESULT 558
ACD18467
ID   ACD18467 standard; DNA; 29 BP.
XX
AC   ACD18467;
XX
DT   25-AUG-2003  (first entry)
XX
DE   Human zinc finger binding motif DNA #16.
XX
KW   Composite binding polypeptide; zinc finger nucleic acid binding domain;
KW   autoimmune disorder; immunosuppressive; zinc finger binding motif; human;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200299084-A2.
XX
PD   12-DEC-2002.
XX
PF   04-APR-2002; 2002WO-US022272.
XX
PR   04-APR-2001; 2001GB-00008491.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Moore M,  Sepp A,  Isalan M,  Choo Y;
XX
DR   WPI; 2003-278214/27.
XX
PT   New composite binding zinc finger polypeptide, useful for designing
PT   sequence-specific binding proteins regulating gene expression in the
PT   fields of molecular biology, and for the diagnosis and treatment of
PT   autoimmune disorders.
XX
PS   Example 4; Page 121; 157pp; English.
XX
CC   The invention relates to a composite binding polypeptide comprising a
CC   first natural binding domain derived from a first natural binding
CC   polypeptide and a second natural binding domain derived from a second
CC   natural binding polypeptide, where the first and second natural binding
CC   polypeptides may be the same or different and where the polypeptide binds
CC   to a target differing from the natural target of both the first and
CC   second binding polypeptides. The invention also relates to a chimeric
CC   polypeptide comprising a binding polypeptide cited above and a biological
CC   effector domain, a library of natural binding domains, a library of
CC   natural zinc finger nucleic acid binding domains comprising a linker
CC   attached to it, a method for selecting a binding polypeptide capable of
CC   binding to a target site and a method for designing a composite binding
CC   polypeptide. The methods and compositions of the present invention are
CC   useful for designing sequence-specific binding proteins for regulation of
```

```
CC   gene expression in the fields of molecular biology. They can also be used
CC   for the diagnosis and treatment of autoimmune disorders, and as research
CC   tools and in transgenic animals. This sequence represents human zinc
CC   finger binding motif DNA used in the scope of the invention
XX
SQ   Sequence 29 BP; 0 A; 2 C; 4 G; 23 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 29;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2155 TTTTTTTCTCCTTTTTTTTTTTTTTTT 2182
              |||||||  |||  ||  ||||||||||
Db          2 TTTTTTTTGCCTGTTGGTTTTTTTTTTT 29


RESULT 559
ABL56892
ID   ABL56892 standard; DNA; 30 BP.
XX
AC   ABL56892;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly e.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||||  |||||||||
Db          2 TATATATTTTTTTTTTTGTTTTTTTT 29


RESULT 560
ABL56896
ID   ABL56896 standard; DNA; 30 BP.
XX
AC   ABL56896;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly i.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
```

```
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTCTTTTTTTTT 29


RESULT 561
ABL56890
ID   ABL56890 standard; DNA; 30 BP.
XX
AC   ABL56890;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly c.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTTT 29


RESULT 562
ABL56891
ID   ABL56891 standard; DNA; 30 BP.
XX
AC   ABL56891;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly d.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
```

```
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTT 29


RESULT 563
ABL56897
ID   ABL56897 standard; DNA; 30 BP.
XX
AC   ABL56897;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly j.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| ||||||||||
Db          2 TATATATTTTTTTTTTGTTTTTTTTT 29


RESULT 564
ABL56889
ID   ABL56889 standard; DNA; 30 BP.
XX
AC   ABL56889;
XX
DT   26-JUL-2002  (first entry)
XX
DE   Synthetic deoxyribooligonucleotide poly b.
XX
KW   Concentration; quantification; mutation detection; polymorphic;
KW   polymerase chain reaction; PCR; ss.
XX
OS   Synthetic.
XX
PN   EP1046717-A2.
XX
PD   25-OCT-2000.
XX
PF   20-APR-2000; 2000EP-00108643.
XX
PR   20-APR-1999;   99JP-00111601.
XX
PA   (NIBI-) JAPAN BIOINDUSTRY ASSOC.
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Kurata S,  Yamada K,  Yokomaku T;
PI   Koyama O,  Furusho K;
XX
DR   WPI; 2000-657765/64.
XX
PT   Determining the concentration of a target nucleic acid, useful e.g. for
PT   detecting genetic mutations, comprises using a fluorescently labeled
PT   probe in which emission is reduced by binding to the target nucleic acid.
XX
PS   Example 5; Page 21; 55pp; English.
XX
CC   The invention relates to the determination of the concentration of a
CC   nucleic acid target, using a fluorescently labeled probe which produces
CC   reduced fluorescence emission when hybridised to the target nucleic acid.
CC   The method comprises measuring the reduction in emission caused by
CC   hybridisation. The new method is particularly used to quantify target
CC   nucleic acids by a real-time polymerase chain reaction, e.g. for
CC   quantifying microbial cells in co-cultures or symbiotic systems, for
CC   detecting gene mutations or polymorphisms, and for analysing melting
CC   curves of target nucleic acids to determine a Tm value. Methods of the
CC   invention allow target nucleic acids to be quantified quickly, easily and
CC   accurately. Particularly there is no need to remove unbound probe, and no
CC   materials are introduced that inhibit amplification by Taq polymerase (so
CC   conventional PCR conditions can be used). The specificity of PCR is kept
CC   high (amplification of primer dimers is delayed), and the limit of
CC   quantitation is reduced. Complex probes are not needed, and amplification
CC   can be monitored in real time. The working graph for data analysis
CC   (automatically generated by a computer) has a higher correlation
CC   coefficient than conventional graphs so more accurate quantitation is
CC   possible. The current sequence represents a synthetic
CC   deoxyribooligonucleotide that was used for investigating the base
CC   selectivity of a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
```

```
                    | | |  |||||||| ||||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTTTT 29


RESULT 565
ABA97613
ID   ABA97613 standard; DNA; 30 BP.
XX
AC   ABA97613;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly b nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                | | |  |||||||| ||||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTTTT 29


RESULT 566
ABA97620
ID   ABA97620 standard; DNA; 30 BP.
XX
AC   ABA97620;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly i nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
                | | |  |||||||| ||||||||||||
Db          2 TATATATTTTTTTTTTCTTTTTTTTTT 29


RESULT 567
ABA97614
ID   ABA97614 standard; DNA; 30 BP.
XX
AC   ABA97614;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly c nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
```

```
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  ||||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 568
ABA97615
ID   ABA97615 standard; DNA; 30 BP.
XX
AC   ABA97615;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly d nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  ||||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 569
ABA97616
ID   ABA97616 standard; DNA; 30 BP.
XX
AC   ABA97616;
XX
DT   11-APR-2002  (first entry)
XX
DE   Poly e nucleotide sequence.
XX
KW   ss; fluorochrome; nucleic acid probe; fluorescence.
XX
OS   Unidentified.
XX
PN   JP2001286300-A.
XX
PD   16-OCT-2001.
XX
PF   20-APR-2000; 2000JP-00120097.
XX
PR   20-APR-1999;   99JP-00111601.
PR   24-AUG-1999;   99JP-00236666.
PR   30-AUG-1999;   99JP-00242693.
PR   01-FEB-2000; 2000JP-00028896.
XX
PA   (BIOI-) BIOINDUSTRY KYOKAI SH.
PA   (KANK-) KANKYO ENG KK.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2002-134193/18.
XX
PT   Measurement of nucleic acids, using a nucleic acid probe and analysis of
PT   the obtained data.
XX
PS   Example 5; Page 17; 34pp; Japanese.
XX
CC   This invention relates to a method for measuring nucleic acids using a
CC   nucleic acid probe labelled with a fluorochrome. The nucleic acid probe
CC   decreases the fluorescence of the fluorochrome when hybridised with a
CC   target nucleic acid, the decrease in the fluorescence is measured. The
CC   method can be used for measuring a target nucleic acid
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  ||||||||| ||||||||||
Db          2 TATATATTTTTTTTTGTTTTTTTTTT 29


RESULT 570
ABL95886
ID   ABL95886 standard; DNA; 30 BP.
XX
AC   ABL95886;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly b for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
```

PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
| | | |||||||| ||||||||||||
Db 2 TATATATTTTTTTTTGTTTTTTTTTTT 29

RESULT 571
ABL95887
ID ABL95887 standard; DNA; 30 BP.
XX
AC ABL95887;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly c for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2159 TTTCTCCTTTTTTTTTTTTTTTTTTTT 2186
| | | |||||||| ||||||||||||
Db 2 TATATATTTTTTTTTGTTTTTTTTTTT 29

RESULT 572
ABL95894
ID ABL95894 standard; DNA; 30 BP.
XX
AC ABL95894;
XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly j for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the

```
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTCTTTTTTTT 29


RESULT 573
ABL95888
ID   ABL95888 standard; DNA; 30 BP.
XX
AC   ABL95888;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly d for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTGTTTTTTTT 29


RESULT 574
ABL95889
ID   ABL95889 standard; DNA; 30 BP.
XX
AC   ABL95889;
XX
DT   19-JUN-2002  (first entry)
XX
DE   Probe poly e for assaying nucleic acids.
XX
KW   Probe; polymorphism detection; mutation detection; disease diagnosis;
KW   microbial identification; ss.
XX
OS   Unidentified.
XX
PN   WO200208414-A1.
XX
PD   31-JAN-2002.
XX
PF   27-JUN-2001; 2001WO-IB001147.
XX
PR   27-JUN-2000; 2000JP-00193133.
PR   03-AUG-2000; 2000JP-00236115.
PR   26-SEP-2000; 2000JP-00292483.
XX
PA   (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA   (KANK-) KANKYO ENG CO LTD.
XX
PI   Kurane R,  Kanagawa T,  Kamagata Y,  Torimura M,  Kurata S,  Yamada K;
PI   Yokomaku T;
XX
DR   WPI; 2002-195876/25.
XX
PT   Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT   their polymorphism and mutation, particularly useful in science and
PT   medicine for e.g. analytical applications, disease diagnosis and
PT   microbial identification.
XX
PS   Example 12; Page 60; 152pp; Japanese.
XX
CC   The present invention relates to nucleic acid probes, which are useful
CC   for assaying nucleic acids by hybridising with a target nucleic acid, in
CC   which a single-stranded oligonucleotide is labelled with a fluorescent
CC   substance and a quencher in a manner that the fluorescence intensity of
CC   the hybridisation reaction system is increased after completion of the
CC   hybridisation but no stem loop structure is formed. The probes are useful
CC   for assaying nucleic acids and their polymorphism and mutation,
CC   particularly useful for e.g. analytical applications, disease diagnosis
CC   and microbial identification. The present sequence was used to illustrate
CC   the invention
XX
SQ   Sequence 30 BP; 4 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   82.1%;  Pred. No. 1.1e+03;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
              | | |  |||||||||| |||||||||
Db          2 TATATATTTTTTTTTTTGTTTTTTTT 29


RESULT 575
ABL95893
ID   ABL95893 standard; DNA; 30 BP.
XX
AC   ABL95893;
```

XX
DT 19-JUN-2002 (first entry)
XX
DE Probe poly I for assaying nucleic acids.
XX
KW Probe; polymorphism detection; mutation detection; disease diagnosis;
KW microbial identification; ss.
XX
OS Unidentified.
XX
PN WO200208414-A1.
XX
PD 31-JAN-2002.
XX
PF 27-JUN-2001; 2001WO-IB001147.
XX
PR 27-JUN-2000; 2000JP-00193133.
PR 03-AUG-2000; 2000JP-00236115.
PR 26-SEP-2000; 2000JP-00292483.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (KANK-) KANKYO ENG CO LTD.
XX
PI Kurane R, Kanagawa T, Kamagata Y, Torimura M, Kurata S, Yamada K;
PI Yokomaku T;
XX
DR WPI; 2002-195876/25.
XX
PT Fluorescently-labeled nucleic acid probes for assaying nucleic acids and
PT their polymorphism and mutation, particularly useful in science and
PT medicine for e.g. analytical applications, disease diagnosis and
PT microbial identification.
XX
PS Example 12; Page 60; 152pp; Japanese.
XX
CC The present invention relates to nucleic acid probes, which are useful
CC for assaying nucleic acids by hybridising with a target nucleic acid, in
CC which a single-stranded oligonucleotide is labelled with a fluorescent
CC substance and a quencher in a manner that the fluorescence intensity of
CC the hybridisation reaction system is increased after completion of the
CC hybridisation but no stem loop structure is formed. The probes are useful
CC for assaying nucleic acids and their polymorphism and mutation,
CC particularly useful for e.g. analytical applications, disease diagnosis
CC and microbial identification. The present sequence was used to illustrate
CC the invention
XX
SQ Sequence 30 BP; 4 A; 1 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 0.7%; Score 20; DB 1; Length 30;
Best Local Similarity 82.1%; Pred. No. 1.1e+03;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2159 TTTCTCCTTTTTTTTTTTTTTTTTTT 2186
Db 2 TATATATTTTTTTTTTCTTTTTTTTT 29

RESULT 576
ADA14837
ID ADA14837 standard; DNA; 30 BP.
XX
AC ADA14837;
XX
DT 06-NOV-2003 (first entry)
XX
DE Hairpin oligonucleotide, #2, used in an example of the invention.
XX
KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW rhodamine B-labelled dye; detection; gold support; ss.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= thiol group"
FT misc_binding 6. .25
FT /*tag= b
FT /bound_moiety= "Target sequence #2"
FT /note= "Forms a doube-stranded region with the target
FT sequence shown in examples 3, 4 and 5"
FT modified_base 30
FT /*tag= c
FT /mod_base= OTHER
FT /note= "OTHER= amino group"
XX
PN US2003013109-A1.
XX
PD 16-JAN-2003.
XX
PF 21-JUN-2002; 2002US-00176055.
XX
PR 21-JUN-2001; 2001US-0299460P.
XX
PA (BALL/) BALLINGER C T.
PA (LOCA/) LOCASCIO M.
PA (LAND/) LANDRY D P.
XX
PI Ballinger CT, Locascio M, Landry DP;
XX
DR WPI; 2003-596312/56.
XX
PT Hairpin sensor useful for detecting a target nucleotide sequence in a
PT sample, comprises a hairpin loop assembly including a complementary probe
PT and a quenchable fluorescing agent.
XX
PS Example 3; Page 11; 16pp; English.
XX
CC The invention discloses a hairpin sensor comprising a hairpin loop
CC assembly including a complementary probe positioned between a first
CC inverse repeat arm and a second inverse repeat arm, and a quenchable
CC fluorescing agent joined, directly or indirectly, to the end of the
CC second inverse repeat arm of the hairpin loop assembly opposite the
CC complementary probe. Also claimed is a microarray comprising the hairpin
CC sensor, where the end of the first inverse repeat arm opposite the
CC complementary probe is bound, directly or indirectly, to a support, a kit
CC for detecting a target nucleotide sequence in a sample comprising the
CC hairpin sensor, and a support, and a hairpin sensor system, in which the
CC particle is conductive or semi-conductive, including at least one of the
CC above hairpin sensor assemblies. The hairpin sensor further comprises a
CC functional group joined to the end of the first inverse repeat arm
CC opposite the complementary probe, or first spacer opposite the first
CC inverse repeat arm, the functional group selected from amino, carboxyl,
CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC between the second inverse repeat arm and the quenchable fluorescing
CC agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC second spacer is positioned between the second inverse repeat arm and the
CC quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC or rhodamine B-labelled dye. Within the microarray the support is capable
CC of accepting a charge. At least one hairpin sensor comprises two or more
CC hairpin sensors. The two or more hairpin sensors include complementary
CC probes that are the same or different and respective quenchable
CC fluorescing agents that are the same or different. The two or more
CC hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC and system are useful for detecting a target nucleotide sequence in a
CC sample. Further, the method involves identifying the target nucleotide
CC sequence by the location of the complementary probe to which the target
CC nucleotide sequence binds. The two or more hairpin sensors include
CC complementary probes or quenchable fluorescing agents, that are
CC different. The sequence presented is the hairpin oligonucleotide, #2,
CC used in an example of the invention.
XX
SQ Sequence 30 BP; 1 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2185
              ||||||||||||||||||||
Db          6 TTTTTTTTTTTTTTTTTTTT 25


RESULT 577
ADA14837/c
ID   ADA14837 standard; DNA; 30 BP.
XX
AC   ADA14837;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Hairpin oligonucleotide, #2, used in an example of the invention.
XX
KW   Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;
KW   quenchable fluorescing agent; microarray; semiconductor; nanocrystal;
KW   rhodamine B-labelled dye; detection; gold support; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= thiol group"
FT   misc_binding    6. .25
FT                   /*tag=  b
FT                   /bound_moiety= "Target sequence #2"
FT                   /note= "Forms a doube-stranded region with the target
FT                   sequence shown in examples 3, 4 and 5"
FT   modified_base   30
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= amino group"
XX
PN   US2003013109-A1.
XX
PD   16-JAN-2003.
XX
PF   21-JUN-2002; 2002US-00176055.
XX
PR   21-JUN-2001; 2001US-0299460P.
XX
PA   (BALL/) BALLINGER C T.
PA   (LOCA/) LOCASCIO M.
PA   (LAND/) LANDRY D P.
XX
PI   Ballinger CT,  Locascio M,  Landry DP;
XX
DR   WPI; 2003-596312/56.
XX
PT   Hairpin sensor useful for detecting a target nucleotide sequence in a
PT   sample, comprises a hairpin loop assembly including a complementary probe
PT   and a quenchable fluorescing agent.
XX
PS   Example 3; Page 11; 16pp; English.
XX
CC   The invention discloses a hairpin sensor comprising a hairpin loop
CC   assembly including a complementary probe positioned between a first
CC   inverse repeat arm and a second inverse repeat arm, and a quenchable
CC   fluorescing agent joined, directly or indirectly, to the end of the
CC   second inverse repeat arm of the hairpin loop assembly opposite the
CC   complementary probe. Also claimed is a microarray comprising the hairpin
CC   sensor, where the end of the first inverse repeat arm opposite the
CC   complementary probe is bound, directly or indirectly, to a support, a kit
CC   for detecting a target nucleotide sequence in a sample comprising the
CC   hairpin sensor, and a support, and a hairpin sensor system, in which the
CC   particle is conductive or semi-conductive, including at least one of the
CC   above hairpin sensor assemblies. The hairpin sensor further comprises a
CC   functional group joined to the end of the first inverse repeat arm
CC   opposite the complementary probe, or first spacer opposite the first
CC   inverse repeat arm, the functional group selected from amino, carboxyl,
CC   thiol and hydroxyl. Further, the sensor comprises a ligand positioned
CC   between the second inverse repeat arm and the quenchable fluorescing
CC   agent, where the ligand is selected from mercapto, hydroxyl, amino,
CC   nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The
CC   second spacer is positioned between the second inverse repeat arm and the
CC   quenchable fluorescing agent which comprises a semiconductor nanocrystal
CC   or rhodamine B-labelled dye. Within the microarray the support is capable
CC   of accepting a charge. At least one hairpin sensor comprises two or more
CC   hairpin sensors. The two or more hairpin sensors include complementary
CC   probes that are the same or different and respective quenchable
CC   fluorescing agents that are the same or different. The two or more
CC   hairpin sensors are arranged in a spatially-defined pattern. The sensor
CC   and system are useful for detecting a target nucleotide sequence in a
CC   sample. Further, the method involves identifying the target nucleotide
CC   sequence by the location of the complementary probe to which the target
CC   nucleotide sequence binds. The two or more hairpin sensors include
CC   complementary probes or quenchable fluorescing agents, that are
CC   different. The sequence presented is the hairpin oligonucleotide, #2,
CC   used in an example of the invention.
XX
SQ   Sequence 30 BP; 1 A; 4 C; 4 G; 21 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       2785 GAAAAAAAAAAAAAAAAAAA 2804
              ||||||||||||||||||||
Db         26 GAAAAAAAAAAAAAAAAAAA 7


RESULT 578
AAV09273
ID   AAV09273 standard; cDNA; 44 BP.
XX
AC   AAV09273;
XX
DT   07-JUL-1998  (first entry)
XX
DE   Nucleotide sequence of the 3' portion of the BG513_19 protein.
XX
KW   BG513_19 protein; human adult brain cDNA library; nutritional activity;
KW   cytokine activity; cell proliferation/differentiation activity; homology;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO9748801-A2.
XX
PD   24-DEC-1997.
XX
PF   16-JUN-1997;   97WO-US010501.
XX
PR   17-JUN-1996;   96US-00664596.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Jacobs K,  Mccoy JM,  Lavallie ER,  Racie LA,  Merberg D,  Treacy M;
PI   Evans C,  Spaulding V,  Bowman M;
XX
DR   WPI; 1998-063142/06.
XX
PT   Poly:nucleotide(s) and proteins obtained from human PBMC, dendritic cell,
PT   adult brain, foetal brain and adult testes cDNA libraries - used in
PT   research, detection and therapy of, e.g. cytokine and cell proliferation
PT   or differentiation.
XX
PS   Claim 19; Page 51; 78pp; English.
```

```
XX
CC   This nucleotide sequence encodes the 3' portion of the BG513_19 protein
CC   which was isolated from a human adult brain cDNA library. The products of
CC   the polynucleotides of the invention can be used in research, detection
CC   and therapy, as they may have nutritional activity, cytokine and cell
CC   proliferation/differentiation activity. A search against the Genbank
CC   database demonstrated that this sequence has no homology with known
CC   sequences
XX
SQ   Sequence 44 BP; 44 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 20;  DB 1;  Length 44;
  Best Local Similarity   65.9%;  Pred. No. 2.2e+03;
  Matches   29;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       2761 AATAAAAGTATTCTTGTTAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              || ||||  |        | ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 44


RESULT 579
ABV77669/c
ID   ABV77669 standard; DNA; 24 BP.
XX
AC   ABV77669;
XX
DT   03-FEB-2003  (first entry)
XX
DE   Human zinc finger protein 9.79 PCR primer #1.
XX
KW   Human; zinc finger protein 9.79; cancer; HIV infection; cytostatic;
KW   anti-HIV; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   CN1343710-A.
XX
PD   10-APR-2002.
XX
PF   19-SEP-2000; 2000CN-00125246.
XX
PR   19-SEP-2000; 2000CN-00125246.
XX
PA   (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-548879/59.
XX
PT   A novel human zinc finger protein 9.79 polypeptide, useful for treating
PT   several diseases e.g. cancer and HIV infection.
XX
PS   Example 2; Page 16 (Disclosure); 31pp; Chinese.
XX
CC   The present invention relates to human zinc finger protein 9.79 (see
CC   ABP59011). The zinc finger protein is useful for treating several
CC   diseases e.g. cancer and HIV infection. The present sequence is a PCR
CC   primer, which was used in an example from the invention
XX
SQ   Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 24;
  Best Local Similarity   91.3%;  Pred. No. 7.2e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
              | |||||||||||||||||||| |
Db         24 AATGAAAAAAAAAAAAAAAAAGA 2


RESULT 580
AAD26900
ID   AAD26900 standard; DNA; 25 BP.
XX
AC   AAD26900;
XX
DT   09-APR-2002  (first entry)
XX
DE   Bacterial PNP DNA fragment with an in-frame polyA tract.
XX
KW   Hypermutable organism; dominant negative allele; mismatch repair gene;
KW   spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
KW   bacteria; ss.
XX
OS   Bacteria.
OS   Unidentified.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .5
FT                   /*tag=  a
FT                   /note= "Bacterial PNP gene"
FT   misc_feature    6. .25
FT                   /*tag=  a
FT                   /note= "In-frame polyA tract"
XX
PN   WO200188192-A2.
XX
PD   22-NOV-2001.
XX
PF   14-MAY-2001; 2001WO-US015376.
XX
PR   17-MAY-2000; 2000US-0204769P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (MORP-) MORPHOTEK INC.
PA   (NICO/) NICOLAIDES N C.
PA   (SASS/) SASS P M.
PA   (GRAS/) GRASSO L.
PA   (VOGE/) VOGELSTEIN B.
PA   (KINZ/) KINZLER K W.
XX
PI   Nicolaides NC,  Sass PM,  Grasso L,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2002-083004/11.
XX
PT   Generating mutation in gene using cells which contain defective mismatch
PT   repair gene, useful to generate genetically altered mutations with new
PT   output traits.
XX
PS   Example 5; Fig 7; 59pp; English.
XX
CC   The patent discloses a method for generating hypermutable organisms.
CC   Dominant negative alleles of human mismatch repair genes can be used to
CC   generate hypermutable cells and organisms. They increase the rate of
CC   spontaneous mutations by reducing the effectiveness of DNA repair and
CC   thereby render the cells or animals hypermutable. The method is used to
CC   produce genetically altered organisms to produce new output traits. The
CC   present sequence is a bacterial poly purine nucleotide phosphorylase
CC   (polyPNP) DNA fragment containing an in-frame polyA tract. This sequence
CC   is used in the exemplification of the invention
XX
SQ   Sequence 25 BP; 21 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 25;
  Best Local Similarity   91.3%;  Pred. No. 8e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
              || | ||||||||||||||||||
Db          1 ATGGCAAAAAAAAAAAAAAAAAA 23


RESULT 581
AAC96419
ID   AAC96419 standard; DNA; 25 BP.
```

```
XX
AC   AAC96419;
XX
DT   26-FEB-2001  (first entry)
XX
DE   HLA DQA1 gene PCR primer #21.
XX
KW   DNA sequence analysis; sequencing; protein sequence; protein structure;
KW   gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
KW   human leukocyte antigen; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200065088-A2.
XX
PD   02-NOV-2000.
XX
PF   20-APR-2000; 2000WO-EP003636.
XX
PR   26-APR-1999;   99EP-00303215.
XX
PA   (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI   Ulfendahl P,  Wong K;
XX
DR   WPI; 2000-679677/66.
XX
PT   Identifying extendible primers for use in identification, or
PT   classification of a nucleic acid of an organism, allele or gene such as
PT   class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT   specific length.
XX
PS   Claim 14; Page 51; 66pp; English.
XX
CC   The present invention provides a method for identifying a set of
CC   extendible primers which can be used in the identification, typing and
CC   classification of genes. This can then be used to predict protein
CC   sequence and structure, in organ donation to match the organ with the
CC   receiver, and to identify bacteria in a sample. The method can be used to
CC   type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
CC   particular
XX
SQ   Sequence 25 BP; 3 A; 2 C; 2 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 25;
  Best Local Similarity   91.3%;  Pred. No. 8e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2172 TTTTTTTTTTTTTTTAACTTTGA 2194
             |||||||||||||||  |||||
Db          1 TTTTTTTTTTTTTTTAGATTTGA 23


RESULT 582
AAD26899
ID   AAD26899 standard; DNA; 26 BP.
XX
AC   AAD26899;
XX
DT   09-APR-2002  (first entry)
XX
DE   Bacterial PNP DNA fragment with an out-of-frame polyA tract.
XX
KW   Hypermutable organism; dominant negative allele; mismatch repair gene;
KW   spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
KW   bacteria; ss.
XX
OS   Bacteria.
OS   Unidentified.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .5
FT                   /*tag=  a
FT                   /note= "Bacterial PNP gene"
FT   misc_feature    6. .26
FT                   /*tag=  a
FT                   /note= "Out-of-frame polyA tract"
XX
PN   WO200188192-A2.
XX
PD   22-NOV-2001.
XX
PF   14-MAY-2001; 2001WO-US015376.
XX
PR   17-MAY-2000; 2000US-0204769P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (MORP-) MORPHOTEK INC.
PA   (NICO/) NICOLAIDES N C.
PA   (SASS/) SASS P M.
PA   (GRAS/) GRASSO L.
PA   (VOGE/) VOGELSTEIN B.
PA   (KINZ/) KINZLER K W.
XX
PI   Nicolaides NC,  Sass PM,  Grasso L,  Vogelstein B,  Kinzler KW;
XX
DR   WPI; 2002-083004/11.
XX
PT   Generating mutation in gene using cells which contain defective mismatch
PT   repair gene, useful to generate genetically altered mutations with new
PT   output traits.
XX
PS   Example 5; Fig 7; 59pp; English.
XX
CC   The patent discloses a method for generating hypermutable organisms.
CC   Dominant negative alleles of human mismatch repair genes can be used to
CC   generate hypermutable cells and organisms. They increase the rate of
CC   spontaneous mutations by reducing the effectiveness of DNA repair and
CC   thereby render the cells or animals hypermutable. The method is used to
CC   produce genetically altered organisms to produce new output traits. The
CC   present sequence is a bacterial poly purine nucleotide phosphorylase
CC   (polyPNP) DNA fragment containing an out-of-frame polyA tract. This
CC   sequence is used in the exemplification of the invention
XX
SQ   Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 26;
  Best Local Similarity   91.3%;  Pred. No. 8.8e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAAA 2804
              || | ||||||||||||||||||
Db          1 ATGGCAAAAAAAAAAAAAAAAA 23


RESULT 583
AAD39650
ID   AAD39650 standard; DNA; 26 BP.
XX
AC   AAD39650;
XX
DT   22-OCT-2002  (first entry)
XX
DE   PolyPNP out-of-frame polyA tract DNA.
XX
KW   Dominant negative allele; mismatch repair gene; D-MMR; gene discovery;
KW   ITRE; inducible transcriptional regulatory element;
KW   recombinant gene mutagenesis; recombinant protein production;
KW   drug target discovery; ds.
XX
OS   Unidentified.
XX
PN   US2002055106-A1.
XX
PD   09-MAY-2002.
```

XX
PF 14-MAY-2001; 2001US-00853646.
XX
PR 12-MAY-2000; 2000US-0203905P.
PR 17-MAY-2000; 2000US-0204769P.
XX
PA (NICO/) NICOLAIDES N C.
PA (SASS/) SASS P M.
PA (GRAS/) GRASSO L.
PA (VOGE/) VOGELSTEIN B.
PA (KINZ/) KINZLER K W.
XX
PI Nicolaides NC, Sass PM, Grasso L, Vogelstein B, Kinzler KW;
XX
DR WPI; 2002-499469/53.
XX
PT Generating a mutation in a gene using a dominant negative allele of a
PT mismatch repair gene which results in mismatch repair deficiency in cells
PT containing the allele is useful in gene and drug target discovery and
PT recombinant technology.
XX
PS Example 5; Fig 7; 25pp; English.
XX
CC The invention relates to methods for generating a mutation in a gene of
CC interesting using a dominant negative allele of a mismatch repair gene (D
CC -MMR) under control of an inducible transcriptional regulatory element
CC (ITRE). The invention is useful to provide new cell lines that can be
CC used for gene discovery, drug target discovery, recombinant gene
CC mutagenesis or recombinant protein production. The present sequence is a
CC polyPNP (purine phosphorylase) out-of-frame polyA tract DNA
XX
SQ Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 8.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAAAAAAAAA 2804
|| | ||||||||||||||||||||
Db 1 ATGGCAAAAAAAAAAAAAAAAAA 23

RESULT 584
AAH43080/c
ID AAH43080 standard; DNA; 27 BP.
XX
AC AAH43080;
XX
DT 15-OCT-2001 (first entry)
XX
DE Nucleotide sequence of a synthetic oligonucleotide.
XX
KW Nucleic acid immobilisation; ss.
XX
OS Synthetic.
XX
PN WO200155365-A1.
XX
PD 02-AUG-2001.
XX
PF 24-JAN-2001; 2001WO-JP000443.
XX
PR 27-JAN-2000; 2000JP-00019301.
XX
PA (TOJO) TOYO KOHAN CO LTD.
XX
PI Tanga M, Okamura H, Takagi K, Takahashi K;
XX
DR WPI; 2001-488794/53.
XX
PT Support for immobilizing nucleotides.
XX
PS Example 1; Page 8; 18pp; Japanese.
XX
CC The specification describes a support for immobilizing nucleotides which
CC contributes to the efficient clarification of DNA without damaging the
CC terminal parts of the DNA. The support is a chemically treated modified
CC substrate on which oligonucleotides with restriction enzyme cleavage
CC sites are immobilised. The support is useful for immobilizing nucleic
CC acids such as DNA. The present sequence represents a synthetic
CC oligonucleotide used in the course of the invention
XX
SQ Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 9.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2168 TTTTTTTTTTTTTTTTTTAACT 2190
|||||||||||||||||||| || |
Db 23 TTTTTTTTTTTTTTTTTTGAATT 1

RESULT 585
ABQ79879/c
ID ABQ79879 standard; DNA; 27 BP.
XX
AC ABQ79879;
XX
DT 23-DEC-2002 (first entry)
XX
DE Nucleotide sequence of a PCR primer #9.
XX
KW Polymerase chain reaction; thermal cycle; immobilisation;
KW genetic engineering; PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2002191369-A.
XX
PD 09-JUL-2002.
XX
PF 27-DEC-2000; 2000JP-00399573.
XX
PR 27-DEC-2000; 2000JP-00399573.
XX
PA (TOJO) TOYO KOHAN CO LTD.
PA (TAKA/) TAKAHASHI K.
XX
DR WPI; 2002-630904/68.
XX
PT Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
PT a substrate on which a DNA is immobilized used in medical, biochemical,
PT molecular biological and gene engineering fields.
XX
PS Example; Page 10; 13pp; Japanese.
XX
CC The invention relates to performing a thermal cycle of PCR by using a
CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
CC method is useful in the medical, biochemical, molecular biological and
CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
CC used in the method of the invention
XX
SQ Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 9.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2168 TTTTTTTTTTTTTTTTTTAACT 2190
|||||||||||||||||||| || |
Db 23 TTTTTTTTTTTTTTTTTTGAATT 1

RESULT 586
ABX12469/c

```
ID   ABX12469 standard; DNA; 27 BP.
XX
AC   ABX12469;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Coxsackie B virus 4 (CBV-4) strain VD2921, PCR primer dT26V.
XX
KW   Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW   strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW   diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW   renal failure; leg amputation; PCR; primer; ss.
XX
OS   Coxsackievirus.
XX
PN   WO2002103060-A2.
XX
PD   27-DEC-2002.
XX
PF   19-JUN-2002; 2002WO-IB003278.
XX
PR   20-JUN-2001; 2001SE-00002198.
XX
PA   (INNO-) INNOVENTUS PROJECT AB.
XX
PI   Tuvemo HT,  Frisk GE,  Yin H;
XX
DR   WPI; 2003-278229/27.
XX
PT   Polymerase chain reaction and primers for detecting nucleic acids from
PT   the diabetogenic coxsackie B virus-4 strain VD2921.
XX
PS   Example 5; Page 44; 79pp; English.
XX
CC   The invention describes a polymerase chain reaction (PCR) and primers for
CC   detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC   strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC   P3C and P3D nucleic acids). The methods and primers are used for the
CC   detection of CBV-4 strain VD2921 which is associated with diabetes
CC   (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC   detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC   cells, can improve prognosis by allowing treatment e.g. with antiviral
CC   drugs, to prevent further loss of beta cells and severe long term
CC   consequences of diabetes including blindness, renal failure and leg
CC   amputations. This sequence represents a primer used to determine the
CC   genomic structure of diabetogenic coxsackie B virus 4 (CBV-4) strain
CC   VD2921
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 27;
  Best Local Similarity   81.5%;  Pred. No. 9.6e+02;
  Matches   22;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2804
             :| ||   ||||||||||||||||||
Db         27 BAAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 587
ADC75074/c
ID   ADC75074 standard; DNA; 27 BP.
XX
AC   ADC75074;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Biosensor related oligonucleotide of the invention SEQ ID NO:2.
XX
KW   ss; biosensor; hybridisation.
XX
OS   Synthetic.
XX
PN   JP2003172737-A.
XX
PD   20-JUN-2003.
XX
PF   07-DEC-2001; 2001JP-00374764.
XX
PR   07-DEC-2001; 2001JP-00374764.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
XX
DR   WPI; 2003-819164/77.
XX
PT   Solid support body comprising crystal resonator on which a surface
PT   treatment layer is formed, and a substrate whose surface treatment layer
PT   is chemically modified, useful as biosensor.
XX
PS   Disclosure; SEQ ID NO 2; 7pp; Japanese.
XX
CC   The invention relates to a novel solid support body comprising a crystal
CC   resonator on which a surface treatment layer is formed. The biosensor is
CC   useful for analysing biological samples e.g., gene, a protein, and a
CC   peptide, and for analysing bioactive substances. Preferably, the
CC   biosensor is useful for analysing base sequences by carrying out
CC   hybridisation. The present sequence is used in the exemplification of the
CC   invention.
XX
SQ   Sequence 27 BP; 20 A; 3 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 27;
  Best Local Similarity   91.3%;  Pred. No. 9.6e+02;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||||| || |
Db         23 TTTTTTTTTTTTTTTTTTGAATT 1


RESULT 588
ADC75075
ID   ADC75075 standard; DNA; 27 BP.
XX
AC   ADC75075;
XX
DT   01-JAN-2004  (first entry)
XX
DE   Biosensor related oligonucleotide of the invention SEQ ID NO:3.
XX
KW   ss; biosensor; hybridisation.
XX
OS   Synthetic.
XX
PN   JP2003172737-A.
XX
PD   20-JUN-2003.
XX
PF   07-DEC-2001; 2001JP-00374764.
XX
PR   07-DEC-2001; 2001JP-00374764.
XX
PA   (TOJO ) TOYO KOHAN CO LTD.
XX
DR   WPI; 2003-819164/77.
XX
PT   Solid support body comprising crystal resonator on which a surface
PT   treatment layer is formed, and a substrate whose surface treatment layer
PT   is chemically modified, useful as biosensor.
XX
PS   Disclosure; SEQ ID NO 3; 7pp; Japanese.
XX
CC   The invention relates to a novel solid support body comprising a crystal
CC   resonator on which a surface treatment layer is formed. The biosensor is
CC   useful for analysing biological samples e.g., gene, a protein, and a
CC   peptide, and for analysing bioactive substances. Preferably, the
```

CC biosensor is useful for analysing base sequences by carrying out
CC hybridisation. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 27 BP; 19 A; 3 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 9.6e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAAAAAAA 2803
|||| |||||||| |||||||||
Db 1 AATTCAAAAAAAATAAAAAAAAA 23

RESULT 589
AAA57856/c
ID AAA57856 standard; DNA; 28 BP.
XX
AC AAA57856;
XX
DT 11-OCT-2000 (first entry)
XX
DE Deoxy-T22-tagged substrate oligonucleotide.
XX
KW Ribozyme; catalytic RNA; analyte detection; effector molecule;
KW nucleic acid substrate; in vitro selection; ribozyme ligase;
KW conformation dependent activity; allosteric activation; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 23. .28
FT /*tag= a
FT misc_binding 24. .28
FT /*tag= b
FT /bound_moiety= "Bases 13-17 of N90 RNA pool (AAA57851)"
XX
PN WO200024931-A2.
XX
PD 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-IL000557.
XX
PR 23-OCT-1998; 98IL-00126731.
XX
PA (INTE-) INTELLIGENE LTD.
XX
PI Nathan A, Ellington A;
XX
DR WPI; 2000-350763/30.
XX
PT Detecting an analyte in a sample comprises providing nucleic acid
PT sequence which is catalytically active in presence of analyte, contacting
PT catalytic nucleic acid with substrate and amplifying catalytic product.
XX
PS Disclosure; Page; 36pp; English.
XX
CC The invention relates to a method of detecting an analyte in a sample.
CC The method comprises providing a nucleic acid sequence which is initially
CC catalytically inactive, but which becomes catalytically active in the
CC presence of an analyte (the effector); providing a nucleic acid substrate
CC for the catalytic activity of the nucleic acid sequence; and contacting
CC the nucleic acid sequence and the substrate with the sample under
CC conditions allowing catalytic activity of nucleic acid sequences. The
CC catalytic nucleic acid sequence will be able to convert the nucleic acid
CC substrate into a nucleic acid product only if the analyte of interest is
CC present. The nucleic acid catalytic product is then amplified, and a
CC significant increase in the amount of product indicates the presence of
CC the analyte in the sample. The method is useful for the qualitative or
CC quantitative determination of an analyte in a sample in diagnostic
CC assays. The invention describes the in vitro selection of a ribozyme
CC ligase (L1; AAA57859, AAA57860) which is catalytically active only in the
CC presence of an oligonucleotide effector (AAA57854). The L1 ribozyme
CC ligase was selected from a pool of RNA molecules comprising a central
CC randomised region 90 nucleotides in length flanked on both sides by
CC constant sequence regions (the N90 RNA pool; AAA57851). In the presence
CC of the effector, selection was performed using one of the tagged
CC substrate molecules AAA57855-A57857. RNAs with ligase activity (i.e.,
CC those which have become ligated to the substrate molecule) were reverse
CC transcribed using the effector oligo, and then PCR amplified using the
CC effector and a DNA primer identical in sequence to the substrate used for
CC the selection. A ribozyme ligase, L1, was selected via this procedure. L1
CC can only adopt its active conformation (AAA57859) in the presence of the
CC effector oligo (analyte). In the absence of the effector, L1 adopts an
CC inactive conformation (AAA57860). The present sequence represents the
CC deoxy-T22-tagged substrate oligonucleotide. The dT22 tag enables
CC successfully ligated products to be isolated using oligo(dA) cellulose
CC Type 7. Note: The present sequence is not given in the specification, but
CC is created from the inforamtion given on page 11
XX
SQ Sequence 28 BP; 1 A; 2 C; 1 G; 22 T; 2 U; 0 Other;

Query Match 0.7%; Score 19.8; DB 1; Length 28;
Best Local Similarity 91.3%; Pred. No. 1e+03;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2782 ATTGAAAAAAAAAAAAAAAAAAA 2804
| || ||||||||||||||||||
Db 28 AGTGCAAAAAAAAAAAAAAAAAA 6

RESULT 590
AAA90025
ID AAA90025 standard; DNA; 29 BP.
XX
AC AAA90025;
XX
DT 20-DEC-2000 (first entry)
XX
DE PCR primer for fatty acid binding protein (FABP) DNA amplification.
XX
KW Vaccine; Japanese schistosomiasis; fatty acid binding protein; FABP;
KW PCR primer; ss.
XX
OS Unidentified.
XX
PN CN1255548-A.
XX
PD 07-JUN-2000.
XX
PF 27-NOV-1998; 98CN-00122043.
XX
PR 27-NOV-1998; 98CN-00122043.
XX
PA (SHAN-) SHANGHAI DOMESTIC ANIMAL PARASITOSIS INS.
XX
PI Lin J, Wu X, Liu J;
XX
DR WPI; 2000-524988/48.
XX
PT Clone of Japanese schistosome fatty acid-binding protein gene and its
PT expression in Bombyx mori system.
XX
PS Claim 3; Page 1; 12pp; Chinese.
XX
CC The present invention relates to the preparation of a vaccine against
CC Japanese schistosomiasis. The vaccine comprises a gene encoding a fatty
CC acid binding protein (FABP). The FABP is expressed in a Bombyx mori
CC system as a fusion protein of 18kD. The fusion protein has an increased
CC immunogenicity and stronger anti-infective action than the wild-type
CC protein. The present sequence represents a PCR primer used to amplify DNA
CC encoding the FABP of the invention
XX
SQ Sequence 29 BP; 2 A; 4 C; 3 G; 20 T; 0 U; 0 Other;

```
  Query Match             0.7%;  Score 19.8;  DB 1;  Length 29;
  Best Local Similarity   91.3%;  Pred. No. 1.1e+03;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       2161 TCTCCTTTTTTTTTTTTTTTTT 2183
              ||  ||||||||||||||||||
Db             7 TCCGCTTTTTTTTTTTTTTTTT 29


RESULT 591
AAS17761/c
ID   AAS17761 standard; DNA; 31 BP.
XX
AC   AAS17761;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Oligo d(T) PCR primer.
XX
KW   Oligo d(T); ss; differential subtraction; PCR primer;
KW   double exponential elimination; tumour.
XX
OS   Synthetic.
XX
PN   US6316192-B1.
XX
PD   13-NOV-2001.
XX
PF   11-MAR-1999;   99US-00268505.
XX
PR   11-MAR-1999;   99US-00268505.
XX
PA   (LUOJ/) LUO J.
XX
PI   Luo J;
XX
DR   WPI; 2002-074371/10.
XX
PT   Selective elimination of non-targeted DNA sequences for rapid isolation
PT   and enrichment of the differences of DNA fragments between two pools of
PT   DNA, comprises converting testers to drivers.
XX
PS   Claim 6; Col 5; 23pp; English.
XX
CC   The invention comprises rapid isolation and enrichment of the differences
CC   of DNA fragments between two pools of DNA, comprises converting
CC   undesirable testers (DNA being subtracted) to drivers (DNA used to
CC   subtract) and re-utilising converted drivers in repeats of subtraction to
CC   achieve double exponential elimination of undesirable tester sequences.
CC   The method comprises (a) attaching a nucleic acid fragment to 1 or more
CC   polymerase chain reaction (PCR) adapters to form an adapter-attached
CC   nucleic acid fragment, followed by amplifying the adapter-attached
CC   nucleic acid fragment through PCR with primers containing nucleic acid
CC   sequences complementary to nucleic acid sequences of the adapter to form
CC   an adapter-attached nucleic acid tester, (b) mixing the adapter-attached
CC   nucleic acid tester with a nucleic acid driver that contains no attached
CC   adapter or contains an attached adapter whose sequence differs from the
CC   adapter, to form a nucleic acid mixture, (c) denaturing and re-annealing
CC   the tester/driver nucleic acid mixture, (d) adding to the nucleic acid
CC   mixture an effective amount of reagents necessary for removing the
CC   adapter sequence from the tester/ driver hetero-duplex and (e) repeating
CC   step (c) to (d) at least once (no amplification takes place and no
CC   additional driver is added). The method is used for rapid isolation and
CC   enrichment of the differences of DNA fragments between two pools of DNA
CC   e.g. in the search for tumour specific sequences. The method has 2
CC   improvements over the methods disclosed by Yang et al. (1996), Lisitsyn
CC   et al. (1993), Straus et al. (1990) by (i) bypassing the need of a
CC   polymerase chain reaction (PCR) amplification or physical separation of
CC   desirable testers from undesirable ones in each repeat of subtraction, it
CC   eliminates the necessity of tester dilution in each repeat of
CC   subtraction, and (ii) by utilising the convened driver from each repeat
CC   of subtraction, it eliminates the need for re-introducing additional
CC   driver into hybridisation in each repeat of subtraction. The present
CC   sequence is an Oligo D(T) PCR primer used in the method of the invention
XX
SQ   Sequence 31 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 1 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 31;
  Best Local Similarity   81.5%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              :| ||   ||||||||||||||||||
Db            31 BAAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 592
AAS09500/c
ID   AAS09500 standard; DNA; 32 BP.
XX
AC   AAS09500;
XX
DT   24-OCT-2001  (first entry)
XX
DE   SMART PCR primer #2.
XX
KW   Heat-labile uracil-DNA glycolsylase; UNG; UDG; PCR primer; SMART;
KW   PCR control; LCR control; ligase chain reaction; carry-over prevention;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO200151623-A1.
XX
PD   19-JUL-2001.
XX
PF   10-JAN-2001; 2001WO-NO000008.
XX
PR   12-JAN-2000; 2000NO-00000163.
PR   27-OCT-2000; 2000NO-00005428.
XX
PA   (BIOT-) BIOTEC ASA.
XX
PI   Lanes O,  Willasen NP,  Guddal PH,  Gjellesvik DR;
XX
DR   WPI; 2001-451854/48.
XX
PT   New cod liver uracil-DNA glycosylase enzyme, useful in monitoring or
PT   controlling a reaction system multiplying DNA sequences or in carry-over
PT   prevention procedures.
XX
PS   Example 2; Page 20; 59pp; English.
XX
CC   The sequence represents a SMART PCR primer used to synthesise first
CC   strand cDNA from Atlantic cod in order to isolate cDNAs encoding heat-
CC   labile uracil-DNA glycosylase, (UNG/UDG). The enzyme is useful in
CC   monitoring and/or controlling a reaction system multiplying DNA
CC   sequences, e.g. PCR (polymerase chain reaction) or LCR (ligase chain
CC   reaction). The enzyme is also useful in carry-over prevention procedures
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 32;
  Best Local Similarity   78.6%;  Pred. No. 1.4e+03;
  Matches   22;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       2777 TTAGAATTGAAAAAAAAAAAAAAAAAAA 2804
              : | ||   ||||||||||||||||||
Db            32 BNAAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 593
ABA01204/c
ID   ABA01204 standard; DNA; 32 BP.
XX
AC   ABA01204;
```

```
XX
DT   11-SEP-2003  (revised)
DT   28-JAN-2002  (first entry)
XX
DE   Mamushi fibrinolytic enzyme, brevinase, PCR primer, BbRP1.
XX
KW   Fibrinolytic enzyme; brevinase; thermostable; thrombolytic agent;
KW   mamushi; PCR primer; ss.
XX
OS   Agkistrodon blomhoffi; brevicaudus.
XX
PN   KR2001045716-A.
XX
PD   05-JUN-2001.
XX
PF   06-NOV-1999;   99KR-00049115.
XX
PR   06-NOV-1999;   99KR-00049115.
XX
PA   (LEEJ/) LEE J W.
PA   (PARK/) PARK W.
XX
PI   Lee JW,  Park W;
XX
DR   WPI; 2001-636862/73.
XX
PT   Fibrinolytic enzyme, brevinase, separated from poison of viper,
PT   agkistrodon blomhoffi brevicaudus.
XX
PS   Example 5; Page 6; 23pp; Korean.
XX
CC   The present invention relates to fibrinolytic enzyme, brevinase (see
CC   AAG79000), which is separated from the poison of Agkistordon blomhoffi
CC   brevicaudus (mamushi). The enzyme shows stability at high temperatures
CC   and is thus useful in developing thrombolytic agents. The present
CC   sequence is a PCR primer, which was used in an example from the present
CC   invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 2 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 32;
  Best Local Similarity   81.5%;  Pred. No. 1.4e+03;
  Matches   22;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAAAA 2804
              :| ||   ||||||||||||||||||||
Db         31 BAAAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 594
ADA26489
ID   ADA26489 standard; DNA; 32 BP.
XX
AC   ADA26489;
XX
DT   20-NOV-2003  (first entry)
XX
DE   DNA nanolithography method example oligonucleotide G1.
XX
KW   ss; direct-write nanolithography; nanoscopic tip; nanoscale pattern;
KW   patterning; scanning probe microscopic tip; nanoparticle; nanoarray.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   32
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "contains a thiol group (CH2)3SH) at the 5' end"
XX
PN   WO2003048314-A2.
XX
PD   12-JUN-2003.
XX
PF   02-DEC-2002; 2002WO-US038252.
XX
PR   30-NOV-2001; 2001US-0337598P.
PR   07-MAR-2002; 2002US-0362924P.
XX
PA   (UYNW-) UNIV NORTHWESTERN TECHNOLOGY TRANSFER PR.
XX
PI   Mirkin CA,  Demers ML,  Ginger DS;
XX
DR   WPI; 2003-671287/63.
XX
PT   Depositing nucleic acid on substrate by direct-write nanolithography, by
PT   positioning nanoscopic tip relative to substrate, to transfer nucleic
PT   acid to substrate and generate stable nucleic acid nanoscale pattern.
XX
PS   Disclosure; Page 38; 76pp; English.
XX
CC   The invention relates to a method of depositing nucleic acid onto a
CC   substrate by direct-write nanolithography, by positioning at least one
CC   nanoscopic tip relative to a substrate so that the tip and substrate
CC   approach each other, and the nucleic acid is transferred from the tip to
CC   the substrate to generate a stable nucleic acid nanoscale pattern on the
CC   substrate which is hybridizable with complementary nucleic acid. The
CC   method is useful for generating nanoscale patterns of nucleic acid on a
CC   substrate, in which before transfer the tip is modified to allow the
CC   nucleic acid to wet the tip and the nucleic acid is modified to chemisorb
CC   or covalently bond to the substrate upon transfer. The method is also
CC   useful for direct patterning of modified nucleic acid onto a substrate,
CC   by inking a scanning probe microscopic tip with a modified nucleic acid
CC   and positioning the inked tip close enough to the substrate to effect
CC   transfer of the nucleic acid to the substrate to form a nanoscale
CC   pattern. Another use for the method is for assembling nanoparticles (e.g.
CC   gold nanoparticles) to form nanoscale patterns, by depositing from a
CC   nanoscopic tip a first nucleic acid onto a substrate to form a deposit
CC   with lateral nanoscale features of 1000 mm or less by direct write
CC   nanolithography, hybridizing the nucleic acid deposit with the
CC   nanoparticle, where the nanoparticle is functionalized with a second
CC   nucleic acid which is either complementary to the first or complementary
CC   to the nucleic acid of a linking strand which links the second nucleic
CC   acid to the first. Deposition of nucleic acid on the substrate is
CC   repeated to form a nanoarray of the nucleic acid and the hybridization is
CC   carried out with the nanoarray. The method is suitable for writing
CC   preconceived nanoscale features directly, without use of expensive and
CC   potentially destructive methods such as electron beam and
CC   photolithographic methods. The structures can be built up, if desired,
CC   without degrading existing structures. Complicated stamps and resists are
CC   not needed. Improvements in the consistency and stability of the
CC   nanolithography can be observed. This sequence represents an example of a
CC   nucleic acid that can be used in the method of the invention.
XX
SQ   Sequence 32 BP; 23 A; 4 C; 1 G; 4 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.8;  DB 1;  Length 32;
  Best Local Similarity   77.4%;  Pred. No. 1.4e+03;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2774 TTGTTAGAATTGAAAAAAAAAAAAAAAAAA 2804
              | | |  | |  ||||||||||||||||||
Db          1 TAGCTCAACTCTAAAAAAAAAAAAAAAAAA 31


RESULT 595
AAD03682/c
ID   AAD03682 standard; DNA; 26 BP.
XX
AC   AAD03682;
XX
DT   19-JUN-2001  (first entry)
XX
DE   Human full length zcytor13 cDNA isolating polyA PCR primer, ZC7764b.
XX
KW   Human; phosphodiesterase; PDE; zcytor13; antiasthmatic; antiarthritic;
```

```
KW   antipsoriatic; cytostatic; antiatherosclerotic; antiinfertility;
KW   cardiant; antiinflammatory; dermatological; wound healing; antiviral;
KW   antibacterial; therapy; inflammatory bowel disease; diverticulitis;
KW   spermatogenesis; sperm capacitation; immunocontraceptive; vaccine;
KW   cancer; reperfusion ischaemia; psoriasis; melanoma; myocarditis; PID;
KW   pelvic inflammatory disease; eczema; scleroderma; vasoconstriction;
KW   heart arrhythmia; congestive heart disease; muscle spasm; fatigue;
KW   chromosomal abnormality; gene therapy; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200125444-A2.
XX
PD   12-APR-2001.
XX
PF   06-OCT-2000; 2000WO-US027734.
XX
PR   07-OCT-1999;   99US-00414025.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Novak JE,  Gao Z;
XX
DR   WPI; 2001-266312/27.
XX
PT   Novel human phosphodiesterase polypeptide, zcytor13 and polynucleotide
PT   encoding it, for detecting human chromosomal abnormalities, identifying
PT   modulators and treating inflammatory and cardiovascular diseases.
XX
PS   Example 1C; Page 118; 122pp; English.
XX
CC   The patent discloses novel human phosphodiesterase (PDE), zcytor13 cDNA
CC   and its corresponding protein. Zcytor13 protein is used to promote wound
CC   healing in tissues, to exhibit anti-bacterial and anti-viral effects and
CC   to identify modulators (e.g. agonists or antagonists). Zcytor13, its
CC   agonists or antagonists are useful in the treatment of inflammatory heart
CC   or cardiovascular conditions, muscle inflammation, inflammation during
CC   and after surgery, arthritis, asthma, inflammatory bowel disease or
CC   diverticulitis, for modulating spermatogenesis, sperm capacitation, as
CC   immunocontraceptive or anti-fertility vaccine and for treating male
CC   infertility. Zcytor13 protein and its antibodies are used to diagnose
CC   cancer, reperfusion ischaemia, asthma, psoriasis and melanoma. Zcytor13
CC   proteins are used to enhance fertilisation. Zcytor13 antagonists are used
CC   to treat myocarditis, atherosclerosis, pelvic inflammatory disease (PID),
CC   psoriasis, eczema, scleroderma and other inflammatory diseases. Zcytor13
CC   sequences and/or its antibodies are useful for treatment of disorders
CC   associated with vasoconstriction, heart arrhythmia, congestive heart
CC   disease, muscle spasms and fatigue. They are used for detecting human
CC   chromosomal abnormalities. Zcytor13 cDNAs are used in gene therapy.
CC   Zcytor13-cytokine fusion proteins or antibody-cytokine fusion proteins
CC   are useful for enhancing in vivo killing of target tissue. The present
CC   sequence is a polyA PCR primer, ZC7764b which is used to isolate full
CC   length zcytor13 cDNA by screening human placental cDNA library
XX
SQ   Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
             || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 596
AAS20596/c
ID   AAS20596 standard; DNA; 26 BP.
XX
AC   AAS20596;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human zsig63 cDNA sequencing primer ZC7764a.
XX
KW   Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KW   microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KW   gastrointestinal disease; urinary tract infection; vaginal infection;
KW   skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KW   acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
KW   chronic bronchitis; gene therapy; protein therapy; primer; ZC7764a.
XX
OS   Homo sapiens.
XX
PN   US6331413-B1.
XX
PD   18-DEC-2001.
XX
PF   17-MAR-2000; 2000US-00527345.
XX
PR   17-MAR-1999;   99US-0124820P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2002-096707/13.
XX
PT   Polynucleotides encoding salivary proteins useful as anti-microbial
PT   agents.
XX
PS   Example 1; Col 53; 29pp; English.
XX
CC   The invention relates to a polynucleotide derived from the 4q12-4q13
CC   region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC   secreted salivary protein with anti-microbial activity. Due to their
CC   microbial activity, the sequences can be used in the study of microbial
CC   infections, e.g. for recombinant production of anti-microbial proteins.
CC   The sequences can be used in the treatment of tooth decay, periodontal
CC   disease, thrush, gastrointestinal disease, urinary tract infections,
CC   vaginal infections, skin infections, epithelial wounds, chronic tissue
CC   damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC   infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC   represents a sequencing primer for cDNA encoding human zsig63
XX
SQ   Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
             || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 597
ABS52638/c
ID   ABS52638 standard; DNA; 26 BP.
XX
AC   ABS52638;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human secreted salivary protein zsig63 PCR primer ZC7764a.
XX
KW   Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
KW   antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KW   fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KW   tooth decay; periodontal disease; thrush; gastrointestinal disease;
KW   urinary tract infection; vaginal infection; skin infection; microflora;
KW   epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KW   chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KW   incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KW   chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KW   digestion; PCR; primer; ss.
```

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XX
OS   Homo sapiens.
XX
PN   US2002081701-A1.
XX
PD   27-JUN-2002.
XX
PF   03-AUG-2001; 2001US-00922480.
XX
PR   17-MAR-1999;   99US-0124820P.
PR   17-MAR-2000; 2000US-00527345.
XX
PA   (ADLE/) ADLER D A.
PA   (SHEP/) SHEPPARD P O.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2002-635468/68.
XX
PT   Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT   useful for treating microbial infections, inflammatory conditions, dental
PT   caries and lung infections associated with cystic fibrosis.
XX
PS   Example 1; Page 29; 33pp; English.
XX
CC   The present invention relates to a new secreted salivary protein, zsig63.
CC   The invention is useful for detecting in a test sample, the presence of
CC   an antagonist or agonist of zsig63 protein activity. The invention is
CC   also useful as an immunogen for producing an antibody to zsig63
CC   polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC   protein are useful for enhancing in vivo killing of target tissues.
CC   Pharmaceutical composition comprising purified zsig63 polypeptide are
CC   useful in the treatment of conditions associated with pathological
CC   microbes, including bacterial, fungal and viral infections. High
CC   expression of zsig63 in salivary gland suggests that anti-microbial
CC   polypeptides are useful for treatment of dental caries (tooth decay),
CC   periodontal disease, thrush and gastrointestinal disease. Other
CC   applications can be used in urinary tract infections, vaginal infections,
CC   prevention of infection in skin and other epithelial wounds. The
CC   polypeptides can be used to establish normal microflora and protect
CC   against pathogenic colonisation and invasion. The invention is useful
CC   when pro-inflammatory activity is desired. Applications for such pro-
CC   inflammatory activity include the treatment of chronic tissue damage,
CC   particularly in areas having a limited or damaged vascular system e.g.,
CC   damage in extremities associated with diabetes. Antagonists to zsig63
CC   polypeptides may be useful as anti-inflammatory agents. The invention is
CC   useful for the treatment of patients having incompetent immune system,
CC   such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC   that have undergone chemotherapy, radiation treatment. The invention is
CC   also useful for the treatment of lung infections associated with cystic
CC   fibrosis and its agonists or antagonists are useful for aiding digestion.
CC   The present nucleic acid sequence represents a PCR primer that was used
CC   in the methods of the invention for identification of zsig63
XX
SQ   Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
                || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 598
AAD45055/c
ID   AAD45055 standard; DNA; 26 BP.
XX
AC   AAD45055;
XX
DT   27-DEC-2002  (first entry)
XX
DE   ZC7764a primer used in the identification of human zsig63 DNA.
XX
KW   Human; secreted salivary protein; zsig63 protein; host defense protein;
KW   immune modulating factor; antipathogenic; cell-cell signalling molecule;
KW   growth factor; cytokine; growth factor hormone activity; dental carries;
KW   infection; tooth decay; periodontal disease; gastrointestinal disease;
KW   thrush; urinary tract infection; vaginal infection; diabetes; obesity;
KW   anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
KW   gene therapy; salivary gland dysfunction; prostate gland dysfunction;
KW   forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2002090677-A1.
XX
PD   11-JUL-2002.
XX
PF   03-AUG-2001; 2001US-00923236.
XX
PR   17-MAR-1999;   99US-0124820P.
PR   17-MAR-2000; 2000US-00527345.
XX
PA   (ADLE/) ADLER D A.
PA   (SHEP/) SHEPPARD P O.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2002-642378/69.
XX
PT   Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
PT   agent for treating microbial infection, dental carries, periodontal
PT   disease, thrush gastrointestinal disease, and for aiding digestion.
XX
PS   Example 1; Page 30; 33pp; English.
XX
CC   The invention relates to human secreted salivary polypeptide designated
CC   as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
CC   can be used in detecting agonists and antagonists of its activity, and is
CC   also useful as a host defense polypeptide, immune modulating factor,
CC   antipathogenic polypeptide, cell-cell signalling molecule, growth factor,
CC   cytokine, or as secreted extracellular matrix associated proteins with
CC   growth factor hormone activity. It is useful for treating conditions
CC   associated with pathological microbes, including bacterial, fungal and
CC   viral infections, for treating dental carries (tooth decay), periodontal
CC   disease, thrush and gastrointestinal disease, for treating urinary tract
CC   infection, vaginal infection and for preventing infection in skin and
CC   other epithelial wounds. zsig63 is useful for establishing normal
CC   microflora and protect against pathogenic colonisation and invasion, for
CC   treating chronic tissue damage e.g. damage in extremities associated with
CC   diabetes and useful as anti-inflammatory agents. It is useful as a marker
CC   of lung dysfunction, salivary gland dysfunction, or dysfunction of
CC   prostate gland. It is also therapeutically useful for aiding digestion.
CC   Polynucleotides of the invention are used in gene therapy for increasing
CC   or inhibiting zsig63 activity, for detecting abnormalities on human
CC   chromosome 4 associated with disease or other human traits and as
CC   diagnostics in forensic DNA profiling. Sequences of the invention are
CC   useful for stimulating proliferation or differentiation of cardiac
CC   myocytes, for proliferation or differentiation of adipocytes and for
CC   inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The
CC   present sequence is a primer used in the identification of human zsig63
CC   DNA
XX
SQ   Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
                || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 599
AAS20671/c
ID   AAS20671 standard; DNA; 26 BP.
XX
AC   AAS20671;
XX
DT   09-APR-2002  (first entry)
XX
DE   Human zalpha11 Ligand sequencing primer ZC7764a.
XX
KW   Cytokine; zalpha11 Ligand; zalpha11 receptor; NK cell progenitor;
KW   natural killer cell proliferation; T-cell proliferation;
KW   B-cell proliferation; anti-tumour response; immune system;
KW   immunostimulant; cytostatic; human; sequencing primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6307024-B1.
XX
PD   23-OCT-2001.
XX
PF   09-MAR-2000; 2000US-00522217.
XX
PR   09-MAR-1999;   99US-0123547P.
PR   11-MAR-1999;   99US-0123904P.
PR   01-JUL-1999;   99US-0142013P.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Novak JE,  Presnell SR,  Sprecher CA,  Foster DC,  Holly RD;
PI   Gross JA,  Johnston JV,  Nelson AJ,  Dillon SR,  Hammond AK;
XX
DR   WPI; 2002-040208/05.
XX
PT   New zalpha11 ligand polypeptides and polynucleotides, useful for
PT   stimulating proliferation, activation, differentiation and/or induction
PT   of inhibition of specialized cell function, or for stimulating an
PT   antigenic response.
XX
PS   Example 7; Col 139; 105pp; English.
XX
CC   The present invention relates to the isolation of a novel cytokine,
CC   zalpha11 Ligand and the polynucleotide encoding it. The invention also
CC   gives the sequence for the zalpha11 receptor and the polynucleotide
CC   encoding it. The zalpha11 Ligand polypeptide stimulates proliferation of
CC   natural killer (NK) cells or NK cell progenitors, the activation of NK
CC   cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC   anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC   reduces proliferation of B-cells stimulated with anti-IgM antibodies. The
CC   zalpha11 Ligand polypeptide is also useful in preparing antibodies that
CC   bind to zalpha11 Ligand epitopes. The zalpha11 Ligand polynucleotides can
CC   be used as probes or primers to clone regions of a zalpha11 Ligand gene,
CC   and in gene therapy. Zalpha11 Ligand may also be used to identify
CC   inhibitors of its activity, to enhance the generation of anti-tumour
CC   responses with or without the infusion of donor lymphocytes, and to
CC   activate or stimulate the immune system. The present sequence represents
CC   a sequencing primer used to sequence cDNA clones in the isolation of
CC   human zalpha11 Ligand
XX
SQ   Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
                || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 600
ABX93599/c
ID   ABX93599 standard; DNA; 26 BP.
XX
AC   ABX93599;
XX
DT   28-MAY-2003  (first entry)
XX
DE   Human zsig63 PCR/sequencing primer ZC7764a.
XX
KW   ss; PCR; zsig63; adhesin; salivary gland; dental carries;
KW   periodontal disease; thrush; gastrointestinal disease; epithelial wound;
KW   urinary tract infection; vaginal infection; skin infection; primer;
KW   pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
KW   lung infection; cystic fibrosis; lung dysfunction; digestive;
KW   salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
KW   chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
KW   cell culture media; gene therapy; human chromosome 4q12-4q13;
KW   dentinogenesis imperfecta; dentin dysplasia type II.
XX
OS   Synthetic.
XX
PN   US2002173027-A1.
XX
PD   21-NOV-2002.
XX
PF   03-AUG-2001; 2001US-00922469.
XX
PR   17-MAR-1999;   99US-0124820P.
PR   17-MAR-2000; 2000US-00527345.
XX
PA   (ADLE/) ADLER D A.
PA   (SHEP/) SHEPPARD P O.
XX
PI   Adler DA,  Sheppard PO;
XX
DR   WPI; 2003-328428/31.
XX
PT   Novel isolated zsig63 polypeptide, member of the adhesin family, useful
PT   for treating dental carries, periodontal disease, thrush,
PT   gastrointestinal disease, urinary tract infections, vaginal infections,
PT   skin infections.
XX
PS   Example 1; Page 29; 32pp; English.
XX
CC   The invention relates to an isolated zsig63 polypeptide comprising at
CC   least 90% identity to an amino acid sequence which comprises domain 1 of
CC   zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also
CC   included are the polynucleotide encoding zsig63, a zsig63 expression
CC   vector, a cultured cell comprising the vector and expressing the protein,
CC   a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
CC   126, 127-219 or 16-219 of zsig63 and an additional protein), using a
CC   zsig63 reporter gene construct to identify zsig63 agonists, and producing
CC   an anti-zsig63 antibody using zsig63 immunogenic peptides, Zsig63 is
CC   useful for detecting in a test sample, the presence of antagonist of
CC   zsig63 protein activity. Zsig63 has antimicrobial activity and since
CC   exhibits high expression in salivary gland, can be used for treating
CC   dental carries, periodontal disease, thrush, and gastrointestinal
CC   disease, urinary tract infections, vaginal infections, skin infections
CC   and other epithelial wounds. The polypeptides can be used to establish
CC   normal microflora and protect against pathogenic colonization and
CC   invasion. Zsig63 can also be used for providing pro-inflammatory activity
CC   for treating chronic, tissue damage particularly in areas having limited
CC   or damaged vascular system, e.g. in diabetes, and for treating
CC   immunocompromised AIDS patients or in individuals that have undergone
CC   chemotherapy, radiation treatment, for treating lung infections e.g. in
CC   cystic fibrosis. Detection of zsig63 polypeptide at relatively high
CC   levels in the trachea may indicate that such polypeptides may serve as a
CC   marker of lung dysfunction. Zsig63 is also useful in diagnosing
CC   conditions associated with salivary gland or lung dysfunction including
CC   salivary gland carcinoma, Pneumocystis carinii infection, emphysema,
CC   chronic bronchitis, prostate dysfunctions such as prostate
CC   adenocarcinoma, aiding digestion, and as components of defined cell
CC   culture media and may be used to replace serum that is commonly used in
CC   culture. The DNA is useful in gene therapy applications to increase or
CC   inhibit zsig63 activity, and for detecting abnormalities on human
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```
CC   chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta,
CC   and dentin dysplasia type II). Zsig63 is an adhesin family member. The
CC   present sequence is a primer used to isolate and sequence nucleic acdis
CC   encoding human zsig63
XX
SQ   Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2778 TAGAATTGAAAAAAAAAAAAAAAAAA 2803
                || ||   ||||||||||||||||||
Db         26 TAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 601
AAN70276/c
ID   AAN70276 standard; DNA; 26 BP.
XX
AC   AAN70276;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC060 (HL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 602
AAN70275/c
ID   AAN70275 standard; DNA; 26 BP.
XX
AC   AAN70275;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC059 (HL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 603
AAN92241/c
ID   AAN92241 standard; DNA; 26 BP.
XX
AC   AAN92241;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRC059.
XX
KW   Probe MRC059; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .10
```

```
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    11. .14
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    15. .26
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO59 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 604
AAN92242/c
ID   AAN92242 standard; DNA; 26 BP.
XX
AC   AAN92242;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRCO60.
XX
KW   Probe MRCO60; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .12
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    13. .16
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    17. .26
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO60 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 605
AAF77536/c
ID   AAF77536 standard; DNA; 26 BP.
XX
AC   AAF77536;
XX
DT   23-MAY-2001  (first entry)
XX
DE   CDNA library production method related oligonucleotide SEQ ID NO: 5.
XX
KW   cDNA library production; SCLA; gene chip technology;
KW   differential screening; pathological diagnosis; genetic identification;
KW   single-cell cDNA library amplification; ds.
XX
OS   Synthetic.
XX
PN   US6197554-B1.
XX
PD   06-MAR-2001.
XX
PF   20-NOV-1998;   98US-00197951.
XX
PR   20-NOV-1998;   98US-00197951.
XX
PA   (LINS/) LIN S.
PA   (CHUO/) CHUONG C.
```

```
PA   (YING/) YING S.
XX
PI   Lin S,  Chuong C,  Ying S;
XX
DR   WPI; 2001-243448/25.
XX
PT   Generating a complete full-length cDNA library from single cells for use
PT   in gene chip technology, involves reverse transcribing intracellular
PT   mRNAs, adding polynucleotide tail and amplifying formed cDNAs.
XX
PS   Disclosure; Col 11-12; 11pp; English.
XX
CC   The present invention describes a method of producing full-length cDNA
CC   libraries from single cells, designated single-cell cDNA library
CC   amplification (SCLA). The method is useful in gene chip technology,
CC   differential screening, pathological diagnosis, physiological prognosis
CC   and genetic identification. No further information about this sequence is
CC   given in the specification
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 606
AAF23526/c
ID   AAF23526 standard; DNA; 26 BP.
XX
AC   AAF23526;
XX
DT   22-MAR-2001  (first entry)
XX
DE   Primer #4.
XX
KW   Primer; mRNA; amplification; ss.
XX
OS   Unidentified.
XX
PN   WO200075356-A1.
XX
PD   14-DEC-2000.
XX
PF   04-JUN-1999;   99WO-US012461.
XX
PR   04-JUN-1999;   99WO-US012461.
XX
PA   (LINS/) LIN S.
PA   (YING/) YING S.
PA   (CHUO/) CHUONG C.
PA   (WIDE/) WIDELITZ R B.
XX
PI   Lin S,  Ying S,  Chuong C,  Widelitz RB;
XX
DR   WPI; 2001-061734/07.
XX
PT   Generating amplified messenger RNA sequences from single cells, involves
PT   cycling steps of reverse transcription, denaturation, double-stranded DNA
PT   sequences and in vitro transcription.
XX
PS   Disclosure; Page 17; 31pp; English.
XX
CC   The present invention relates to generating amplified messenger RNAs with
CC   polymerase reaction activity, comprising cycling steps of reverse
CC   transcription, denaturation, double-stranded cDNA synthesis and in vitro
CC   transcription. The invention is used for generating amplified mRNAs from
CC   limited mRNAs from single cells
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 607
AAD43853/c
ID   AAD43853 standard; DNA; 26 BP.
XX
AC   AAD43853;
XX
DT   14-NOV-2002  (first entry)
XX
DE   Primer #2 used to illustrate the method of the invention.
XX
KW   Single stranded polynucleotide tag; cleavage agent; gene expression;
KW   primer; ss.
XX
OS   Unidentified.
XX
PN   WO200259357-A2.
XX
PD   01-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-DK000052.
XX
PR   24-JAN-2001; 2001DK-00000126.
PR   12-FEB-2001; 2001US-0267704P.
XX
PA   (GENO-) GENOMIC EXPRESSION APS.
XX
PI   Pedersen ML;
XX
DR   WPI; 2002-636542/68.
XX
PT   Obtaining single stranded polynucleotide tags from a biological sample,
PT   for analyzing gene expression or diagnosing clinical conditions,
PT   comprises employing nicking endonucleases that cleave complementary
PT   strands.
XX
PS   Example; Page 294; 302pp; English.
XX
CC   The invention relates to a method for obtaining a single stranded
CC   polynucleotide tag from a biological sample by cleaving one of the
CC   complementary strands of a double stranded polynucleotide with a cleavage
CC   agent capable of recognising a double stranded polynucleotide comprising
CC   complementary strands and cleaving only one of the strands of the
CC   polynucleotide in the process of generating a single stranded
CC   polynucleotide tag. The method is useful for separating, analysing,
CC   quantifying or obtaining single stranded polynucleotides comprising tags
CC   originating partly, and preferably wholly from a source of DNA and/or RNA
CC   in a sample comprising biological cells. The method is particularly for
CC   analysing gene expression (expression profiling or differential gene
CC   expression), or in diagnosing clinical conditions. The present sequence
CC   is a primer used in the exemplification of the invention
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1
```

```
RESULT 608
ABZ24784/c
ID   ABZ24784 standard; DNA; 26 BP.
XX
AC   ABZ24784;
XX
DT   07-APR-2003  (first entry)
XX
DE   Oligodeoxynucleic acid molecule ODN 24.
XX
KW   Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .26
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "thiophosphate backbone"
XX
PN   WO200295027-A2.
XX
PD   28-NOV-2002.
XX
PF   17-MAY-2002; 2002WO-EP005448.
XX
PR   21-MAY-2001; 2001AT-00000805.
XX
PA   (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI   Lingnau K,  Schellack C,  Schmidt W;
XX
DR   WPI; 2003-183880/18.
XX
PT   New oligodeoxynucleic acid molecules useful for the preparation of
PT   vaccine.
XX
PS   Example 8; Page 32; 57pp; English.
XX
CC   The present sequence is that of a thiosubstituted oligodeoxynucleic acid
CC   (ODN) molecule, ODN 24, including deoxyuridine monophosphates. The
CC   invention is based on the discovery that ODNs containing deoxyuridine
CC   residues (U-ODNs) have an immunostimulatory effect comparable to, or in
CC   many instances greater than, ODNs containing CpG motifs, producing higher
CC   numbers of specific T cells to a given antigen. The U-ODNs do not induce
CC   the systemic production of pro-inflammatory cytokines and, in contrast to
CC   CpG ODNs, are not dependent on a specific motif or a palindromic
CC   sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
CC   Combining the U-ODN with an antigen strongly increases the potential of
CC   the antigen to raise the protection/immune response of a vaccinated
CC   individual. An example of the invention demonstrated the generation of a
CC   specific immune response against a melanoma-derived peptide (see
CC   ABP58360) by injection of mice with the peptide in combination with ODN
CC   24
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 1 T; 25 U; 0 Other;

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 609
ACA62282/c
ID   ACA62282 standard; DNA; 26 BP.
XX
AC   ACA62282;
XX
DT   12-AUG-2003  (first entry)
XX
DE   Oligo (dT) primer #1.
XX
KW   ss; PCR; primer; antisense therapy; mRNA expression profile;
KW   promoter containing primer.
XX
OS   Synthetic.
XX
PN   US2003022318-A1.
XX
PD   30-JAN-2003.
XX
PF   07-SEP-2001; 2001US-00949305.
XX
PR   25-JAN-2000; 2000US-00494212.
XX
PA   (EPIC-) EPICLONE INC.
XX
PI   Lin S,  Ying S;
XX
DR   WPI; 2003-479488/45.
XX
PT   Improved polymerase thermocycling reaction for nucleic acid
PT   amplification, by thermal cycling of promoter-linked nucleic acid
PT   template synthesis and in vitro transcriptional amplification of nucleic
PT   acid sequences.
XX
PS   Example 4; Page 14; 28pp; English.
XX
CC   The invention relates to an improved polymerase thermocycling reaction
CC   (M1) for linear amplification of nucleic acid sequences, involves
CC   denaturing a number of nucleic acid templates (I), combining the
CC   denatured (I) with a promoter-containing primer (P1), a primer (P2), a
CC   number of deoxynucleotide triphosphates and ribonucleotide triphosphates,
CC   a reverse transcription enzyme, a DNA-dependent DNA polymerase and RNA
CC   polymerase, contacting P1 with (I) to generate a number of promoter-
CC   containing templates, denaturing the promoter-containing templates,
CC   contacting P2 with the denatured promoter-containing templates to
CC   generate a number of promoter-containing double-stranded DNA templates,
CC   where the double-stranded nucleic acid templates are flanked by P1 in one
CC   end and P2 in the other end of the other orientation, transcribing the
CC   promoter-containing double-stranded DNA templates to form a number of
CC   amplified RNA sequences, including the primer region of the promoter-
CC   containing double-stranded DNA templates, contacting the amplified RNA
CC   sequences with P2 to form a number of cDNAs and a number of DNA-RNA
CC   hybrid templates, and denaturing the DNA-RNA hybrid templates. The method
CC   is useful for improved polymerase thermocycling reaction for linear
CC   amplification of nucleic acid sequences, and thus for producing mRNA
CC   expression profile of a cell by M1 to generate multiple copies of the
CC   mRNA. M1 is also useful for determining aberrant protein production of
CC   cells in a diseased state, by generating an expression profile by the
CC   above method, of cells in both normal and diseased states, comparing the
CC   expression profile of the cells in the normal and diseased states,
CC   determining the differences in mRNA composition of the cell(s) in the
CC   diseased state, isolating the mRNA sequences of cell(s) in the diseased
CC   state that differ from mRNA in cell(s) in non-diseased state, amplifying
CC   the isolated mRNA by M1, and determining aberrant protein function of the
CC   protein coded for by the isolated mRNA. M1 is also useful for treating a
CC   cell in a diseased state caused by aberrant protein production, by
CC   determining protein expression of a cell in a diseased state, determining
CC   the mRNA sequence for the aberrant proteins, synthesising an antisense
CC   sequence of the mRNA, amplifying the antisense mRNA sequences by M1, and
CC   delivering a pharmaceutically effective dosage of a composition
CC   comprising the anti-sense mRNA and a compatible lipid based biological
CC   carrier. M1 is also useful for predicting the efficacy of a proposed drug
CC   targeted against an aberrant protein, by determining aberrant protein
CC   production of cell in a diseased state by the above method, amplifying
CC   the aberrant protein by M1 and using recombinant techniques to determine
CC   the effect of proposed drug on the aberrant protein. M1 is also useful
CC   for differential screening of tissue-specific gene expression at a
CC   cellular level, for preparing labeled RNA/DNA probes for a gene chip
```

```
CC   technology, and for determining the efficacy of a drug regiment against a
CC   gene or its cDNAs. The present sequence is an Oligo (dT) primer used to
CC   produce second strand cDNA in the method of the invention
XX
SQ   Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||||
Db         26 AAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 610
AAT99265
ID   AAT99265 standard; DNA; 26 BP.
XX
AC   AAT99265;
XX
DT   15-APR-1998  (first entry)
XX
DE   Human PUR-alpha gene primer PDT-01.
XX
KW   PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
KW   cancer; PCR; primer; amplification.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5672479-A.
XX
PD   30-SEP-1997.
XX
PF   07-JUN-1995;   95US-00486421.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
PR   06-JUN-1995;   95US-00470911.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1997-488859/45.
XX
PT   Assays for PUR protein ligands or modulators - using immobilised PUR
PT   protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
PS   Disclosure; Col 9; 64pp; English.
XX
CC   The primers AAT99265-T99269 were used to PCR amplify and isolate the
CC   complete sequence of the human PUR-alpha gene (AAT99264). The PUR
CC   sequence can be used to identify chemical or biological compounds that
CC   bind to PUR or binding fragments of PUR. Inhibitors of PUR activity may
CC   be used to treat hyperproliferative diseases such as cancer
XX
SQ   Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTT 2184
                | |||  |  ||||||||||||||||||
Db          1 TATCTGCAGTTTTTTTTTTTTTTTTT 26


RESULT 611
AAT93819
ID   AAT93819 standard; DNA; 26 BP.
XX
AC   AAT93819;
XX
DT   25-MAR-2003  (revised)
DT   24-FEB-1998  (first entry)
XX
DE   Antitumoural phosphodiester oligonucleotide 9 with cytotoxic activity.
XX
KW   Phosphodiester; selective binding; cell viability; growth;
KW   tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW   lymphoblastic tumour; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .26
FT                    /*tag=  a
FT                    /note= "phosphodiester oligonucleotide"
XX
PN   WO9720924-A1.
XX
PD   12-JUN-1997.
XX
PF   04-DEC-1996;   96WO-EP005388.
XX
PR   04-DEC-1995;   95IT-MI002539.
XX
PA   (SAIC-) SAICOM SRL.
XX
PI   Scaggiante B,  Quadrifoglio F;
XX
DR   WPI; 1997-319771/29.
XX
PT   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT   selective cytotoxic effect on tumour cells, for treating both solid and
PT   liquid tumours.
XX
PS   Claim 10; Page 5; 38pp; English.
XX
CC   Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC   generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-
CC   (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''- (G-gTg')g''-N', where: N and
CC   N' = T or G, equal or different from each other; x = 0-8, equal or
CC   different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC   different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC   or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC   16, equal or different from each other; The oligonucleotides are believed
CC   to selectively bind and sequester some proteins which are essential to
CC   the viability and growth of tumoural cell line. They have specific and
CC   selective cytotoxic activity against tumour cells, and can be used for
CC   treating tumours of the liquid type, in particular of lymphoblastic
CC   origin, and of solid type, in particular lymphomas. The present
CC   phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC   reduced growth of CCRF-CEM tumoural cells by 76%, which is detectable 48
CC   hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 26 BP; 0 A; 0 C; 2 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTT 2181
                ||||||  |  ||||||| ||||||||
Db          1 TTTTTTTTGTTTTTTTTGTTTTTTT 26


RESULT 612
AAV12482/c
ID   AAV12482 standard; DNA; 26 BP.
XX
AC   AAV12482;
XX
DT   15-MAY-1998  (first entry)
```

```
XX
DE   Oligonucleotide SEQ ID NO:5 from US5174320 Example 2.
XX
KW   Synthesis; selection; amplification; circular oligonucleotide;
KW   rolling circle synthesis; diagnosis; therapeutic agent; ss.
XX
OS   Synthetic.
XX
PN   US5714320-A.
XX
PD   03-FEB-1998.
XX
PF   23-FEB-1995;   95US-00393439.
XX
PR   15-APR-1993;   93US-00047860.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-144278/13.
XX
PT   Rolling circle synthesis of oligo:nucleotide(s) - using primed circular
PT   template to produce oligonucleotide multimer for cleavage.
XX
PS   Example 2; Col 45; 38pp; English.
XX
CC   The present sequence represents an oligonucleotide used in an example of
CC   the present invention. The present invention describes a method for
CC   synthesising a selected oligonucleotide (I) having well defined ends. The
CC   method comprises: (a) annealing a primer to a single-stranded (ss)
CC   circular template to yield a primed circular template, where the template
CC   comprises: (i) at least one nucleotide sequence complementary to (I); and
CC   (ii) at least one nucleotide effective to produce a cleavage site in the
CC   oligonucleotide multimer; (b) combining the primed circular template with
CC   at least two types of nucleotide triphosphates and a polymerase enzyme
CC   without the addition of auxiliary proteins to yield a ss oligonucleotide
CC   multimer complementary to the circular oligonucleotide template,
CC   comprising multiple copies of (I); and (c) cleaving the oligonucleotide
CC   multimer at the cleavage site to produce (I) having well defined ends.
CC   The method is used for the large-scale synthesis of DNA and RNA oligomers
CC   for use, e.g. as probes and diagnostic agents and/or therapeutic agents
XX
SQ   Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||| ||||||   ||||
Db         26 TTTTTTTTTTTTGTTTTTTTTTTTTG 1


RESULT 613
AAV59215/c
ID   AAV59215 standard; DNA; 26 BP.
XX
AC   AAV59215;
XX
DT   14-DEC-1998  (first entry)
XX
DE   Circular template for linear oligomer dT12.
XX
KW   ss; circular; cyclic; RNA oligonucleotide; probe; standard; diagnostic;
KW   therapeutic agent.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_binding    1
FT                   /*tag=  a
FT                   /note= "Position 1 optionally bound to position 26"
FT   misc_binding    26
FT                   /*tag=  b
FT                   /note= "Position 26 optionally bound to position 1"
XX
PN   WO9838300-A1.
XX
PD   03-SEP-1998.
XX
PF   26-FEB-1998;   98WO-US003784.
XX
PR   26-FEB-1997;   97US-00805631.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1998-481202/41.
XX
PT   Synthesis of oligo:nucleotide(s) - using a single-stranded circular
PT   oligo:nucleotide template ribonucleotide tri:phosphate(s) and a
PT   polymerase to form multimer(s) which can be cleaved.
XX
PS   Example 2; Page 36; 100pp; English.
XX
CC   The circular template was used for the synthesis of the oligomer dT12 in
CC   an example of the method of the invention for synthesising an RNA
CC   oligonucleotide, comprising combining a single-stranded circular
CC   oligonucleotide template comprising at least one copy of a nucleotide
CC   sequence complementary to the sequence of the desired RNA oligonucleotide
CC   with at least 2 types of ribonucleotide triphosphate and a polymerase
CC   enzyme to yield a single-stranded RNA oligonucleotide multimer
CC   complementary to the circular oligonucleotide template, where the RNA
CC   oligonucleotide multimer comprises multiple copies of the desired RNA
CC   oligonucleotide. The methods can be used for producing RNA
CC   oligonucleotides having a specific sequence and well defined ends. The
CC   RNA oligonucleotides produced can be used as probes, standards and
CC   diagnostic or therapeutic agents. They can be used for modifying the
CC   structure or function of a target molecule. They can also be used to
CC   cleave disease-associated RNA, DNA or protein
XX
SQ   Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTTTG 2193
              ||||||||||||| ||||||   ||||
Db         26 TTTTTTTTTTTTGTTTTTTTTTTTTG 1


RESULT 614
AAV31721
ID   AAV31721 standard; DNA; 26 BP.
XX
AC   AAV31721;
XX
DT   24-SEP-1998  (first entry)
XX
DE   Nucleotide sequence of the PUR specific PCR primer.
XX
KW   PUR-alpha gene; inhibition; viral infection; cancer; PCR; primer;
KW   hyperproliferative disease; amplification; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5756684-A.
XX
PD   26-MAY-1998.
XX
PF   06-JUN-1995;   95US-00470911.
XX
```

```
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1998-321632/28.
XX
PT   PUR protein and its fragments - that inhibit PUR protein binding to PUR
PT   element or other proteins.
XX
PS   Disclosure; Col 9; 63pp; English.
XX
CC   This is the nucleotide sequence of the PUR psecific PCR primer used for
CC   amplification in the method of the invention, involving the use of the
CC   PUR protein and its fragments, which inhibit PUR protein binding to PUR
CC   element or other proteins. Inhibitors of PUR activity may be useful for
CC   treating viral infections and hyperproliferative diseases such as cancer
XX
SQ   Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTT 2184
              | ||| |  ||||||||||||||||
Db          1 TATCTGCAGTTTTTTTTTTTTTTTT 26


RESULT 615
AAX04087
ID   AAX04087 standard; DNA; 26 BP.
XX
AC   AAX04087;
XX
DT   12-APR-1999  (first entry)
XX
DE   PUR-alpha RACE reaction primer PDT-01.
XX
KW   PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
KW   monoclonal antibody; identification; characterisation; RACE primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US5869622-A.
XX
PD   09-FEB-1999.
XX
PF   07-JUN-1995;   95US-00486809.
XX
PR   28-AUG-1992;   92US-00938189.
PR   02-FEB-1993;   93US-00014943.
PR   06-JUN-1995;   95US-00470911.
XX
PA   (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
PI   Bergemann AD,  Johnson EM;
XX
DR   WPI; 1999-152881/13.
XX
PT   Monoclonal antibody specific for PUR protein - useful for treating
PT   cancer.
XX
PS   Example; Col 9; 64pp; English.
XX
CC   The present invention describes a monoclonal antibody that specifically
CC   binds to an epitope of the PUR protein. Antibodies that bind to the PUR
CC   protein and neutralise PUR activity may be used to treat
CC   hyperproliferative diseases such as cancer. PUR antibodies may be used
CC   diagnostically to detect aberrant expression of the PUR protein and/or
CC   mutations in the PUR gene. The present sequence represents a PUR-alpha
CC   RACE primer which is used in an example from the present invention
XX
SQ   Sequence 26 BP; 2 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2159 TTTCTCCTTTTTTTTTTTTTTTTTT 2184
              | ||| |  ||||||||||||||||
Db          1 TATCTGCAGTTTTTTTTTTTTTTTT 26


RESULT 616
AAX30018/c
ID   AAX30018 standard; DNA; 26 BP.
XX
AC   AAX30018;
XX
DT   16-JUN-1999  (first entry)
XX
DE   Precircle DNA oligonucleotide SEQ ID NO:5.
XX
KW   Multimer; probe; diagnosis; synthesis; detection; polymerase; ss.
XX
OS   Synthetic.
XX
PN   WO9909216-A2.
XX
PD   25-FEB-1999.
XX
PF   13-AUG-1998;   98WO-US016776.
XX
PR   13-AUG-1997;   97US-00910632.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 1999-181062/15.
XX
PT   New detectably labelled oligonucleotide multimer, comprising multiple
PT   contiguous copies of a repeated oligonucleotide - useful for detecting
PT   target molecules in diagnosis and medicinal applications.
XX
PS   Example 2; Page 41; 103pp; English.
XX
CC   The present invention describes a detectably labelled oligonucleotide
CC   multimer, comprising multiple contiguous copies of a repeated
CC   oligonucleotides. The detectably labelled oligonucleotide multimer is
CC   useful for detecting a target molecule. Oligonucleotide multimers may be
CC   produced in sufficient quantity to be useful for diagnostic and medical
CC   applications. The multimers are useful for affinity labelling of
CC   proteins, and for signal amplification in highly sensitive affinity
CC   capture and sequence identification applications. The method provides a
CC   faster, cheaper and simpler way for large-scale production of DNA and RNA
CC   oligomers and multimers. The incorporation of labels enables the
CC   oligonucleotide multimers to be useful in diagnostics and medicine. The
CC   present sequence represents an oligonucleotide used in an example from
CC   the present invention
XX
SQ   Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTTTG 2193
              |||||||||||| ||||||   ||||
Db         26 TTTTTTTTTTTGTTTTTTTTTTTTG 1
```

```
RESULT 617
ADC65872/c
ID   ADC65872 standard; DNA; 26 BP.
XX
AC   ADC65872;
XX
DT   18-DEC-2003  (first entry)
XX
DE   DNA oligonucleotide #5.
XX
KW   RNA oligonucleotide synthesis; ribonucleotide triphosphate; polymerase;
KW   electroporation; calcium phosphate treatment; lipid-mediated delivery;
KW   cation-mediated delivery; bacterial infection; viral infection;
KW   drug resistant infection; double stranded DNA oligomer; ss.
XX
OS   Synthetic.
XX
PN   US2003087241-A1.
XX
PD   08-MAY-2003.
XX
PF   30-NOV-2001; 2001US-00997931.
XX
PR   15-APR-1993;   93US-00047860.
PR   23-FEB-1995;   95US-00393439.
PR   26-FEB-1997;   97US-00805631.
PR   11-MAY-2000; 2000US-00569344.
XX
PA   (UYRP ) UNIV ROCHESTER.
XX
PI   Kool ET;
XX
DR   WPI; 2003-755141/71.
XX
PT   Synthesizing RNA oligonucleotide involves combining single-stranded
PT   circular oligonucleotide, ribonucleotide triphosphate and polymerase
PT   enzyme to yield desired RNA complementary to circular oligonucleotide
PT   template.
XX
PS   Example 2; SEQ ID NO 5; 78pp; English.
XX
CC   The invention relates to a method for synthesising an RNA
CC   oligonucleotide, comprising combining a single-stranded circular
CC   oligonucleotide template with at least two types of ribonucleotide
CC   triphosphate and a polymerase enzyme to yield a single-stranded RNA
CC   oligonucleotide multimer complementary to the circular oligonucleotide
CC   template, where the RNA oligonucleotide multimer comprises multiple
CC   copies of the desired RNA oligonucleotide. The method is useful for
CC   synthesising an RNA oligonucleotide with well-defined ends. The circular
CC   oligonucleotide is introduced into the cell using direct injection,
CC   electroporation, calcium phosphate treatment, lipid-mediated delivery, or
CC   cation-mediated delivery. The method is useful for treating bacterial
CC   and/or viral infections in mammals, particularly drug resistant
CC   infections, and for producing double stranded DNA oligomers. The method
CC   is performed in the absence of an oligonucleotide primer, or without the
CC   addition of auxiliary proteins. This sequence represents an
CC   oligonucleotide used in the method of the invention.
XX
SQ   Sequence 26 BP; 24 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 26;
  Best Local Similarity   84.6%;  Pred. No. 9.5e+02;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTTAACTTTG 2193
             ||||||||||||| ||||||    ||||
Db         26 TTTTTTTTTTTTGTTTTTTTTTTTTG 1


RESULT 618
AAN70281/c
ID   AAN70281 standard; DNA; 27 BP.
XX
AC   AAN70281;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC071 (HL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2


RESULT 619
AAN70274/c
ID   AAN70274 standard; DNA; 27 BP.
XX
AC   AAN70274;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC046 (PL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
```

```
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 620
AAN92240/c
ID   AAN92240 standard; DNA; 27 BP.
XX
AC   AAN92240;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRCO46.
XX
KW   Probe MRCO46; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .10
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    11. .16
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    17. .27
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO46 is bound by a permanent linkage to a solid support at its 3'
CC   end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 621
AAN92247/c
ID   AAN92247 standard; DNA; 27 BP.
XX
AC   AAN92247;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRCO71.
XX
KW   Probe MRCO71; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .15
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    16. .17
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    18. .27
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
```

```
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO71 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 622
AAQ40854
ID   AAQ40854 standard; DNA; 27 BP.
XX
AC   AAQ40854;
XX
DT   23-SEP-1993  (first entry)
XX
DE   DNA sequence used in DNA replication method.
XX
KW   ss.
XX
OS   Synthetic.
XX
PN   JP05103673-A.
XX
PD   27-APR-1993.
XX
PF   26-AUG-1991;   91JP-00240525.
XX
PR   26-AUG-1991;   91JP-00240525.
XX
PA   (UYAR-) UNIV ARIZONA.
XX
DR   WPI; 1993-171830/21.
XX
PT   Replication of DNA - useful in genetic engineering and medical
PT   applications.
XX
PS   Disclosure; Page 20; 20pp; Japanese.
XX
CC   The sequence is given in the disclosure to illustrate the invention
XX
SQ   Sequence 27 BP; 27 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 623
AAF99706/c
ID   AAF99706 standard; DNA; 27 BP.
XX
AC   AAF99706;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #822.
XX
KW   Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW   immunostimulatory; tumour; viral infection; bacterial infection;
KW   fungal infection; parasitic infection; cancer; asthma;
KW   infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS   Synthetic.
XX
PN   WO200122972-A2.
XX
PD   05-APR-2001.
XX
PF   25-SEP-2000; 2000WO-US026383.
XX
PR   25-SEP-1999;   99US-0156113P.
PR   27-SEP-1999;   99US-0156135P.
PR   23-AUG-2000; 2000US-0227436P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
PA   (COLE-) COLEY PHARM GMBH.
XX
PI   Krieg AM,  Schetter C,  Vollmer J;
XX
DR   WPI; 2001-273485/28.
XX
PT   Vaccinating against tumors, infectious diseases, allergies and asthma
PT   using immunostimulatory Py-rich and TG nucleic acids.
XX
PS   Claim 101; Page 56; 338pp; English.
XX
CC   The present invention relates to a method for stimulating an immune
CC   response. The method comprises administering an immunostimulatory nucleic
CC   acid to a non-rodent subject in sufficient quantity to stimulate an
CC   immune response. The present sequence is one such immunostimulatory
CC   nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC   (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC   against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC   and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC   haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC   staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC   also useful for preventing cancer, asthma, infectious disease, allergy or
CC   immune deficiency. The present sequence can also be used to redirect a
CC   Th2 to a Th1 immune response and to activate immune cells. Note: the
CC   present sequence may have a phosphorothioate backbone
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 624
ABS78427/c
ID   ABS78427 standard; DNA; 27 BP.
XX
AC   ABS78427;
XX
DT   13-DEC-2002  (first entry)
XX
DE   Angiogenesis inhibitory oligonucleotide #911.
XX
```

```
KW   Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW   tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW   diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW   corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW   rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW   plaque neovascularisation; telangiectasia; haemophiliac joint;
KW   angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW   scleroderma; hypertrophic scar.
XX
OS   Synthetic.
XX
PN   WO200253141-A2.
XX
PD   11-JUL-2002.
XX
PF   14-DEC-2001; 2001WO-US048458.
XX
PR   14-DEC-2000; 2000US-0255534P.
XX
PA   (COLE-) COLEY PHARM GROUP INC.
XX
PI   Bratzler RL;
XX
DR   WPI; 2002-566690/60.
XX
PT   Inhibiting angiogenesis in a subject, involves administering at least one
PT   antiangiogenic nucleic acid molecule to the subject.
XX
PS   Claim 2; Page 35; 276pp; English.
XX
CC   The invention relates to inhibiting angiogenesis in a subject, comprising
CC   administering at least one antiangiogenic nucleic acid molecule. Also
CC   included is a kit comprising a first container housing the antiangiogenic
CC   nucleic acids, and instructions for administering them to a subject
CC   having a condition characterised by unwanted angiogenesis. The method is
CC   useful for inhibiting angiogenesis associated with solid tumour growth,
CC   tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC   diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC   corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC   rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC   neovascularisation, telangiectasia, haemophiliac joints, angiofibroma,
CC   wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC   hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC   acid of the invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 625
ABL39406/c
ID   ABL39406 standard; DNA; 27 BP.
XX
AC   ABL39406;
XX
DT   16-APR-2002  (first entry)
XX
DE   Immunostimulatory nucleic acid SEQ ID NO: 842.
XX
KW   Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW   angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .27
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "phosphorothioate backbone"
XX
PN   WO200197843-A2.
XX
PD   27-DEC-2001.
XX
PF   22-JUN-2001; 2001WO-US020154.
XX
PR   22-JUN-2000; 2000US-0213346P.
XX
PA   (IOWA ) UNIV IOWA RES FOUND.
XX
PI   Weiner G,  Hartmann G;
XX
DR   WPI; 2002-154611/20.
XX
PT   Treating or preventing cancer, such as basal cell carcinoma, comprises
PT   administering immunostimulatory nucleic acids that induce expression of
PT   cell surface antigens and antibodies to a subject having or at risk of
PT   developing cancer.
XX
PS   Disclosure; Page 310; 312pp; English.
XX
CC   The present invention relates to methods for treating or preventing
CC   cancer, involving administering to a subject having or at risk of
CC   developing cancer immunostimulatory nucleic acids that induce expression
CC   of cell surface antigens and antibodies. The methods are useful for
CC   treating or preventing cancer such as basal cell carcinoma, bladder
CC   cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC   breast cancer, cervical cancer, colon and rectum cancer, connective
CC   tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC   cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC   Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC   cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC   cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC   present sequence is an immunostimulatory oligonucleotide described in the
CC   exemplification of the invention
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 626
ACH03245/c
ID   ACH03245 standard; DNA; 27 BP.
XX
AC   ACH03245;
XX
DT   25-SEP-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #880.
XX
KW   Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW   antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW   psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW   inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS   Synthetic.
XX
PN   US2003050268-A1.
XX
PD   13-MAR-2003.
XX
PF   29-MAR-2002; 2002US-00112653.
```

```
XX
PR   29-MAR-2001; 2001US-0279642P.
XX
PA   (KRIE/) KRIEG A M.
PA   (BERG/) BERG D J.
XX
PI   Krieg AM,  Berg DJ;
XX
DR   WPI; 2003-521815/49.
XX
PT   Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT   allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT   disease by administering an immunostimulatory nucleic acid.
XX
PS   Disclosure; Page 32; 229pp; English.
XX
CC   The invention describes a method of treating non-allergic inflammatory
CC   disease comprising administering to a subject having or at risk of
CC   developing a non-allergic inflammatory disease an immunostimulatory
CC   nucleic acid for prevention or treatment of the disease. The method is
CC   useful for treating non-allergic inflammatory diseases, such as
CC   psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC   inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC   This sequence represents an immunostimulatory nucleic acid
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 627
ADB37208/c
ID   ADB37208 standard; DNA; 27 BP.
XX
AC   ADB37208;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Immunostimulatory nucleic acid #822.
XX
KW   ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW   hypo-responsive subject; immunostimulatory.
XX
OS   Synthetic.
XX
PN   US2003087848-A1.
XX
PD   08-MAY-2003.
XX
PF   02-FEB-2001; 2001US-00776479.
XX
PR   03-FEB-2000; 2000US-0179991P.
XX
PA   (BRAT/) BRATZLER R L.
PA   (PETE/) PETERSEN D M.
PA   (FOUR/) FOURON Y.
XX
PI   Bratzler RL,  Petersen DM,  Fouron Y;
XX
DR   WPI; 2003-657977/62.
XX
PT   Treating and/or preventing allergy or asthma using an immunostimulatory
PT   nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS   Disclosure; Page 17; 221pp; English.
XX
CC   The invention relates to a method of treating or preventing allergy or
CC   asthma which comprises administering to a subject a poly-G nucleic acid
CC   in an aerosol formulation. The methods and compositions of the present
CC   invention are useful for diagnosing and/or treating asthma and allergy
CC   especially in a hypo-responsive subject. The present sequence represents
CC   an immunostimulatory nucleic acid of the invention.
XX
SQ   Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 27;
  Best Local Similarity   84.6%;  Pred. No. 1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         27 AAAAAAAAAAAAAAAAAAAAAAAAAA 2

RESULT 628
AAQ05003/c
ID   AAQ05003 standard; DNA; 29 BP.
XX
AC   AAQ05003;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-1990  (first entry)
XX
DE   Sequence binding to and inhibiting the GSTpi gene.
XX
KW   C-myc; cancer; HIV-I; AIDS; collagenase; Alzheimers disease; EGF;
KW   epidermal growth factor; GSTpi; HMGCoA; thallasemia;
KW   Herpes simplex virus; nerve growth factor receptor; globin; ss.
XX
OS   Synthetic.
XX
PN   EP375408-A.
XX
PD   27-JUN-1990.
XX
PF   20-DEC-1989;   89EP-00313391.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
PA   (HOGA/) HOGAN M E.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1990-195509/26.
XX
PT   Synthetic oligo-nucleotide(s) which bind target duplex DNA - forming co-
PT   linear triplex to control transcription process in gene-specific fashion.
XX
PS   Claim 39; Page 30; 40pp; English.
XX
CC   Sequence forms triplex with the double stranded target sequence with G
CC   binding to G-C and T to A-T. The strand runs 3' to 5' in an antiparallel
CC   orientation and when targeted to a specific sequence will deactivate it.
CC   This allows for growth inhibition in cancerous cells; manipulation of
CC   cellular structural protein content; inhibition of IL-2 chain receptor;
CC   disbursing plaque formation in Alzheimer's disease; inhibiting EGF gene;
CC   modulating cholestrol synthesis through the HMGCoA gene; suppressing NGF
CC   gene expression; arresting HSV-I replication and suppressing Beta- globin
CC   expression in thallassaemia and sicle cell anaemia patients. (Updated on
CC   25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA
CC   field.)
XX
SQ   Sequence 29 BP; 0 A; 0 C; 0 G; 29 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
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                    | ||   ||||||||||||||||||||
Db         29 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 4

RESULT 629
AAA94315
ID   AAA94315 standard; DNA; 29 BP.
XX
AC   AAA94315;
XX
DT   11-JAN-2001  (first entry)
XX
DE   RNA-protein fusion oligonucleotide 30-P.
XX
KW   RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   29
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "attached to puromycin, a peptide acceptor"
XX
PN   WO200047775-A1.
XX
PD   17-AUG-2000.
XX
PF   01-FEB-2000; 2000WO-US002589.
XX
PR   09-FEB-1999;   99US-00247190.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 2000-533022/48.
XX
PT   Producing protein or DNA libraries which are useful for improving
PT   existing proteins, by in vitro translating protein coding sequences to
PT   produce RNA-protein fusions and incubating these protein fusions under
PT   high salt conditions.
XX
PS   Disclosure; Page 43; 121pp; English.
XX
CC   The present sequence is one of a number of oligonucleotides which were
CC   used for the generation of RNA-protein fusions, including fusions having
CC   a myc epitope tag. The RNA-protein fusions comprise a protein covalently
CC   linked to the 3' end of its own mRNA. This is accomplished by synthesis
CC   and in vitro or in situ translation of an mRNA molecule with a peptide
CC   acceptor attached to its 3' end. The RNA-protein fusions are incubated
CC   under high salt conditions to produce a protein library. This method is
CC   useful for improving or altering existing proteins, as well as for
CC   isolating new proteins and nucleic acid or small molecule targets. It may
CC   also be used to improve human or humanised single-chain antibodies for
CC   the treatment of a number of diseases. The method is useful for the
CC   isolation of proteins with specific binding properties, for screening
CC   cDNA libraries and cloning new genes on the basis of protein-protein
CC   interactions. Unlike prior art, the new method does not rely on
CC   maintaining the integrity of an mRNA:ribosome:nascent chain ternary
CC   complex, which is very fragile and is therefore of limited use. The
CC   method does not rely on topological links between the protein and the
CC   nucleic acid so that the information of the protein is retained and can
CC   be recovered in readable, nucleic acid form
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||||

Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 630
AAS00066
ID   AAS00066 standard; DNA; 29 BP.
XX
AC   AAS00066;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Synthetic branched encoding molecule sequence.
XX
KW   Addressing element; microarray; protein display;
KW   branched encoding molecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   9. .10
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "AXA, where X is a branching monomer, linked to
FT                   nucleotide 16 of sequence in AAS00065 via a (Hexaethylene
FT                   oxide)n linkage"
FT   modified_base   30
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Other= Covalently linked to puromycin"
XX
PN   WO200116352-A1.
XX
PD   08-MAR-2001.
XX
PF   25-AUG-2000; 2000WO-US023414.
XX
PR   27-AUG-1999;   99US-0151261P.
XX
PA   (PHYL-) PHYLOS INC.
XX
PI   Kuimelis RG;
XX
DR   WPI; 2001-183261/18.
XX
PT   Encoding and sorting in vitro translated proteins, useful for the
PT   identification of desired binding partners, comprises attaching a nucleic
PT   acid linker to the protein and binding an encoding molecule to the
PT   linker.
XX
PS   Example 3; Fig 9B; 48pp; English.
XX
CC   The sequence represents part of a branched encoding molecule used in
CC   methods to hybridise a capture probe to the addressing element of a DNA
CC   linker attached to an in vitro translated protein, in order to immobilise
CC   the protein to a solid support. The new methods are useful for tagging or
CC   encoding in vitro translated proteins with unique and minimal encoding
CC   molecules and sorting these molecules onto solid supports. They are also
CC   useful for the identification of a desired binding partner. The method
CC   allows the use of pre-made sets of universal encoding molecules, such as
CC   nucleic acid(s) (analogues). These can be used in conjunction with
CC   corresponding universal microarrays or sets of microparticles to create
CC   new protein display systems which are flexible, modular, scalable and
CC   cost effective. The method allows the use of nucleic acid analogue which
CC   are not susceptible to enzymatic incorporation or polymerisation and are
CC   superior to conventional DNA/RNA. The proteins can also be labelled with
CC   fluorescent groups which can be used to monitor the protein in real time.
CC   The absence of RNA is advantageous as they can adopt secondary structures
CC   which are difficult to predict and can interfere with hybridisation steps
CC   and protein folding/function
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
```

```
  Best Local Similarity   84.6%;  Pred. No. 1.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 631
AAH20990
ID   AAH20990 standard; DNA; 29 BP.
XX
AC   AAH20990;
XX
DT   31-AUG-2001  (first entry)
XX
DE   C-myc epitope puromycin linker primer #1.
XX
KW   C-myc; epitope; detection; amplification; biomedical diagnosis;
KW   environmental monitoring; primer; ss.
XX
OS   Unidentified.
XX
PN   WO200142494-A2.
XX
PD   14-JUN-2001.
XX
PF   20-OCT-2000; 2000WO-EP010336.
XX
PR   10-DEC-1999;   99DE-01059857.
XX
PA   (AVET ) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.
XX
PI   Burgstaller P,  Konz D;
XX
DR   WPI; 2001-381706/40.
XX
PT   System for detecting immobilized analyte, useful e.g. for biomedical
PT   diagnosis, has as detection agent specific polypeptide coupled to nucleic
PT   acid for signal amplification.
XX
PS   Example; Page 6; 12pp; German.
XX
CC   This invention describes a novel test system (A) which comprises at least
CC   one immobilized analyte (I) on an insoluble carrier and a polypeptide
CC   detection agent (II), specific for (I) and conjugated, via a linker, to
CC   an amplifier (III). (A) is used for direct, in vitro detection of (I)
CC   with amplification of the signal by polymerase chain reaction (PCR), or a
CC   related technique, applied to (III). The method is useful in biomedical
CC   diagnosis and environmental monitoring and can be used to detect a wide
CC   range of (I), e.g. diagnostic or pharmaceutical agents, secondary
CC   metabolites, herbicides or pesticides. (A) allow simultaneous, parallel
CC   detection of many different analytes (high throughput capacity),
CC   relatively simply (only a few incubation and washing steps are required)
CC   and with high sensitivity and selectivity. This sequence represents
CC   primer used in the ampification of the c-myc DNA fragment which encodes
CC   an epitope used to illustrate the method of the invention
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 632
AAK98637
ID   AAK98637 standard; DNA; 29 BP.
XX
AC   AAK98637;
XX
DT   19-APR-2002  (first entry)
XX
DE   S cerevisiae alpha factor receptor STE2 vector linker.
XX
KW   Biological material detection; electrophoresis; bioprobe isolation;
KW   alpha factor receptor; STE2; linker; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   29
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "modified by puromycin"
XX
PN   WO200204656-A2.
XX
PD   17-JAN-2002.
XX
PF   26-JUN-2001; 2001WO-EP007259.
XX
PR   07-JUL-2000; 2000DE-01033194.
XX
PA   (XZIL-) XZILLION GMBH & CO KG.
XX
PI   Wagner P,  Polakowski T;
XX
DR   WPI; 2002-154934/20.
XX
PT   Detecting and purifying biological material by (di)electrophoresis,
PT   useful e.g. for separating tissues and viruses, comprises using a probe
PT   that alters (di)electrophoretic properties.
XX
PS   Example 1; Page 12; 20pp; German.
XX
CC   The present invention relates to a method for the detection or
CC   purification of biological material by electrophoresis, which comprises
CC   (i) treating the biological material containing different species with a
CC   bioprobe and (ii) establishing an electric field for detection or
CC   purification of at least one complex formed between the biological
CC   material being tested and a specifically bound bioprobe. The method is
CC   used for detection and purification of tissue, cells, cell organelles,
CC   viruses, proteins, nucleic acids, lipids and/or other organic compounds.
CC   It can also be used for the isolation of specific bioprobes from a
CC   library of bioprobes. The present sequence is a linker described in the
CC   exemplification of the invention
XX
SQ   Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 29;
  Best Local Similarity   84.6%;  Pred. No. 1.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 633
AAN70277/c
ID   AAN70277 standard; DNA; 30 BP.
XX
AC   AAN70277;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC064 (HL).
XX
KW   Hybridisation; probe; ss.
XX
```

```
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 634
AAN92243/c
ID   AAN92243 standard; DNA; 30 BP.
XX
AC   AAN92243;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRCO64.
XX
KW   Probe MRCO64; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .12
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    13. .20
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    21. .30
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO64 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 22 T; 8 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 635
AAQ36302/c
ID   AAQ36302 standard; DNA; 30 BP.
XX
AC   AAQ36302;
XX
DT   25-MAR-2003  (revised)
DT   07-JUN-1993  (first entry)
XX
DE   GST3anti, for GSTpi gene target sequence.
XX
KW   Glutathione-s-transferase pi; cancer; drug resistance; chemotherapy;
KW   sensitisation; triplex; target; duplex; ss.
XX
OS   Synthetic.
XX
PN   US5176996-A.
XX
PD   05-JAN-1993.
XX
PF   22-DEC-1989;   89US-00453532.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1993-035718/04.
XX
PT   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT   which bind to target sequence in duplex DNA forming colinear triplex by
PT   binding to major groove.
XX
```

```
PS   Example 8; Col 27; 29pp; English.
XX
CC   Overexpression of the enzyme glutathione-s-transferase pi has been
CC   implicated as being responsible for the broad range drug resistance which
CC   develops in a variety of cancers. Expression of the gene may be prevented
CC   by the formation of a triplex between the duplex target DNA sequence and
CC   an anti parallel or parallel synthetic oligonucleotide. A suitable target
CC   sequence is that from base -499 to -410 of GSTpi, an unusual repetitive
CC   DNA segment within the control domain. Oligonucleotides targetted against
CC   this sequence will repress GSTpi transcription. See also AAQ36219-362.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 636
AAQ36301/c
ID   AAQ36301 standard; DNA; 30 BP.
XX
AC   AAQ36301;
XX
DT   25-MAR-2003  (revised)
DT   07-JUN-1993  (first entry)
XX
DE   GST3par, for GSTpi gene target sequence.
XX
KW   Glutathione-s-transferase pi; cancer; drug resistance; chemotherapy;
KW   sensitisation; triplex; target; duplex; ss.
XX
OS   Synthetic.
XX
PN   US5176996-A.
XX
PD   05-JAN-1993.
XX
PF   22-DEC-1989;   89US-00453532.
XX
PR   20-DEC-1988;   88US-00287359.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Hogan ME,  Kessler DJ;
XX
DR   WPI; 1993-035718/04.
XX
PT   Synthetic oligo-nucleotide(s), prodn. useful e.g. for HIV-1 inhibition -
PT   which bind to target sequence in duplex DNA forming colinear triplex by
PT   binding to major groove.
XX
PS   Example 8; Col 27; 29pp; English.
XX
CC   Overexpression of the enzyme glutathione-s-transferase pi has been
CC   implicated as being responsible for the broad range drug resistance which
CC   develops in a variety of cancers. Expression of the gene may be prevented
CC   by the formation of a triplex between the duplex target DNA sequence and
CC   an anti parallel or parallel synthetic oligonucleotide. A suitable target
CC   sequence is that from base -499 to -410 of GSTpi, an unusual repetitive
CC   DNA segment within the control domain. Oligonucleotides targetted against
CC   this sequence will repress GSTpi transcription. See also AAQ36219-362.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 637
AAX57020/c
ID   AAX57020 standard; DNA; 30 BP.
XX
AC   AAX57020;
XX
DT   19-JUL-1999  (first entry)
XX
DE   WO9923258 oligonucleotide primer 2.
XX
KW   Visual; nucleic acid detection; target; hybridisation; probe; primer;
KW   agglutination; bridging molecule; ss.
XX
OS   Synthetic.
XX
PN   WO9923258-A1.
XX
PD   14-MAY-1999.
XX
PF   30-OCT-1998;   98WO-US023267.
XX
PR   31-OCT-1997;   97US-0063969P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Weisburg WG,  Stull PD,  Reshatoff MR;
XX
DR   WPI; 1999-326994/27.
XX
PT   Optical detection of hybridization complexes for specific target nucleic
PT   acid sequences.
XX
PS   Example 1; Page 40; 46pp; English.
XX
CC   This invention describes a novel method for the visual detection of
CC   target nucleic acid presence in a sample. A preferred target is a
CC   Mycobacterium complex nucleic acid sequence. The detection method uses
CC   visual detection of a change in the hybridization without aid of
CC   instrumentation. Multiple copies of a target nucleic acid sequence are
CC   mixed with first and second detectable probes under hybridizing
CC   conditions favouring particle agglutination via a bridging molecule
CC   allowing for visual detection of the target nucleic acid sequence. The
CC   bridging molecule enhances or inhibits formation of a hybridization
CC   complex
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 638
AAF99889
ID   AAF99889 standard; DNA; 30 BP.
XX
AC   AAF99889;
XX
DT   12-JUN-2001  (first entry)
XX
DE   Immunostimulatory nucleic acid #1005.
XX
```

KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Example 6; Page 60; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
| || ||||||||||||||||||
Db 1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26

RESULT 639
AAF99888/c
ID AAF99888 standard; DNA; 30 BP.
XX
AC AAF99888;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #1004.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Example 6; Page 60; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

Query Match 0.7%; Score 19.6; DB 1; Length 30;
Best Local Similarity 84.6%; Pred. No. 1.3e+03;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
| || ||||||||||||||||||
Db 30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 640
ABK10416
ID ABK10416 standard; DNA; 30 BP.
XX
AC ABK10416;
XX
DT 21-MAY-2002 (first entry)
XX
DE Synthetic primer sequence 5'-A30-3'.
XX
KW ss; 5'-A30-3'; double stranded DNA generation; promiscuous base;
KW target molecule; primer.
XX
OS Synthetic.
XX
PN US6326143-B1.
XX
PD 04-DEC-2001.
XX
PF 22-MAY-1998; 98US-00083123.
XX
PR 22-NOV-1996; 96WO-EP005149.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Orum H, Seeger C;

```
XX
DR   WPI; 2002-214947/27.
XX
PT   Determining an analyte in a sample, for generating multiple double
PT   stranded nucleic acids, comprises employing a single primer sequence with
PT   a nucleobase sequence having affinity to the sequence contained in a
PT   target nucleic acid.
XX
PS   Example 1; Col 14; 25pp; English.
XX
CC   The invention relates to determining an analyte in a sample comprising
CC   (a) providing a target nucleic acid comprising a region A, a nucleobase
CC   sequence B, and a sequence I linked to the 5' terminus of the nucleobase
CC   sequence B, where the nucleobase sequence B is not specific for the
CC   analyte, and the region A specifically binds to the analyte, (b) binding
CC   the target nucleic acid to the analyte, separating the analyte bound to
CC   the target nucleic acid from the remaining part of the sample, (d)
CC   hybridising a primer to the target nucleic acid, where the primer
CC   comprises a nucleobase sequence B', and the nucleobase sequence B'
CC   hybridises to the nucleobase sequence B, (e) elongating the hybridised
CC   primer to produce an elongation product E using the target nucleic acid
CC   as a template and using nucleotides, where at least 30 % of the
CC   nucleotides contain at least one promiscuous base which is capable of
CC   base pairing with each of adenine, guanine, cytosine, and thymine, (f)
CC   separating the target nucleic acid from the elongation product E, (g)
CC   hybridising a further primer which comprises the nucleobase sequence B'
CC   to the elongation product E, where the elongation product E is capable of
CC   acting as a template for the elongation of the further primer, (h)
CC   elongating the hybridised further primer of step (g) to produce an
CC   elongation product E' using the elongation product E as a template and
CC   using nucleotides, where at least 30 % of the nucleotides contain at
CC   least one promiscuous base, (i) separating the elongation product E from
CC   the elongation product E', (j) hybridising a further primer comprising a
CC   nucleobase sequence B' to the target nucleic acid or the elongation
CC   product E, (k) elongating the further primer of step (j) to produce
CC   another elongation product E using the target nucleic acid or elongation
CC   product E as a template and using nucleotides, where at least 30 % of the
CC   nucleotides contain at least one promiscuous base, (l) separating product
CC   E of step (k) from the target nucleic acid or elongation product E, (m)
CC   optionally repeating steps (g) - (l) a sufficient number of times to
CC   generate a desired amount of double stranded nucleic acids and (n)
CC   determining the elongation product E and/or elongation product E' as a
CC   measure of the presence or amount of the analyte, where the lengths of
CC   the sequence I and the nucleobase sequence B are chosen such that, when
CC   the further primer hybridises to the elongation product E in step (g),
CC   the further primer spans a sequence formed by elongation of the
CC   hybridised primer of step (e) and overlaps at least a part of the 3'
CC   region of the hybridized primer of step (e) by an overlap length. The
CC   method is useful determining an analyte in a sample. In particular, the
CC   method is useful for generating multiple double stranded nucleic acids.
CC   The present sequence is a primer molecule used to exemplify the method of
CC   the invention
XX
SQ   Sequence 30 BP; 30 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 641
ABK10412/c
ID   ABK10412 standard; DNA; 30 BP.
XX
AC   ABK10412;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Synthetic primer sequence 5'-T30-3'.
XX
KW   ss; 5'-T30-3'; double stranded DNA generation; promiscuous base;
KW   target molecule; primer.
XX
OS   Synthetic.
XX
PN   US6326143-B1.
XX
PD   04-DEC-2001.
XX
PF   22-MAY-1998;   98US-00083123.
XX
PR   22-NOV-1996;   96WO-EP005149.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Orum H,  Seeger C;
XX
DR   WPI; 2002-214947/27.
XX
PT   Determining an analyte in a sample, for generating multiple double
PT   stranded nucleic acids, comprises employing a single primer sequence with
PT   a nucleobase sequence having affinity to the sequence contained in a
PT   target nucleic acid.
XX
PS   Example 1; Col 14; 25pp; English.
XX
CC   The invention relates to determining an analyte in a sample comprising
CC   (a) providing a target nucleic acid comprising a region A, a nucleobase
CC   sequence B, and a sequence I linked to the 5' terminus of the nucleobase
CC   sequence B, where the nucleobase sequence B is not specific for the
CC   analyte, and the region A specifically binds to the analyte, (b) binding
CC   the target nucleic acid to the analyte, separating the analyte bound to
CC   the target nucleic acid from the remaining part of the sample, (d)
CC   hybridising a primer to the target nucleic acid, where the primer
CC   comprises a nucleobase sequence B', and the nucleobase sequence B'
CC   hybridises to the nucleobase sequence B, (e) elongating the hybridised
CC   primer to produce an elongation product E using the target nucleic acid
CC   as a template and using nucleotides, where at least 30 % of the
CC   nucleotides contain at least one promiscuous base which is capable of
CC   base pairing with each of adenine, guanine, cytosine, and thymine, (f)
CC   separating the target nucleic acid from the elongation product E, (g)
CC   hybridising a further primer which comprises the nucleobase sequence B'
CC   to the elongation product E, where the elongation product E is capable of
CC   acting as a template for the elongation of the further primer, (h)
CC   elongating the hybridised further primer of step (g) to produce an
CC   elongation product E' using the elongation product E as a template and
CC   using nucleotides, where at least 30 % of the nucleotides contain at
CC   least one promiscuous base, (i) separating the elongation product E from
CC   the elongation product E', (j) hybridising a further primer comprising a
CC   nucleobase sequence B' to the target nucleic acid or the elongation
CC   product E, (k) elongating the further primer of step (j) to produce
CC   another elongation product E using the target nucleic acid or elongation
CC   product E as a template and using nucleotides, where at least 30 % of the
CC   nucleotides contain at least one promiscuous base, (l) separating product
CC   E of step (k) from the target nucleic acid or elongation product E, (m)
CC   optionally repeating steps (g) - (l) a sufficient number of times to
CC   generate a desired amount of double stranded nucleic acids and (n)
CC   determining the elongation product E and/or elongation product E' as a
CC   measure of the presence or amount of the analyte, where the lengths of
CC   the sequence I and the nucleobase sequence B are chosen such that, when
CC   the further primer hybridises to the elongation product E in step (g),
CC   the further primer spans a sequence formed by elongation of the
CC   hybridised primer of step (e) and overlaps at least a part of the 3'
CC   region of the hybridized primer of step (e) by an overlap length. The
CC   method is useful determining an analyte in a sample. In particular, the
CC   method is useful for generating multiple double stranded nucleic acids.
CC   The present sequence is a primer molecule used to exemplify the method of
CC   the invention
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
```

```
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 642
ABK70490/c
ID   ABK70490 standard; DNA; 30 BP.
XX
AC   ABK70490;
XX
DT   15-JUL-2002  (first entry)
XX
DE   In-situ analysis synthetic probe #58.
XX
KW   Human; oligonucleotide label-domain; CMV; cytomegalovirus; EBV;
KW   Epstein-Barr virus; lambda-immunoglobulin light chain; hapten;
KW   kappa-immunoglobulin light chain; repetitive Alu sequence; EBER;
KW   Epstein-Barr early RNA; probe; ss.
XX
OS   Synthetic.
XX
PN   WO200222874-A2.
XX
PD   21-MAR-2002.
XX
PF   06-SEP-2001; 2001WO-US028014.
XX
PR   15-SEP-2000; 2000US-0233177P.
XX
PA   (VENT-) VENTANA MEDICAL SYSTEMS INC.
XX
PI   Utermohlen JG,  Connaughton J;
XX
DR   WPI; 2002-371972/40.
XX
PT   Novel oligonucleotide label-domain for incorporation into oligonucleotide
PT   probes useful for detecting or localizing nucleic acid target genes
PT   within a cell or tissue sample.
XX
PS   Disclosure; Page 69; 71pp; English.
XX
CC   The present invention relates to a new oligonucleotide label-domain
CC   comprising the sequence (CTATTTT)_n and its complement (AAAATAG)_n, where
CC   n is 1. The probe sets of the invention are useful for detecting kappa or
CC   lambda-immunoglobulin light chain mRNA or corresponding heteronuclear
CC   RNA, CMV (cytomegalovirus) immediate early RNA, EBV (Epstein-Barr virus)
CC   early RNA 1 and RNA 2, and human Alu repetitive satellite genomic
CC   sequences. The invention is a useful generic sequence for incorporation
CC   into oligonucleotide probes for detecting gene-specific sequences within
CC   cells or tissue samples in in situ hybridisation analysis and for
CC   attaching a label to immunoglobulins or other proteins for detecting
CC   haptens and antigens in immunohistochemical analyses. The present nucleic
CC   acid sequence represents one of a collection (ABK70376-ABK70501) of
CC   oligonucleotide probes that were used in the invention for detecting or
CC   localising a plurality nucleic acid target gene or antigen within a cell
CC   or tissue sample
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 643
ABS53961/c
ID   ABS53961 standard; DNA; 30 BP.
XX
AC   ABS53961;
XX
DT   26-NOV-2002  (first entry)
XX
DE   Method of measuring nucleic acid related oligonucleotide dT30mer.
XX
KW   Fluorescent intercalative dye; nucleic acid detection; gene diagnosis;
KW   clinical diagnostics; Stokes shift; ds.
XX
OS   Synthetic.
XX
PN   EP1223226-A2.
XX
PD   17-JUL-2002.
XX
PF   11-JAN-2002; 2002EP-00000723.
XX
PR   11-JAN-2001; 2001JP-00003432.
XX
PA   (TOYJ ) TOSOH CORP.
XX
PI   Tokunaga T,  Ishiguro T,  Horie R;
XX
DR   WPI; 2002-645688/70.
XX
PT   Fluorescent dye or its salt, hydrate, solvate or stereoisomer for nucleic
PT   acid probe for measuring nucleic acid(s) containing specific nucleic acid
PT   sequence in sample, has specific formula.
XX
PS   Example 5; Page 33; 40pp; English.
XX
CC   The invention describes a novel fluorescent dye and method of detecting
CC   nucleic acid. The dye and method are useful for nucleic acid probes for
CC   measuring nucleic acid(s) containing a specific nucleic acid sequence in
CC   a sample, and for qualitative/quantitative assay of target RNA containing
CC   specific base sequence anticipated in gene mixture. The assay is useful
CC   in gene diagnosis and other areas of clinical diagnostics and in
CC   identification/quantification microorganisms in biological samples such
CC   as serum, plasma and urine, microbially contaminated samples from food,
CC   rooms, soil, rivers and sea. The fluorescent intercalative dye shows a
CC   large fluorescent enhancement upon intercalation into double-stranded
CC   nucleic acid, and shows a great difference between excitation and
CC   emission wavelengths (has a large Stokes shift) and does not have a
CC   fluorescent spectrum that overlaps with those of conventionally known
CC   fluorescent intercalation dyes. Viruses, microbial RNAs, specific
CC   sequences in one RNA, are detected or quantified in a short time, hence
CC   the detection method is applicable to clinical diagnosis which requires
CC   high reliability. Amplification and extraction efficiencies of the target
CC   nucleic acid, are checked. This sequence represents a synthetic DNA used
CC   as the target in an assay to detect double stranded DNA
XX
SQ   Sequence 30 BP; 0 A; 0 C; 0 G; 30 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||
Db         30 AAAAAAAAAAAAAAAAAAAAAAAAAA 5


RESULT 644
AAV48087
ID   AAV48087 standard; DNA; 30 BP.
XX
AC   AAV48087;
XX
DT   27-OCT-1998  (first entry)
XX
```

```
DE   Oligonucleotide 30-P.
XX
KW   In situ translation; RNA-protein fusion; binding reagent; antibody;
KW   industrial catalyst; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   30
FT                   /*tag=  a
FT                   /note= "Puromycin"
XX
PN   WO9831700-A1.
XX
PD   23-JUL-1998.
XX
PF   14-JAN-1998;    98WO-US000807.
XX
PR   21-JAN-1997;    97US-0035963P.
PR   06-NOV-1997;    97US-0064491P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
XX
PI   Szostak JW,  Roberts RW,  Liu R;
XX
DR   WPI; 1998-414032/35.
XX
PT   Selection of specific protein by screening protein-RNA fusions generated
PT   in vitro or in situ - useful for, e.g. identifying enzymes and antibodies
PT   with altered properties, potentially useful as catalysts or for therapy
PT   or diagnosis.
XX
PS   Disclosure; Page 39; 94pp; English.
XX
CC   The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and
CC   variations were used to generate RNA-protein fusions. These were used in
CC   the selection of a specific protein or RNA, by in vitro or in situ
CC   translation of candidate RNA molecules to produce RNA-protein fusions,
CC   then selecting specific RNA protein fusions. The method is used to select
CC   proteins (or DNA encoding them) having altered properties, e.g. for
CC   identification of new binding reagents, to identify improved human
CC   antibodies or new enzymes. These proteins are potentially useful in
CC   diagnosis and therapy, or as industrial catalysts. The methods allow many
CC   rounds of selection and amplification to be performed, resulting in
CC   enrichment of even very rare molecules and allowing isolation of proteins
CC   that bind specifically to almost any compound or catalyse almost any
CC   reaction
XX
SQ   Sequence 30 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 1 Other;

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 645
AAQ83940
ID   AAQ83940 standard; DNA; 30 BP.
XX
AC   AAQ83940;
XX
DT   25-MAR-2003  (revised)
DT   04-OCT-1995  (first entry)
XX
DE   Oligonucleotide clamp o, for producing comb-type brached polymer.
XX
KW   HIV; pol; nef; oligonucleotide clamp; branched; macromolecule; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "Modified with SP(O-)(=O)-"
XX
PN   WO9501365-A1.
XX
PD   12-JAN-1995.
XX
PF   05-JUL-1994;    94WO-US007557.
XX
PR   02-JUL-1993;    93US-00087386.
XX
PA   (LYNX-) LYNX THERAPEUTICS INC.
XX
PI   Gryaznov SM;
XX
DR   WPI; 1995-060944/08.
XX
PT   Synthesis of branched polymers and novel branched polymeric structures -
PT   used as molecular probes esp. for detecting poly-nucleotide(s).
XX
PS   Example 8; Page 33; 52pp; English.
XX
CC   The sequences given in AAQ83938, AAQ83952 and AAQ83940 are used in the
CC   construction of an oligonucleotide clamp. The clamp is a comb-type
CC   branched polymer which has 3' termini and was used to bind a target
CC   sequence comprising a segment of the HIV pol and nef genes in single
CC   stranded or double stranded forms. An oligonucleotide clamp is a compound
CC   capable of forming a covalently closed macromolecule or a stable circular
CC   complex after specifically binding to the target polynucleotide.
CC   Oligonucleotide clamps generally comprise one or more oligonucleotide
CC   moieties capable of specific binding to the target molecule and one or
CC   more pairs of binding moieties covalently linked to the oligonucleotide
CC   moieties. Upon annealing of the oligonucleotides moieties to the target
CC   polynucleotide, the binding moieties of a pair are bought into
CC   juxtaposition so that they form a stable covalent or non-covalent linkage
CC   or complex. The interaction of the binding moieties effectively clamps
CC   the specifically annealed oligonucleotide moieties to the target
CC   polynucleotide. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db          4 ACAAAAAAAAAAAAAAAAAAAAAAAA 29


RESULT 646
AAF60462
ID   AAF60462 standard; DNA; 30 BP.
XX
AC   AAF60462;
XX
DT   27-APR-2001  (first entry)
XX
DE   Oligonucleotide clamp #22.
XX
KW   Oligonucleotide clamp; ds.
XX
OS   Unidentified.
XX
PN   US6180777-B1.
XX
PD   30-JAN-2001.
XX
PF   03-JAN-1997;    97US-00787321.
XX
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PR   12-JAN-1996;   96US-0009918P.
XX
PA   (FARB ) BAYER CORP.
XX
PI   Horn T;
XX
DR   WPI; 2001-201911/20.
XX
PT   Synthesizing branched nucleic acids useful as diagnostic and molecular
PT   probes, involves combining first units having haloalkylamino groups and
PT   second units having thiol or phosphorothioate groups.
XX
PS   Example 8; Col 19; 20pp; English.
XX
CC   The present invention relates to a method for synthesising a branched or
CC   multiply connected macromolecular structure, comprising oligonucleotide
CC   clamps (OC). The macromolecular structure is capable of specifically
CC   binding to a target molecule, and can therefore be used as probes. At
CC   least one OC comprises a target binding sequence that binds specifically
CC   and stably with the target molecule, and at least two OCs comprise signal
CC   generation moieties capable of generating a detectable signal in the
CC   presence of the target molecule. In addition the OCs are connected to one
CC   another by thioalkylamino, or thiophosphorylalkylamino bridges. The
CC   present sequence is an OC used in the present invention
XX
SQ   Sequence 30 BP; 27 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||||
Db          4 ACAAAAAAAAAAAAAAAAAAAAAAAA 29


RESULT 647
AAV62858/c
ID   AAV62858 standard; DNA; 30 BP.
XX
AC   AAV62858;
XX
DT   05-MAR-1999  (first entry)
XX
DE   Primer for PR-Q gene.
XX
KW   Chemically regulatable DNA promoter; expression control; pesticide;
KW   herbicide tolerance; pathogenesis-related gene; PR gene; primer; ss.
XX
OS   Synthetic.
OS   Nicotiana acuminata.
XX
PN   US5851766-A.
XX
PD   22-DEC-1998.
XX
PF   31-MAY-1995;   95US-00456262.
XX
PR   31-MAY-1995;   95US-00456262.
XX
PA   (NOVS ) NOVARTIS FINANCE CORP.
XX
PI   Harms C,  Ryals JA;
XX
DR   WPI; 1999-080396/07.
XX
PT   Isolating chemically regulatable DNA sequences in plants - useful for
PT   chemically controlling expression in transformed plants.
XX
PS   Example 72; Col 96; 175pp; English.
XX
CC   This sequence represents a primer used to isolate the tobacco
CC   pathogenesis-related (PR) gene. The PR gene can be isolated using the
CC   method of the invention. The method is for isolating a chemically
CC   regulatable DNA promoter fragment from the 5' flanking region of a
CC   chemically regulatable gene in a plant tissue. The method allows
CC   isolation of sequences which will be useful for the controlled expression
CC   of genes, under the control of a non-coding regulatable sequence. This is
CC   useful in plants with a herbicide or pesticide detoxification mechanism
CC   under the control of a chemical regulator, the regulator being applied
CC   before or with the herbicide or pesticide to give optimal tolerance. The
CC   promoter fragment is useful for controlling sequences which encode traits
CC   such as height, shape, development, male or female sterility, and the
CC   ability of the plant to withstand cold, heat, salt and drought. The
CC   chemical induction of the promoter allows the regulation of production of
CC   compounds, e.g. flavours, fragrances, pigments, natural sweeteners,
CC   industrial feedstocks, antimicrobials and pharmaceuticals, by
CC   biosynthesis or metabolite conversion, whose biosynthesis is controlled
CC   by endogenous or foreign genes. The method allows control over the time
CC   and rate of gene expression either throughout the whole plant, or in
CC   localized tissues, to achieve e.g. fungal or insect resistance by for
CC   instance dusting the leaves with the chemical regulator. Controlling the
CC   developmental processes by the application of a regulating chemical in
CC   e.g. the commercial production of cultivated crops allows processes such
CC   as germination, flower formation and fruit ripening to be synchronised at
CC   a given time
XX
SQ   Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
                ||| | |||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTTGAATT 5


RESULT 648
AAV81666/c
ID   AAV81666 standard; DNA; 30 BP.
XX
AC   AAV81666;
XX
DT   25-FEB-1999  (first entry)
XX
DE   Oligonucleotide SEQ ID NO:85 used in Example 72.
XX
KW   Regulation; transcription; plant tissue; chimeric construction; PR;
KW   pathogenesis-related protein; anti-pathogenic; transgenic plant;
KW   beta-1,3-glucanase activity; pest resistance; primer; ss.
XX
OS   Synthetic.
XX
PN   US5847258-A.
XX
PD   08-DEC-1998.
XX
PF   31-MAY-1995;   95US-00457364.
XX
PR   08-MAR-1988;   88US-00165667.
PR   06-FEB-1989;   89US-00305566.
PR   24-MAR-1989;   89US-00329018.
PR   20-JUN-1989;   89US-00368672.
PR   20-OCT-1989;   89US-00425504.
PR   07-SEP-1990;   90US-00580431.
PR   21-DEC-1990;   90US-00632441.
PR   01-APR-1991;   91US-00678378.
PR   27-SEP-1991;   91US-00768122.
PR   06-MAR-1992;   92US-00848506.
PR   06-NOV-1992;   92US-00973197.
PR   06-APR-1993;   93US-00042847.
PR   12-APR-1993;   93US-00045957.
PR   16-JUL-1993;   93US-00093301.
PR   13-JAN-1994;   94US-00181271.
PR   31-MAY-1995;   95US-00457364.
```

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XX
PA   (NOVS ) NOVARTIS FINANCE CORP.
XX
PI   Payne GB,  Ward ER,  Moyer MB,  Ryals JA;
XX
DR   WPI; 1999-059180/05.
XX
PT   DNA encoding pathogenesis-related glucanase proteins - useful for
PT   producing transgenic plants with enhanced disease or pest resistance.
XX
PS   Example 72; Col 93; 169pp; English.
XX
CC   The present invention describes a DNA molecule encoding a pathogenesis-
CC   related (PR) protein having beta-1,3-glucanase activity selected from PR-
CC   2, PR-2', PR-2'', PR-N, PR-O and PR-O'. Also described are: (i) a
CC   chimeric gene comprising the above DNA molecule linked to a heterologous
CC   promoter; (ii) a vector containing the chimeric gene; (iii) a host cell
CC   containing the chimeric gene; (iv) a transgenic plant containing the
CC   chimeric gene; and (v) a seed from the transgenic plant. The DNA molecule
CC   is used to produce transgenic plants with enhanced disease or pest
CC   resistance. The present sequence represents an oligonucleotide from the
CC   present invention
XX
SQ   Sequence 30 BP; 20 A; 3 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2165 CTTTTTTTTTTTTTTTTTTTTAACT 2190
              ||| | ||||||||||||||||| || |
Db         30 CTTATGTTTTTTTTTTTTTTTGAATT 5


RESULT 649
AAI65862
ID   AAI65862 standard; DNA; 30 BP.
XX
AC   AAI65862;
XX
DT   03-JAN-2002  (first entry)
XX
DE   Nucleotide sequence of triplex forming oligonucleotide for Hprt gene.
XX
KW   DNA-modifying molecule; DNA repair-deficient cell; transgenic cell;
KW   disease model; Hprt gene; triplex forming oligonucleotide; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /note= "psoralen attached"
XX
PN   WO200173001-A2.
XX
PD   04-OCT-2001.
XX
PF   22-MAR-2001; 2001WO-US009218.
XX
PR   24-MAR-2000; 2000US-0191996P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Seidman MM,  Majumdar A;
XX
DR   WPI; 2001-616491/71.
XX
PT   Modifying nucleotide sequence, including recombination of genes in (non-
PT   )human cell, comprises introducing DNA-modifying molecule into cell cycle
PT   synchronized cell.
XX
PS   Example 4; Page 49; 67pp; English.
XX
CC   The specification describes a method for modifying a nucleotide sequence
CC   in the genome of a cell. The method comprises providing a cell and a DNA-
CC   modifying molecule, manipulating the cell to generate a synchronized cell
CC   and contacting the synchronized cell with the DNA-modifying molecule
CC   under conditions such that a modification in the nucleotide sequence is
CC   produced. The method is useful for modifying nucleotide sequences in the
CC   genome of a human or non-human cell including a fertilized egg cell from
CC   an animal such as sheep, pig, rabbit, cattle and a mouse cell such as
CC   blastomere, eight-cell embryo cell, blastocoele, midgestation embryo cell
CC   and embryonic stem cell. The cell is preferably DNA repair-deficient. The
CC   method is useful for introducing a modification into the genome of a cell
CC   for determining the effect of the modification on the cell. The method
CC   generates transgenic cells and animals useful as models for diseases, and
CC   for screening therapeutic agents. The method also facilitates targeted
CC   recombination for producing gene knockout organisms and/or replacement of
CC   detective genes with non-defective genes. Further the method is useful
CC   for determining the function of a gene of unknown function. AAI65861-62
CC   represent triplex forming oligonucleotides, which were used in the method
CC   of the invention to modify a fragment of the Hprt gene
XX
SQ   Sequence 30 BP; 0 A; 6 C; 0 G; 24 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 30;
  Best Local Similarity   84.6%;  Pred. No. 1.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2156 TTTTTTCTCCTTTTTTTTTTTTTTT 2181
              |||||||| ||||| ||| ||||| |
Db          5 TTTTTTCTTCTTTTCTTTCTTTTTCT 30


RESULT 650
AAN70278/c
ID   AAN70278 standard; DNA; 32 BP.
XX
AC   AAN70278;
XX
DT   03-OCT-2002  (revised)
DT   26-MAY-1991  (first entry)
XX
DE   Sequence of scissile link probe MRC068 (HL).
XX
KW   Hybridisation; probe; ss.
XX
OS   Synthetic.
XX
PN   EP227976-A.
XX
PD   08-JUL-1987.
XX
PF   04-DEC-1986;   86EP-00116906.
XX
PR   05-DEC-1985;   85US-00805279.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R,  Crosby W,  Robertson JG;
XX
DR   WPI; 1987-186567/27.
XX
PT   Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT   linked by a scissile linkage.
XX
PS   Example; p29; 46pp; English.
XX
CC   The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC   NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC   linkage; n= 1 or 1,000, which is used for the detection of specific DNA
CC   or RNA sequences in a test soln. The scissile link probes may be PL
CC   (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC   Support). The differential liability of DNA and RNA may be exploited in a
CC   heterogenous system when the scissile linkage is an RNA molecule. In the
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CC   examples, counter probe molecules 9 through 16 were used to determine
CC   suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC   OS field.)
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 32;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAAAAAAAAAA 7


RESULT 651
AAN92244/c
ID   AAN92244 standard; DNA; 32 BP.
XX
AC   AAN92244;
XX
DT   25-MAR-2003  (revised)
DT   31-OCT-2002  (revised)
DT   25-APR-1990  (first entry)
XX
DE   SS probe MRCO68.
XX
KW   Probe MRCO68; solid support; ribonuclease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1. .14
FT                   /*tag=  a
FT                   /note= "deoxyribonucleotides."
FT   misc_feature    15. .22
FT                   /*tag=  b
FT                   /note= "ribonucleotides."
FT   misc_feature    23. .32
FT                   /*tag=  c
FT                   /note= "deoxyribonucleotides."
XX
PN   WO8910415-A.
XX
PD   02-NOV-1989.
XX
PF   29-APR-1988;   88US-00187814.
XX
PR   29-APR-1988;   88US-00187814.
XX
PA   (MEIO-) MEIOGENICS INC.
XX
PI   Duck P,  Bender R;
XX
DR   WPI; 1989-339977/46.
XX
PT   Detecting target nucleic acid molecules - using excess complementary
PT   nucleic acid probes and nicking to complete a cycling sequence.
XX
PS   Disclosure; Page 24; 34pp; English.
XX
CC   Probe MRCO68 is bound by a hydrolysable linkage to a solid support at its
CC   3' end. It is used by reacting excess probe with a target nucleic acid;
CC   nicking hybridised probe at least once within a predetermined sequence to
CC   form 2 or more probe fragments hybridised to the target sequence, which
CC   results in the probe fragments becoming hybridised to another probe; and
CC   identifying probe fragments, so detecting the target sequence. The probe
CC   can react with target sequence to complete a cycling sequence. Using this
CC   system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC   be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC   RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
CC   (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 24 T; 8 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 32;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAAAAAAAAAA 7


RESULT 652
ADC33445/c
ID   ADC33445 standard; DNA; 32 BP.
XX
AC   ADC33445;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Template oligonucleotide #SEQ ID 2.
XX
KW   Binding; tandem repeat; label; analyte detection; ss.
XX
OS   Synthetic.
XX
PN   WO2003072721-A2.
XX
PD   04-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005301.
XX
PR   21-FEB-2002; 2002US-0359223P.
PR   08-MAY-2002; 2002US-0379360P.
XX
PA   (DISC-) DISCOVERX INC.
XX
PI   Wu M,  Ullman E;
XX
DR   WPI; 2003-712717/67.
XX
PT   Detecting a label comprising employing (as the label) a reagent having a
PT   3' extendable terminus hybridized to a tandem repeat template in
PT   combination with a DNA polymerase and dNTPs necessary for repetitively
PT   replicating the tandem repeat.
XX
PS   Example; SEQ ID NO 2; 38pp; English.
XX
CC   The invention relates to a method for detecting a label, comprising
CC   employing (as the label) a reagent having a 3' extendable terminus
CC   hybridised to a tandem repeat template in combination with a DNA
CC   polymerase and dNTPs necessary for repetitively replicating the tandem
CC   repeat. The method involves detecting a binding event between first and
CC   second binding members, employing a label to determine the occurrence of
CC   the binding event. The tandem repeating units are polyT. The method of
CC   the invention is useful in detecting an analyte using repetitive
CC   extension along a tandem repeat. The extended nucleic acid may be used
CC   for detecting a moiety, particularly involved in a binding event
CC   employing a reagent. The current sequence represents a template member
CC   oligonucleotide containing a polyT tandem repeat that binds to the
CC   extendable oligonucleotide given in ADC33444.
XX
SQ   Sequence 32 BP; 0 A; 0 C; 0 G; 32 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 32;
  Best Local Similarity   84.6%;  Pred. No. 1.5e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         32 AAAAAAAAAAAAAAAAAAAAAAAAAA 7


RESULT 653
```

```
AAF29153/c
ID   AAF29153 standard; DNA; 33 BP.
XX
AC   AAF29153;
XX
DT   04-APR-2001  (first entry)
XX
DE   PCR primer SEQ ID 24 used to amplify SRSV specific cDNA.
XX
KW   Small round structured virus; SRSV; food poisoning; PCR primer; ss.
XX
OS   Small round structured virus.
XX
PN   WO200079280-A1.
XX
PD   28-DEC-2000.
XX
PF   22-JUN-2000; 2000WO-JP004095.
XX
PR   22-JUN-1999;   99JP-00175928.
XX
PA   (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA   (DENK-) DENKA SEIKEN KK.
XX
PI   Takeda N,  Natori K,  Miyamura T,  Kamata K,  Sato T,  Sato S;
XX
DR   WPI; 2001-080848/09.
XX
PT   Kit for the detection and typing of small round-structured virus (SRSV)
PT   strains for investigation of food poisoning outbreaks, contains
PT   antibodies.
XX
PS   Example 1; Page 75; 84pp; Japanese.
XX
CC   This invention relates to a kit for the detection and typing of small
CC   round structured virus (SRSV) strains. The kit contains antibodies
CC   directed against peptides represented in sequences AAB49700 - AAB49710,
CC   which are each SRSV strain specific. Polynucleotide sequences AAF20141 -
CC   AAF20151 represent cDNA encoding the strain specific proteins. The kit is
CC   used for detecting and typing strains of SRSV in order to prevent the
CC   spread of infection and to examine the epidemiology of outbreaks. PCR
CC   primers AAF29152 - AAF29163 are used to amplify SRSV strain specific cDNA
CC   sequences
XX
SQ   Sequence 33 BP; 0 A; 0 C; 0 G; 33 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 33;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAAAA 8


RESULT 654
AAX88521/c
ID   AAX88521 standard; DNA; 33 BP.
XX
AC   AAX88521;
XX
DT   13-SEP-1999  (first entry)
XX
DE   Conus stercusmuscarum contryphan PCR primer DHOG 496.
XX
KW   Contryphan; leu-tryphan; anticonvulsant; neuroprotective; venom;
KW   cone snail; neurodegenerative disorder; epilepsy; neurotoxic injury;
KW   hypoxia; anoxia; ischaemia; stroke; cerebrovascular accident;
KW   brain trauma; spinal chord trauma; myocardial infarct; physical trauma;
KW   drowning; suffocation; perinatal asphyxia; hypoglycaemia; migraine;
KW   senile dementia; Alzheimer's disease; amyotrophic lateral sclerosis;
KW   Parkinson's disease; Huntington's disease; Down's syndrome; PCR primer;
KW   Korsakoff's disease; schizophrenia; neuronal damage; seizure; ss.
XX
OS   Synthetic.
OS   Conus stercusmuscarum.
XX
PN   WO9933865-A1.
XX
PD   08-JUL-1999.
XX
PF   16-DEC-1998;   98WO-US026789.
XX
PR   24-DEC-1997;   97US-0068737P.
PR   16-APR-1998;   98US-00061026.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Jacobsen R,  Jimenez E,  Cruz LJ,  Olivera BM,  Gray WR,  Grilley M;
PI   Watkins M,  Hillyard DR;
XX
DR   WPI; 1999-419087/35.
XX
PT   New pure contryphan peptides.
XX
PS   Example 3; Page 20; 48pp; English.
XX
CC   The present sequence sequence represents a PCR primer for a contryphan
CC   peptide sequence. Contryphan peptides are found in the venom of cone
CC   snails. The contryphan peptides are useful as anticonvulsant agents, as
CC   neuroprotective agents, for managing pain, and for treating
CC   neurodegenerative disorders, especially those resulting from an
CC   overstimulation of excitatory amino acid receptors. The contryphans are
CC   useful for the treatment and alleviation of epilepsy and as a general
CC   anticonvulsant agent. The contryphans are also useful to reduce
CC   neurotoxic injury associated with conditions of hypoxia, anoxia, or
CC   ischaemia which typically follows stroke, cerebrovascular accident, brain
CC   or spinal chord trauma, myocardial infarct, physical trauma, drownings,
CC   suffocation, perinatal asphyxia, or hypoglycaemic events. The contryphans
CC   are further useful for the treatment of Alzheimer's disease, senile
CC   dementia, amyotrophic lateral sclerosis, Parkinson's disease,
CC   Huntington's disease, Down's syndrome, Korsakoff's disease,
CC   schizophrenia, AIDS dementia, multi-infarct dementia, and neuronal damage
CC   associated with uncontrolled seizures. The contryphans are further useful
CC   in controlling pain and are effective in the treatment of migraine. They
CC   can be used prophylactically or to relieve the symptoms associated with a
CC   migraine episode
XX
SQ   Sequence 33 BP; 0 A; 1 C; 2 G; 30 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 33;
  Best Local Similarity   84.6%;  Pred. No. 1.6e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         33 AAAAAAAAAAAAAAAAAAAAAAAAAA 8


RESULT 655
AAT93827/c
ID   AAT93827 standard; DNA; 34 BP.
XX
AC   AAT93827;
XX
DT   25-MAR-2003  (revised)
DT   24-FEB-1998  (first entry)
XX
DE   Antitumoural phosphodiester oligonucleotide 17 with cytotoxic activity.
XX
KW   Phosphodiester; selective binding; cell viability; growth;
KW   tumoural cell line; cytotoxic activity; tumour cell; lymphoma;
KW   lymphoblastic tumour; ss.
XX
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   modified_base   1. .34
FT                   /*tag=  a
FT                   /note= "phosphodiester oligonucleotide"
XX
PN   WO9720924-A1.
XX
PD   12-JUN-1997.
XX
PF   04-DEC-1996;    96WO-EP005388.
XX
PR   04-DEC-1995;    95IT-MI002539.
XX
PA   (SAIC-) SAICOM SRL.
XX
PI   Scaggiante B,  Quadrifoglio F;
XX
DR   WPI; 1997-319771/29.
XX
PT   New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and
PT   selective cytotoxic effect on tumour cells, for treating both solid and
PT   liquid tumours.
XX
PS   Claim 10; Page 6; 38pp; English.
XX
CC   Novel phosphodiesteric oligonucleotides AAT93811-27 are based on the
CC   generic formula, in the 3'-5' or 5'-3' direction: (GaTa')a''-(GbTb')b''-
CC   (GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''- (G-gTg')g''-N', where: N and
CC   N' = T or G, equal or different from each other; x = 0-8, equal or
CC   different from each other; a, b, c, d, e, f, and g = 0-10, equal or
CC   different from each other; a', b', c', d', e', f', and g' = 0-30, equal
CC   or different from each other; a'', b'', c'', d'', e'', f'', and g'' = 1-
CC   16, equal or different from each other; The oligonucleotides are believed
CC   to selectively bind and sequester some proteins which are essential to
CC   the viability and growth of tumoural cell line. They have specific and
CC   selective cytotoxic activity against tumour cells, and can be used for
CC   treating tumours of the liquid type, in particular of lymphoblastic
CC   origin, and of solid type, in particular lymphomas. The present
CC   phosphodiester oligonucleotide, at a concentration of 15 micromolar,
CC   reduced growth of CCRF-CEM tumoural cells by 71%, which is detectable 48
CC   hours after administration. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 34 BP; 0 A; 0 C; 2 G; 32 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 34;
  Best Local Similarity   84.6%;  Pred. No. 1.7e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         34 ACAAAAAAAAAAAAAAAAAAAAAAAA 9


RESULT 656
AAL07488
ID   AAL07488 standard; DNA; 38 BP.
XX
AC   AAL07488;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human reproductive system related antigen DNA SEQ ID NO: 10176.
XX
KW   Human; reproductive system related antigen; reproductive system disorder;
KW   cancer; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155320-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001339.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
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PR   11-JUL-2000; 2000US-0217487P.
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PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
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PR   14-AUG-2000; 2000US-0225213P.
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PR   14-AUG-2000; 2000US-0225266P.
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PR   14-AUG-2000; 2000US-0225270P.
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PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
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PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
PR   08-SEP-2000; 2000US-0231243P.
PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
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PR   08-SEP-2000; 2000US-0232080P.
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PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
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PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
PR   14-SEP-2000; 2000US-0233065P.
PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236369P.
PR   29-SEP-2000; 2000US-0236370P.
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PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0237040P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240960P.
PR   20-OCT-2000; 2000US-0241221P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
PR   20-OCT-2000; 2000US-0241808P.
PR   20-OCT-2000; 2000US-0241809P.
PR   20-OCT-2000; 2000US-0241826P.
PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0246474P.
PR   08-NOV-2000; 2000US-0246475P.
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PR   08-NOV-2000; 2000US-0246478P.
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PR   08-NOV-2000; 2000US-0246524P.
PR   08-NOV-2000; 2000US-0246525P.
PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0246527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
PR   08-NOV-2000; 2000US-0246609P.
PR   08-NOV-2000; 2000US-0246610P.
PR   08-NOV-2000; 2000US-0246611P.
PR   08-NOV-2000; 2000US-0246613P.
PR   17-NOV-2000; 2000US-0249207P.
PR   17-NOV-2000; 2000US-0249208P.
PR   17-NOV-2000; 2000US-0249209P.
PR   17-NOV-2000; 2000US-0249210P.
PR   17-NOV-2000; 2000US-0249211P.
PR   17-NOV-2000; 2000US-0249212P.
PR   17-NOV-2000; 2000US-0249213P.
PR   17-NOV-2000; 2000US-0249214P.
PR   17-NOV-2000; 2000US-0249215P.
PR   17-NOV-2000; 2000US-0249216P.
PR   17-NOV-2000; 2000US-0249217P.
PR   17-NOV-2000; 2000US-0249218P.
PR   17-NOV-2000; 2000US-0249244P.
PR   17-NOV-2000; 2000US-0249245P.
PR   17-NOV-2000; 2000US-0249264P.
PR   17-NOV-2000; 2000US-0249265P.
PR   17-NOV-2000; 2000US-0249297P.
PR   17-NOV-2000; 2000US-0249299P.
PR   17-NOV-2000; 2000US-0249300P.
PR   01-DEC-2000; 2000US-0250160P.
PR   01-DEC-2000; 2000US-0250391P.
PR   05-DEC-2000; 2000US-0251030P.
PR   05-DEC-2000; 2000US-0251988P.
PR   05-DEC-2000; 2000US-0256719P.
PR   06-DEC-2000; 2000US-0251479P.
PR   08-DEC-2000; 2000US-0251856P.
PR   08-DEC-2000; 2000US-0251868P.
PR   08-DEC-2000; 2000US-0251869P.
PR   08-DEC-2000; 2000US-0251989P.
PR   08-DEC-2000; 2000US-0251990P.
PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465570/50.
XX
PT   Isolated nucleic acid molecule encoding a reproductive system antigen is
PT   used in preventing, treating or ameliorating a medical condition.
XX
PS   Disclosure; SEQ ID NO 10176; 1297pp + Sequence Listing; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human reproductive system related antigens. These can be used
CC   in the prevention and treatment of reproductive system disorders,
CC   including cancer. The present sequence is a genomic sequence encoding a
CC   protein of the invention
XX
SQ   Sequence 38 BP; 35 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 38;
  Best Local Similarity   84.6%;  Pred. No. 2.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                |||   ||||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 657
AAZ57404/c
ID   AAZ57404 standard; DNA; 38 BP.
XX
AC   AAZ57404;
XX
DT   07-APR-2000  (first entry)
XX
DE   Hepatitis C virus PCR primer CAC-T35 SEQ ID NO:19.
XX
KW   Hepatitis C virus; RNA virus; replication; viral infection; PCR primer;
KW   ss.
XX
OS   Hepatitis C virus.
XX
PN   WO9967394-A1.
XX
PD   29-DEC-1999.
XX
PF   24-JUN-1999;   99WO-JP003380.
XX
PR   24-JUN-1998;   98JP-00177820.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Kohara M,  Kohara K,  Taira K,  Matsuzaki J,  Ohmori H;
XX
DR   WPI; 2000-106296/09.
XX
PT   Vectors expressing full-length gene of RNA viruses, useful in clarifying
PT   mechanisms of RNA viral replication, infection, and developing remedies
PT   and therapeutics.
XX
PS   Example 2; Page 20; 46pp; Japanese.
XX
CC   The present invention describes a vector comprising a cDNA encoding an
CC   RNA virus gene, constructed to ensure the exact and homogeneous
CC   transcription of both terminals of the RNA virus gene. Also described is
CC   a method for screening drugs for inhibiting the replication of RNA virus
CC   by using the RNA viral infection model animal, particularly one with
CC   hepatitis C viral infection. The vector is useful in clarifying the
CC   mechanism of RNA viral replication, onset of RNA viral infection, and
CC   developing remedies and therapeutics for RNA viral infections,
CC   particularly of a hepatitis C virus. The present sequence represents a
CC   PCR primer which is used in the exemplification of the present invention
XX
SQ   Sequence 38 BP; 1 A; 2 C; 0 G; 35 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 38;
  Best Local Similarity   84.6%;  Pred. No. 2.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
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                    | ||   ||||||||||||||||||||
Db          38 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 13

RESULT 658
AAL07487
ID   AAL07487 standard; DNA; 38 BP.
XX
AC   AAL07487;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human reproductive system related antigen DNA SEQ ID NO: 10175.
XX
KW   Human; reproductive system related antigen; reproductive system disorder;
KW   cancer; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200155320-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001339.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
PR   14-AUG-2000; 2000US-0225266P.
PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
PR   14-AUG-2000; 2000US-0225270P.
PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
PR   22-AUG-2000; 2000US-0226681P.
PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
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PR   08-SEP-2000; 2000US-0231414P.
PR   08-SEP-2000; 2000US-0232080P.
PR   08-SEP-2000; 2000US-0232081P.
PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
PR   14-SEP-2000; 2000US-0233064P.
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PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
PR   27-SEP-2000; 2000US-0235836P.
PR   29-SEP-2000; 2000US-0236327P.
PR   29-SEP-2000; 2000US-0236367P.
PR   29-SEP-2000; 2000US-0236368P.
PR   29-SEP-2000; 2000US-0236369P.
PR   29-SEP-2000; 2000US-0236370P.
PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0237040P.
PR   13-OCT-2000; 2000US-0239935P.
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PR   20-OCT-2000; 2000US-0241221P.
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PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
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PR   20-OCT-2000; 2000US-0241826P.
PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0246474P.
PR   08-NOV-2000; 2000US-0246475P.
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PR   17-NOV-2000; 2000US-0249211P.
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PR   17-NOV-2000; 2000US-0249297P.
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PR   17-NOV-2000; 2000US-0249299P.
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PR   01-DEC-2000; 2000US-0250391P.
PR   05-DEC-2000; 2000US-0251030P.
PR   05-DEC-2000; 2000US-0251988P.
PR   05-DEC-2000; 2000US-0256719P.
PR   06-DEC-2000; 2000US-0251479P.
PR   08-DEC-2000; 2000US-0251856P.
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PR   08-DEC-2000; 2000US-0251869P.
PR   08-DEC-2000; 2000US-0251989P.
PR   08-DEC-2000; 2000US-0251990P.
PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-465570/50.
XX
PT   Isolated nucleic acid molecule encoding a reproductive system antigen is
PT   used in preventing, treating or ameliorating a medical condition.
XX
PS   Disclosure; SEQ ID NO 10175; 1297pp + Sequence Listing; English.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human reproductive system related antigens. These can be used
CC   in the prevention and treatment of reproductive system disorders,
CC   including cancer. The present sequence is a genomic sequence encoding a
CC   protein of the invention
XX
SQ   Sequence 38 BP; 34 A; 1 C; 2 G; 1 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 38;
  Best Local Similarity   84.6%;  Pred. No. 2.1e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db          1 AAAAAAAAAAAAAAAAAAAAAAAAAA 26


RESULT 659
AAQ25031/c
ID   AAQ25031 standard; DNA; 40 BP.
XX
AC   AAQ25031;
XX
DT   13-JUL-1992  (first entry)
XX
DE   Oligonucleotide specific for HIV proviral DNA.
XX
KW   HIV; thiolation; reverse transcriptase; primer; inhibition; homooligomer;
KW   ss.
XX
OS   Synthetic.
XX
PN   WO9203127-A.
XX
PD   05-MAR-1992.
XX
PF   15-AUG-1991;   91WO-US005919.
XX
PR   16-AUG-1990;   90US-00568131.
XX
PA   (UYNY-) RES FOUND UNIV NEW.
XX
PI   Bardos TJ,  Ho YK,  Aradi J,  Schinazi RF;
XX
DR   WPI; 1992-096567/12.
XX
PT   Compsn. contg. 5-thiolated (oligo-poly-)-nucleotide(s) - for treating HIV
PT   infection, AIDS and for preventing HIV-1 infection.
XX
PS   Disclosure; Page 11; 42pp; English.
XX
CC   The oligomer comprises a non-thiolated (binding) homooligonucleotide
CC   region ( d(T)12 ) to promote the binding of the remaining portion of the
CC   5-thiolated oligonucleotide ( MdU_28 ) to a homopurine site of the viral
CC   genome via triple-helix formations. The oligo is used to in the treatment
CC   of HIV. See also AAQ22624-27 and AAQ25017-Q25032
XX
SQ   Sequence 40 BP; 0 A; 0 C; 0 G; 12 T; 28 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 40;
  Best Local Similarity   84.6%;  Pred. No. 2.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         40 AAAAAAAAAAAAAAAAAAAAAAAAAA 15


RESULT 660
AAA39649/c
ID   AAA39649 standard; DNA; 40 BP.
XX
AC   AAA39649;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Primer used in construction of hybrid CAT RNA.
XX
KW   Control element; translation enhancer; pestivirus homology box IV;
KW   immune response; viral infection; primer; ss.
XX
OS   Unidentified.
XX
PN   US6057093-A.
XX
PD   02-MAY-2000.
XX
PF   12-MAY-1995;   95US-00439996.
XX
PR   28-SEP-1992;   92US-00952799.
PR   28-SEP-1993;   93US-00128583.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Han JH,  Spaete RR,  Suh BS,  Selby MJ,  Houghton M,  Yoo BJ;
XX
DR   WPI; 2000-338599/29.
XX
PT   Enhancing translation of coding region of hepatitis C virus involves
PT   making RNA molecule comprising the coding region and 5' untranslated
PT   region comprising a sequence fully homologous to pestivirus homology box
PT   IV.
XX
PS   Disclosure; Col 19-20; 16pp; English.
XX
CC   This invention describes a novel method for enhancing translation of a
CC   coding region which involves making an RNA molecule, comprising the
CC   coding region operably linked to a 5' untranslated region (UTR)
CC   comprising a sequence fully homologous to pestivirus homology box IV, and
CC   then translating it so that the translation of the coding region is
CC   enhanced. The method is useful for enhancing or controlling the
CC   translation of HCV nucleic acid, which allows stronger immune responses,
CC   where blocking or decreasing translation of viral nucleic acid may
CC   decrease the pathology of viral infection. This sequence represents a
CC   primer which is used in the construction of hybrid CAT RNA's described in
CC   the method of the invention
XX
SQ   Sequence 40 BP; 0 A; 0 C; 0 G; 40 T; 0 U; 0 Other;
```

```
  Query Match             0.7%;  Score 19.6;  DB 1;  Length 40;
  Best Local Similarity   84.6%;  Pred. No. 2.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         40 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 15


RESULT 661
AAZ98722/c
ID   AAZ98722 standard; cDNA; 40 BP.
XX
AC   AAZ98722;
XX
DT   20-JUN-2000  (first entry)
XX
DE   PCR primer used for swine vesicular disease virus gene synthesis.
XX
KW   Swine vesicular disease virus; SVDV; swine vesicular disease;
KW   Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
KW   differentiation; vaccine; prevent; PCR primer; ss.
XX
OS   Swine vesicular disease virus.
XX
PN   EP982403-A1.
XX
PD   01-MAR-2000.
XX
PF   14-AUG-1998;   98EP-00306486.
XX
PR   14-AUG-1998;   98EP-00306486.
XX
PA   (BIOT-) DEV CENT BIOTECHNOLOGY.
XX
PI   Hwong CL,  Lo C,  Yang Y,  Jeng K,  Chang EL;
XX
DR   WPI; 2000-258616/23.
XX
PT   Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
PT   to prevent swine vesicular disease.
XX
PS   Example 2; Page 6; 66pp; English.
XX
CC   This sequence represents a PCR primer used to determine the full length
CC   cDNA sequence of the swine vesicular disease virus (SVDV) gene sequence
CC   of Taiwan Yu-Li strain (see AAZ98717). SVDV is the causative agent of
CC   swine vesicular disease, which is very similar to foot and mouth disease.
CC   The invention relates to the wild-type Taiwan Yu-Li strain cDNA sequence,
CC   and the gene sequences of the mutant SVDV strains N3, H21 and SP7. The
CC   mutant SVDV nucleotide sequence can be used in a vaccine for the
CC   prophylaxis of swine vesicular disease. The invention also includes a
CC   method for differentiating the mutant SVDV nucleotide sequences from the
CC   wild type strain of SVDV, coxsackievirus and foot-and-mouth disease virus
CC   through the use of polymerase chain reaction
XX
SQ   Sequence 40 BP; 1 A; 3 C; 3 G; 33 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 40;
  Best Local Similarity   84.6%;  Pred. No. 2.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         40 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 15


RESULT 662
AAQ55168/c
ID   AAQ55168 standard; DNA; 40 BP.
XX
AC   AAQ55168;
XX
DT   25-MAR-2003  (revised)
DT   21-JUL-1994  (first entry)
XX
DE   Sequence of primer for PCR amplification of HIV-LP Pt.1 isolate.
XX
KW   Human immunodeficiency virus; HIV-LP; PCR primer; ss.
XX
OS   Synthetic.
XX
PN   WO9400562-A1.
XX
PD   06-JAN-1994.
XX
PF   23-JUN-1993;   93WO-US006162.
XX
PR   24-JUN-1992;   92US-00903421.
XX
PA   (UYNY ) UNIV NEW YORK MT SINAI SCHOOL MEDICINE.
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Gelman IH,  Laurence JC;
XX
DR   WPI; 1994-026200/03.
XX
PT   HIV-LP useful in vaccine formulations - is novel HIV virus distinct from
PT   HIV-1 and or HIV-2 viruses.
XX
PS   Example; Page 7; 75pp; English.
XX
CC   HIV-LP is a new variant of the HIV family. A cDNA first strand was
CC   synthesised from Pt. 1 pellet using MLV RT. The product was converted
CC   into dsDNA and this cDNA was amplified by PCR using primers AAQ55167 and
CC   AAQ55168. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 40 BP; 3 A; 2 C; 3 G; 32 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 40;
  Best Local Similarity   84.6%;  Pred. No. 2.2e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAAA 2804
              | ||   ||||||||||||||||||||
Db         40 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 15


RESULT 663
AAV03013/c
ID   AAV03013 standard; DNA; 41 BP.
XX
AC   AAV03013;
XX
DT   17-AUG-1998  (first entry)
XX
DE   Aspergillus oryzae alpha-amylase transcription factor PCR primer.
XX
KW   alpha-amylase; promoter; filamentous fungi; transcription factor;
KW   expression; control; production; heterologous polypeptide; medicinal;
KW   industrial enzyme; PCR primer; amyR; ss.
XX
OS   Synthetic.
OS   Aspergillus oryzae.
XX
PN   WO9801470-A1.
XX
PD   15-JAN-1998.
XX
PF   07-JUL-1997;   97WO-DK000305.
XX
PR   05-JUL-1996;   96DK-00000740.
XX
PA   (NOVO ) NOVO-NORDISK AS.
XX
PI   Christensen T;
```

```
XX
DR   WPI; 1998-100998/09.
XX
PT   Transcription factor from Aspergillus oryzae which regulates alpha-
PT   amylase promoter - useful for producing heterologous proteins, especially
PT   medicinal proteins or enzymes, in filamentous fungi.
XX
PS   Example 1; Page 25; 64pp; English.
XX
CC   The sequence is that of PCR primer oligodT which was used in the analysis
CC   of a transcription factor (amyR) which regulates the expression of an
CC   alpha-amylase promoter
XX
SQ   Sequence 41 BP; 2 A; 1 C; 2 G; 36 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 41;
  Best Local Similarity   84.6%;  Pred. No. 2.3e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         41 AAAAAAAAAAAAAAAAAAAAAAAAAA 16


RESULT 664
AAA37946/c
ID   AAA37946 standard; DNA; 42 BP.
XX
AC   AAA37946;
XX
DT   18-AUG-2000  (first entry)
XX
DE   DNA synthesis primer used in PTAN gene isolation.
XX
KW   PTAN; testis specific; prostate cancer; overexpress; chromosome 1q22;
KW   diagnose; cancer; breast; vaccine; primer; ss.
XX
OS   Synthetic.
XX
PN   WO200020589-A2.
XX
PD   13-APR-2000.
XX
PF   30-SEP-1999;   99WO-US022985.
XX
PR   30-SEP-1998;   98US-0102556P.
PR   02-OCT-1998;   98US-0102910P.
PR   21-DEC-1998;   98US-0113229P.
PR   14-APR-1999;   99US-0129518P.
XX
PA   (UROG-) UROGENESYS INC.
PA   (AFAR/) AFAR D E.
PA   (HUBE/) HUBERT R S.
PA   (RAIT/) RAITANO A B.
PA   (MITC/) MITCHELL S C.
XX
PI   Afar DE,  Hubert RS,  Raitano AB,  Mitchell SC;
XX
DR   WPI; 2000-317715/27.
XX
PT   PTAN proteins, and sequences encoding them, used for diagnosing and
PT   treating cancers, especially breast and prostate cancers.
XX
PS   Example 1; Page 31; 71pp; English.
XX
CC   This sequence represents a primer used in the isolation of cDNA fragments
CC   of the PTAN (testis specific protein expressed in prostate cancer) gene.
CC   PTAN is expressed in 3 isoforms PTAN-1, 2, and 3. The PTAN gene is
CC   located on chromosome 1q22. PTAN is overexpressed in prostate cancer, and
CC   has a testis specific expression pattern in adult tissues. PTAN shows no
CC   homology to any known gene. PTAN can be used in methods for the diagnosis
CC   of cancer, especially prostate or breast cancer, where the normal tissue
CC   samples are prostate tissue, or breast tissue, bone tissue, lymphatic
CC   tissue, serum, blood, or urine. A vector containing the PTAN nucleotide
CC   sequence, a vaccine composition targeting PTAN, PTAN, ribozymes specific
CC   for PTAN mRNA and antisense sequences, can be used to treat cancer,
CC   especially breast and prostate cancers. Cancer development can be
CC   inhibited by a vaccine composition targeting PTAN
XX
SQ   Sequence 42 BP; 3 A; 2 C; 2 G; 35 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 42;
  Best Local Similarity   84.6%;  Pred. No. 2.4e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         42 AAAAAAAAAAAAAAAAAAAAAAAAAA 17


RESULT 665
AAD17216/c
ID   AAD17216 standard; DNA; 43 BP.
XX
AC   AAD17216;
XX
DT   29-NOV-2001  (first entry)
XX
DE   Human mRNA hybridisation selection reaction biotin-dT3 oligonucleotide.
XX
KW   Human; multiplex ligation-dependent amplification; amplicon;
KW   single nucleotide polymorphism; hybridisation selection reaction; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1
FT                    /*tag=  a
FT                    /mod_base= OTHER
FT                    /note= "Biotin-labelled Thymidine"
XX
PN   WO200161033-A2.
XX
PD   23-AUG-2001.
XX
PF   15-FEB-2001; 2001WO-EP001739.
XX
PR   15-FEB-2000; 2000EP-00200506.
XX
PA   (SCHO/) SCHOUTEN J P.
XX
PI   Schouten JP;
XX
DR   WPI; 2001-550053/61.
XX
PT   An improved multiplex ligation-dependent amplification method for
PT   detecting specific single stranded target nucleic acids in samples.
XX
PS   Example 8; Page 137; 158pp; English.
XX
CC   The invention relates to an improved multiplex ligation-dependent
CC   amplification method for detecting specific single stranded target
CC   nucleic acids in samples using a plurality of probe sets comprising at
CC   least 2 probes. Each probe comprises a target specific region and a non-
CC   complementary region comprising a primer binding site. The probes in each
CC   set are ligated when hybridised to a target nucleic acid and amplified by
CC   a primer set. The method is used for detecting a nucleotide polymorphism,
CC   especially a single nucleotide polymorphism; detecting multiple single
CC   stranded target nucleic acid sequences (through the detection of multiple
CC   amplicons); determining the absolute or relative abundance of multiple
CC   single stranded nucleic acids in a sample; and detection of a break point
CC   region in rearranged nucleic acids. By using a femtomolar amount of the
CC   probes, a large number of different probe sets can be used to
CC   simultaneously detect and quantify a corresponding large number of target
CC   sequences with high specificity. The present DNA sequence is biotin-dT3
CC   labelled fluorescent oligonucleotide which is used for the hybridisation
```

```
CC   selection reaction of human mRNA samples
XX
SQ   Sequence 43 BP; 0 A; 0 C; 0 G; 43 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 43;
  Best Local Similarity   84.6%;  Pred. No. 2.4e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         43 AAAAAAAAAAAAAAAAAAAAAAAAAA 18


RESULT 666
ADD33791/c
ID   ADD33791 standard; DNA; 44 BP.
XX
AC   ADD33791;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Mouse mitochondrial DNA sequence SEQ ID NO:1564.
XX
KW   ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
KW   mitochondrial disease; oxidative phosphorylation dysfunction;
KW   oxidative stress; apoptosis; aging.
XX
OS   Mus musculus.
XX
PN   WO2003020220-A2.
XX
PD   13-MAR-2003.
XX
PF   30-AUG-2002; 2002WO-US027886.
XX
PR   30-AUG-2001; 2001US-0316323P.
PR   31-AUG-2001; 2001CA-02356540.
XX
PA   (UYEM-) UNIV EMORY.
XX
PI   Wallace DC,  Levy S,  Kerstann K,  Procaccio V;
XX
DR   WPI; 2003-300821/29.
XX
PT   Array containing probes for genes involved in mitochondrial biology,
PT   useful for determining mitochondrial biology gene expression profiles for
PT   use in diagnosing pathologies and identifying biochemical pathways.
XX
PS   Claim 2; SEQ ID NO 1564; 201pp; English.
XX
CC   The invention relates to a novel array comprising at least two isolated
CC   nucleotide molecules, each molecule having a sequence capable of uniquely
CC   hybridising to a nucleic acid molecule which is an expression product of
CC   a gene involved in mitochondrial biology. The array comprises two or more
CC   isolated nucleic acid molecules or spots, each molecule having a sequence
CC   chosen from sequence of 994 human probes and 2046 mouse probes. An array
CC   of the invention is useful for determining an expression profile of a
CC   mouse or human sample containing nucleic acid, by contacting the array
CC   with the sample under conditions allowing selective hybridisation, and
CC   measuring hybridisation of nucleic acid in the sample to the array to
CC   produce an expression profile. The array is also useful for determining
CC   an expression profile of a first labelled sample containing nucleic acid
CC   relative to a second, differently labelled sample containing nucleic
CC   acid. The second sample is a reference or a standard. An array is useful
CC   for determining an expression profile diagnostic of an energy-metabolism-
CC   related physiological condition. An array of the invention is useful for
CC   determining mitochondrial biology gene expression profiles of organisms,
CC   such as human, mice and closely related species, tissue and organs of
CC   such organisms, which are useful for determining expression profiles
CC   diagnostic of energy metabolism-related physiological conditions,
CC   diagnosing such physiological conditions, identifying biochemical
CC   pathways, genes, and mutations involved in such physiological conditions,
CC   identifying therapeutic agents useful for preventing and/or treating such
CC   physiological conditions, evaluating and/or monitoring the efficacy of
CC   such therapies, and creating and identifying animal models of human
CC   energy metabolism-related physiological conditions. An array is also
CC   useful for defining expression signatures or profiles for mitochondrial
CC   diseases, as well as distinguishing clinical disorders that result from
CC   oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,
CC   apoptosis and aging. An array of the invention contains probes of genes
CC   not previously recognised to participate in mitochondrial biology. The
CC   sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA
CC   clones used to make the probes of the invention. Some sequences are not
CC   present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
CC   1906, 2408 and 2643.
XX
SQ   Sequence 44 BP; 1 A; 1 C; 0 G; 42 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.6;  DB 1;  Length 44;
  Best Local Similarity   84.6%;  Pred. No. 2.5e+03;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       2779 AGAATTGAAAAAAAAAAAAAAAAAAA 2804
                | ||   ||||||||||||||||||
Db         44 AAAAAAAAAAAAAAAAAAAAAAAAAA 19


RESULT 667
AAQ75758
ID   AAQ75758 standard; DNA; 21 BP.
XX
AC   AAQ75758;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;  93JP-00112515.
XX
PR   16-APR-1993;  93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTAAC 2189
                ||||||||||||||||| |||
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Db          1 TTTTTTTTTTTTTTTTCAAC 21


RESULT 668
AAQ75630
ID   AAQ75630 standard; DNA; 21 BP.
XX
AC   AAQ75630;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAAC 2189
             ||||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTGAAC 21


RESULT 669
AAQ75648
ID   AAQ75648 standard; DNA; 21 BP.
XX
AC   AAQ75648;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
             |||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTGTTA 21


RESULT 670
AAQ75676
ID   AAQ75676 standard; DNA; 21 BP.
XX
AC   AAQ75676;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
```

```
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2168 TTTTTTTTTTTTTTTTTTAA 2188
              |||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTATAA 21


RESULT 671
AAQ75681
ID   AAQ75681 standard; DNA; 21 BP.
XX
AC   AAQ75681;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTATTT 21


RESULT 672
AAQ75629/c
ID   AAQ75629 standard; DNA; 21 BP.
XX
AC   AAQ75629;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2802
              ||| ||||||||||||||||
Db         21 ATTCAAAAAAAAAAAAAAAA 1


RESULT 673
AAQ75725
ID   AAQ75725 standard; DNA; 21 BP.
XX
AC   AAQ75725;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
```

```
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTAAAT 21


RESULT 674
AAQ75725/c
ID   AAQ75725 standard; DNA; 21 BP.
XX
AC   AAQ75725;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2802
              ||| |||||||||||||||
Db         21 ATTTAAAAAAAAAAAAAAAA 1


RESULT 675
AAQ75729
ID   AAQ75729 standard; DNA; 21 BP.
XX
AC   AAQ75729;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTAACT 2190
              |||||||||||||||||| |
Db          1 TTTTTTTTTTTTTTTTAATT 21


RESULT 676
AAQ75729/c
ID   AAQ75729 standard; DNA; 21 BP.
XX
AC   AAQ75729;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
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PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2781 AATTGAAAAAAAAAAAAAAA 2801
              |||| ||||||||||||||||
Db         21 AATTAAAAAAAAAAAAAAAA 1


RESULT 677
AAQ75773/c
ID   AAQ75773 standard; DNA; 21 BP.
XX
AC   AAQ75773;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||
Db         21 ATAGAAAAAAAAAAAAAAAA 1


RESULT 678
AAQ75780/c
ID   AAQ75780 standard; DNA; 21 BP.
XX
AC   AAQ75780;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              ||| ||||||||||||||||
Db         21 TGAGAAAAAAAAAAAAAAAA 1


RESULT 679
AAQ75660/c
ID   AAQ75660 standard; DNA; 21 BP.
XX
AC   AAQ75660;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
```

```
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2803
              ||| ||||||||||||||||||
Db         21 TTGCAAAAAAAAAAAAAAAAA 1


RESULT 680
AAQ75684/c
ID   AAQ75684 standard; DNA; 21 BP.
XX
AC   AAQ75684;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAA 2804
              ||| ||||||||||||||||||
Db         21 TGATAAAAAAAAAAAAAAAAA 1


RESULT 681
AAQ75741/c
ID   AAQ75741 standard; DNA; 21 BP.
XX
AC   AAQ75741;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match              0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAA 2802
              || ||||||||||||||||||
Db         21 ATCGAAAAAAAAAAAAAAAA 1
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RESULT 682
AAQ75652/c
ID   AAQ75652 standard; DNA; 21 BP.
XX
AC   AAQ75652;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2784 TGAAAAAAAAAAAAAAAAAAA 2804
              ||| ||||||||||||||||||
Db         21 TGACAAAAAAAAAAAAAAAAAA 1


RESULT 683
AAQ75753/c
ID   AAQ75753 standard; DNA; 21 BP.
XX
AC   AAQ75753;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2782 ATTGAAAAAAAAAAAAAAAAA 2802
              | ||||||||||||||||||
Db         21 ACTGAAAAAAAAAAAAAAAAA 1


RESULT 684
AAQ75788/c
ID   AAQ75788 standard; DNA; 21 BP.
XX
AC   AAQ75788;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
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```
SQ   Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAA 2803
              ||| ||||||||||||||||||
Db         21 TTGGAAAAAAAAAAAAAAAAA 1


RESULT 685
AAQ75680
ID   AAQ75680 standard; DNA; 21 BP.
XX
AC   AAQ75680;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTA 2187
              |||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTATTA 21


RESULT 686
AAQ75649
ID   AAQ75649 standard; DNA; 21 BP.
XX
AC   AAQ75649;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2166 TTTTTTTTTTTTTTTTTTTT 2186
              |||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTGTTT 21


RESULT 687
AAQ75726
ID   AAQ75726 standard; DNA; 21 BP.
XX
AC   AAQ75726;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 8; 11pp; Japanese.
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XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2169 TTTTTTTTTTTTTTTTTTAAC 2189
              ||||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTAAAC 21


RESULT 688
AAQ75692/c
ID   AAQ75692 standard; DNA; 21 BP.
XX
AC   AAQ75692;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2783 TTGAAAAAAAAAAAAAAAAAA 2803
              ||| ||||||||||||||||||
Db         21 TTGTAAAAAAAAAAAAAAAAA 1


RESULT 689
AAQ75776
ID   AAQ75776 standard; DNA; 21 BP.
XX
AC   AAQ75776;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 9; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2167 TTTTTTTTTTTTTTTTTTTTA 2187
              ||||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTCTTA 21


RESULT 690
AAQ75697
ID   AAQ75697 standard; DNA; 21 BP.
XX
AC   AAQ75697;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
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PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2171 TTTTTTTTTTTTTTTTAACTT 2191
              ||||||||||||||||| ||||
Db          1 TTTTTTTTTTTTTTTTTACTT 21


RESULT 691
AAQ75637
ID   AAQ75637 standard; DNA; 21 BP.
XX
AC   AAQ75637;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 6; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||| |||
Db          1 TTTTTTTTTTTTTTTTTGACT 21


RESULT 692
AAQ75685
ID   AAQ75685 standard; DNA; 21 BP.
XX
AC   AAQ75685;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
KW   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993;   93JP-00112515.
XX
PR   16-APR-1993;   93JP-00112515.
XX
PA   (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR   WPI; 1995-018287/03.
XX
PT   Analysis of cDNA and gene expression - by amplification of mRNA followed
PT   by digestion with restriction enzymes.
XX
PS   Disclosure; Page 7; 11pp; Japanese.
XX
CC   A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC   labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC   and using the aggregate of mRNAs as the template for each reverse
CC   transcription primer; (b) digesting each of the prepared aggregates of
CC   the double-stranded cDNAs with restriction enzyme and; (c)
CC   electrophoresing the digested aggregate of cDNAs in seperate lanes. The
CC   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

  Query Match             0.7%;  Score 19.4;  DB 1;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 6e+02;
  Matches   20;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2170 TTTTTTTTTTTTTTTTTAACT 2190
              ||||||||||||||||| ||
Db          1 TTTTTTTTTTTTTTTTTATCT 21


RESULT 693
AAQ75717
ID   AAQ75717 standard; DNA; 21 BP.
XX
AC   AAQ75717;
XX
DT   04-AUG-1995  (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
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